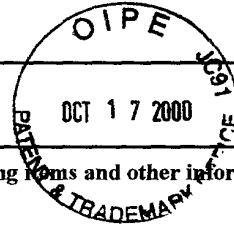
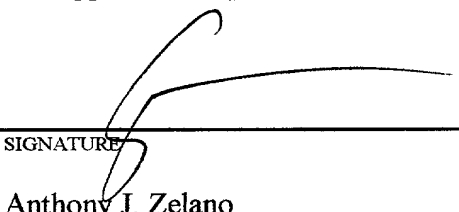


525 Rec'd PCT/PTO 17 OCT 2000

FORM PTO-1390 (REV 10-95)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER	
<b>TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. §371</b>				SCH 1780	
				U.S. APPLICATION NO (If known, see 37 CFR §1.5) <b>09/673395</b>	
INTERNATIONAL APPLICATION NO.		INTERNATIONAL FILING DATE		PRIORITY DATE CLAIMED	
PCT/DE99/01174		15 April 1999		17 April 1998	
TITLE OF INVENTION					
HUMAN NUCLEIC ACID SEQUENCES FROM ENDOMETRIAL TUMOR TISSUE					
APPLICANT(S) FOR DO/EO/US					
SPECHT, Thomas, et al.					
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:					
<ol style="list-style-type: none"> <li>1. <input checked="" type="checkbox"/> This is a <b>FIRST</b> submission of items concerning a filing under 35 U.S.C. §371.</li> <li>2. <input type="checkbox"/> This is a <b>SECOND</b> or <b>SUBSEQUENT</b> submission of items concerning a filing under 35 U.S.C. §371.</li> <li>3. <input type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).</li> <li>4. <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19<sup>th</sup> month from the earliest claimed priority date.</li> <li>5. <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. §371(c)(2))             <ol style="list-style-type: none"> <li>a. <input type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau).</li> <li>b. <input checked="" type="checkbox"/> has been transmitted by the International Bureau.</li> <li>c. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US).</li> </ol> </li> <li>6. <input checked="" type="checkbox"/> A translation of the International Application into English (35 U.S.C. §371(c)(2)).</li> <li>7. <input type="checkbox"/> A copy of the International Search Report (PCT/ISA/210).</li> <li>8. <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))             <ol style="list-style-type: none"> <li>a. <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau).</li> <li>b. <input type="checkbox"/> have been transmitted by the International Bureau.</li> <li>c. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired.</li> <li>d. <input checked="" type="checkbox"/> have not been made and will not be made.</li> </ol> </li> <li>9. <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).</li> <li>10. <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).</li> <li>11. <input type="checkbox"/> A copy of the International Preliminary Examination Report (PCT/IPEA/409).</li> <li>12. <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).</li> </ol>					
Items 13. to 19. below concern document(s) or information included:					
<ol style="list-style-type: none"> <li>13. <input type="checkbox"/> An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.</li> <li>14. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.</li> <li>15. <input checked="" type="checkbox"/> A FIRST preliminary amendment.             <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.</li> <li>16. <input type="checkbox"/> A substitute specification.</li> <li>17. <input type="checkbox"/> A change of power of attorney and/or address letter.</li> <li>18. <input type="checkbox"/> Certificate of Mailing by Express Mail</li> <li>19. <input type="checkbox"/> Other items or information.</li> </ol>					



U.S. APPLICATION NO. (if known, see 37 CFR §1.5) <b>09/673395</b>		INTERNATIONAL APPLICATION NO. PCT/DE99/01174		ATTORNEY'S DOCKET NUMBER SCH 1780	
17. <input checked="" type="checkbox"/> The following fees are submitted: <b>BASIC NATIONAL FEE ( 37 CFR §1.492 (a) (1) - (5)):</b> Search Report has been prepared by the EPO or JPO..... \$860.00 International preliminary examination fee paid to USPTO (37 CFR §1.482). ..... \$690.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO. .... \$1,000.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100.00  <b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b>				<b>CALCULATIONS</b> PTO USE ONLY	
Surcharge of <b>\$130.00</b> for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30				\$0.00	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	38 - 20 =	18	x \$ 18.00	\$324.00	
Independent claims	6 - 3 =	3	x \$ 80.00	\$240.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00		
<b>TOTAL OF ABOVE CALCULATIONS =</b>				\$1,424.00	
Reduction of ½ for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
<b>SUBTOTAL =</b>				\$1,424.00	
Processing fee of <b>\$130.00</b> for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
<b>TOTAL NATIONAL FEE =</b>				\$1,424.00	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
<b>TOTAL FEES ENCLOSED =</b>				\$1,424.00	
				Amount to be refunded:	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,424.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
<b>NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.</b>					
SEND ALL CORRESPONDENCE TO:					
MILLEN, WHITE, ZELANO & BRANIGAN, P.C. Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333					
Filed: October 17, 2000  aek:k:\pat\sche\1780\natl phase transmlt				SIGNATURE	
				 Anthony J. Zelano NAME	
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				REGISTRATION NUMBER	



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: ALBRE-12

In re patent application of

SPECHT, THOMAS et al.

Serial No. 09/673,395

Filed: October 17, 2000

For: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents  
Washington, D.C. 20231  
**Box SEQUENCE**

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

~~James~~/A. Coburn

Intellectual Property Services  
1500A Lafayette Road  
Suite 262  
Portsmouth, N.H.  
800-318-3021

09/673395

529 Rec'd PCT/PTC 17 OCT 2000

## Sequence Protocol

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&lt;120&gt; Human Nucleic Acid Sequences from Uterus Tumor Tissue

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 <212> DNA  
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<400> 29

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<400> 30

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<400> 33

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<400> 34

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<210> 35  
 <211> 1559  
 <212> DNA  
 <213> homo sapiens

<400> 35

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caactttgag caaatagcag tgatgtttta ggaactgaaa tgccacactt aaagtcttca 180
gcccagctac ttccctatct ttggcgggga gaagagggcc tgattagaac tgttctgggt 240
gtgtttggcg ggaggggaat aatttttgtt cagtccttct tagtgacca actttaattt 300
```

```

ttaagaataa tatattgact tactgaactg aagcattctg agttgaaagg agctccagag 360
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acctatcttc agatattccg ccatttttcat ctcttcatta tagtcaaaca gtgtgacttg 480
agagtgttgc tctgggtgtct gtattctggc ttatgaagat ttttgaaaa agaactctta 540
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gttaccaagg cagctttttt cctcaaaagt aacctgttcc tctttggaat agcacatttt 840
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<210> 36  
 <211> 1072  
 <212> DNA  
 <213> homo sapiens

<400> 36

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catcttcttc atgattgaca gcttcgagga ggtgttcagc gacatgaccg tagggaagga 180
gagatgggtct gtgtggagct ggtggctagt gacaaaacca acacgttcca gggggtcac 240
tttcagggct ccattccgcta cgaggcgctc aagaagggtg atgacaaccg ggtgagcgtg 300
gccgcccgcg tggcacagaa gatgtcgttt ggcttctaca agtacagcaa catggagtgt 360
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acaggtgaca cagccccctg tgggactgaa gaggactcca gccagcttc gcccatgcac 480
gagcgggtga cctccttcag cagaccccc accccagaac ggaacaaccg gcctgccttc 540
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<210> 37  
 <211> 454  
 <212> DNA  
 <213> homo sapiens

<400> 37

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agaaaaccgc tcctgtgtgg gccctgagtg ctgaggagga agctgccatg cacttttccc180
tggcattttt cctgcatggt tcgtctgttt ttttgcaaat aacatgttgt catgaatttt240
tatgcatgag gcatatttca tcatgtctgt atgctgaagt ccccttcac ctttcaattg300
gttggtggac aggagagaga ggtccaaggt gccctacatc gtgcgccagt gccgtgggag360
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gacatccagg cactgaaggc agccttcaac gtca 454

```

<210> 38  
<211> 700  
<212> DNA  
<213> homo sapiens

<400> 38

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gtcattccgt aaagtaaaca tcatcatctt ggtcctgggt gttgctctct tcttactggt180
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aattgtaggg cctcaaccta tagactttgt cccaaatgct ctccgacatg cagtagatgg300
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tctcaacaat acagcagacc atctccgggt ctgggtcaac agtgattccc tgaaaagcat480
cagatacaaaa attgtcaatt ttgaccctaa acttttggaa ggaaaagtaa aggaggatcc540
tgaccagggg gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg600
ttcccagcgg caaaggaagg cccgtttaca tgggggtgat gatgttattt gtggcaggtg660
ggattttttg ccctttacat tacagcagtg aggccggggc 700
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<210> 39  
<211> 914  
<212> DNA  
<213> homo sapiens

<400> 39

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gagggggaag ggatccagca ccggtcctc ctccggcaac cacggtggga gcggcggagg180
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tggtattcag ggcttcagag gacagggttg ttccagcaac atgagggaaa taagcaaaga300
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cagtggagga ggtgacgctg ttggtggagt caatactgtg aactctgaga cgtctcctgg420
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<210> 40  
<211> 1669  
<212> DNA  
<213> homo sapiens

<400> 40

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tgctcctacc cacctctcct ggctgagcct tgctgatac agcagcccgg aggcaccact 120
tgcttcccgga gtctcaccct cccaggcagc tctacactc aactgcttct ctaggaaagg 180
tctcacctcc agcctggagc agtcgggatt acagaaagcc ccctccttg cttaggggagc 240
gccatgacga ctgaaattgg ttggtggaag ctgactttcc tccggaaaaa gaaatccact 300
cccaaagtgc tgtatgagat cctgacacc tatgccaaa cagaggggaga tgcagaacct 360
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gacaagagca caaagggcaa gcacgtcaag gtctccaact caggacgctt caaggagaag 480
aagaaaagtga gagccacgct ggcagagaac cctaacctct ttgatgatca cgaggaaagg 540
cggatcatcaa agtgaagggt tgaggagggt gctagcacct cttgggtccc tgccatcagc 600
cagatctgag acaggacctt gccacgctgg cctctttggc catagctgaa gctgtggggc 660
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aaaaaaaaa	aaaaa					2535

<210> 44  
 <211> 805  
 <212> DNA  
 <213> homo sapiens

<400> 44

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cccaagtacc	aggaagagct	ggaggacagg	ctgcatttct	acgtggagga	atgtgactac	180
ttgcagggct	tccagatcct	gtgtgacctg	cacgatggct	tctctggggg	aggcggaag	240
gcggcagagc	tgctacaaga	tgaatattca	gggcggggaa	taataacctg	gggcctgcta	300
cctggtccct	accatcgtgg	ggaggcccag	agaaacatct	atcgtctatt	aaacacagct	360
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cctgattccc	tgatgcagtt	tgaggagcc	accccatgga	ccccactgtg	tgcatgtggg	720
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<210> 45  
 <211> 1279  
 <212> DNA  
 <213> homo sapiens

<400> 45

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<210> 46  
 <211> 1923

<212> DNA  
<213> homo sapiens

<400> 46

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gaaagtgatg gaaaatcaag atggttctac tcaccgtggg tgttggtaga atgttacatg 480  
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<210> 47  
<211> 706  
<212> DNA  
<213> homo sapiens

<400> 47

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<210> 48  
<211> 749  
<212> DNA  
<213> homo sapiens



<400> 48

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<210> 49

<211> 857

<212> DNA

<213> homo sapiens

<400> 49

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gaccacaaa atgtattgtt aaaaaaaat tgaaaaccag cagtgatttg ggtccccctg180
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<210> 50

<211> 268

<212> DNA

<213> homo sapiens

<400> 50

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<210> 51

<211> 297

<212> DNA

<213> homo sapiens

<400> 51

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atttattgct taatccaaca taggctatga aagttttgag tttcctcttg tgtattagaa180
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tttcattcct atttgttgta gagagtatag tacggggaat cagtaaatta aatgaagtaa240  
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<210> 52  
<211> 590  
<212> DNA  
<213> homo sapiens

<400> 52

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gtattaccag gtccaaacat aaaaaccacc tctgttcaaa aaataaatgt tcagagagct240  
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caagaatatt agtcatataa agaacttag aatTTTTttc cccaagtaca agctatcttt360  
tgctccaaaa cagttctgaa ggttttattt atattttatc ttatcccgag ggaccaacag420  
caggcatacc tttgccaggc cttcttgagc aaagacacag agccgtaaag gcaaaaataa480  
aattgcaata aagtatatgg tattgggggc aggggagaacc agaaaccctc aaggggacca540  
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<210> 53  
<211> 1714  
<212> DNA  
<213> homo sapiens

<400> 53

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cgcgagagccg gcgcgctcgt gagggggctg gcacggggag tcggcggtc ttgtgcatct 180  
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<210> 54  
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<212> DNA  
<213> homo sapiens

<400> 54

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gcggagaagg ggagaggcat ggagctatcc gacctgattg ttttcaatgg gaaactctac 180
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cacgagaact ggggtgtccaa ctacaacgcc ctgcgggctg ctgccggcat ccagccgcca 480
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<210> 55

<211> 765

<212> DNA

<213> homo sapiens

<400> 55

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ataagcatct tgaaacacca tggctgtagc tgcagtaaaa tgggtgatgt caaagagaac 180
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gaatctgaat cctccaaaag acagatgatg cggaggttcc tgggggaatc aaagagaaat 600
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aataatgata aaatatcttt tcatatatta gaatgtgtac ttttatataa agtaattctg 720
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<210> 56

<211> 1647

<212> DNA

<213> homo sapiens

<400> 56

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agaagttgct aaacatccgg cctcctcctc gggcacagtg gatccgagtg ctgtttggag 540
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gagtgtctgg agcccgaaatg catgctgctt atatccggcc aggaggagtg caccaggacc 720
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aaaaaaaaaa aaaaaaaaaa aaaaaaa 1647

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<210> 57  
 <211> 1166  
 <212> DNA  
 <213> homo sapiens

<400> 57

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accaagtgga agaccagca ctaagtgagc ctggggagga acctcagcgc ccttccccct 660
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aacggcttgt aacagggttc aggttg 1166

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<210> 58  
 <211> 487  
 <212> DNA  
 <213> homo sapiens

<400> 58

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agagcggctc tcggctgttt gcatcgccga tagagaagag aaaggatgca cgtcccagga180
gggaggaact actccaactt ttctatttca gaaacaaaga aaaaagatta ttcaagctgt240
gagggacaat tcattcctta ttgttactgg aaatacagga agtggtaaaa caactcaact300
cccaaaatat ctatatgaag cagggttttc acaacatggt atgattggtg taactcaacc360
acgaaaagta gctgctatat cagttgctca gagagtagct gaagaaatga aatgcacttt420
gggatccaaa gtaggatacc aagttcgttt tgatgattgc agttctaagg agacagcaat480

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caaatat

487

<210> 59  
<211> 1630  
<212> DNA  
<213> homo sapiens

<400> 59

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tgtgaacctt tcaaaaaaac ctcaggttgg gaaaagaccc ccaaaccctt ttttaaggat 180
catttgtctc gcccatcaca ggatcttggg aatgtttccc taggggtgtg aaaaattaac 240
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gcagagagac ctgctcctgc ttgcccggct acaggggcca ctgtggagtc aactgaggc 360
tgtgaccggc cataagccca ggagagcccg tggcagctgt gccgaggcgc caggacctct 420
aagcgggaag tccccaaagt aggaatggag caacactgca atgaaatgtg tccaccaagc 480
tcattgttcc tcccgggtgc ttataaagct cagatgtata gtgacgtatg gacaaatata 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gcctttcttt ctacaggca taagacacaa 600
attatatatt gttatgaagc actttttacc aacggctcagt ttttacattt tatagctgcg 660
tgcgaaaggc ttccagatgg gagaccatc tctcttgtgc tccagacttc atcacaggct 720
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<210> 60  
<211> 1272  
<212> DNA  
<213> homo sapiens

<400> 60

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ctgacacccg gcggctgatc accaagccgc agaacctgaa tgacgcctac ggacccccca 180
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<210> 61  
 <211> 1914  
 <212> DNA  
 <213> homo sapiens

<400> 61

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 tgctccatag gaaggcgaca ggtccgggtg tagaacaggc agtgagaggc cttgttcttg 300  
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<210> 62  
 <211> 608  
 <212> DNA  
 <213> homo sapiens

<400> 62

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<210> 63  
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 <213> homo sapiens

<400> 63

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<210> 64  
 <211> 326  
 <212> DNA  
 <213> homo sapiens

<400> 64

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acacagctcc	tgcaacaatt	ccatcggaat	gggacagacc	tacttgacat	gcagatgcat240
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<210> 65  
 <211> 888  
 <212> DNA  
 <213> homo sapiens

<400> 65

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<210> 66  
 <211> 202  
 <212> DNA  
 <213> homo sapiens

<400> 66

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acatcaaaag	aagttgaacc	tttcaacaat	attgatattg	aaattttctat	gtttgaaaaa180
gggaagggtac	ctaagattgt	ca			202

<210> 67  
 <211> 1225  
 <212> DNA  
 <213> homo sapiens

<400> 67

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gccatggcgg	agctgttgca	ggaggagctc	tcggctcctg	ccgcgatttt	ctgcaggccc 120
cacgagtggg	aggtgctgag	ccgctcagag	acagatggga	ccgtgttcag	aattcacaca 180
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aattatcctt	catgtctacc	tggatatctg	attaactctg	aacagttgac	cagggcccag 300
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gttcatgagc	tggttctctg	gattcagcag	aatctcaggc	atatcctcag	ccaaccagaa 420
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```

1225

<210> 68

<211> 1093

<212> DNA

<213> homo sapiens

<400> 68

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1093

<210> 69

<211> 309

<212> DNA

<213> homo sapiens

<400> 69

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309

<210> 70

<211> 380

<212> DNA

<213> homo sapiens

<400> 70

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380

<210> 71

<211> 1253  
<212> DNA  
<213> homo sapiens

<400> 71

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<212> DNA  
<213> homo sapiens

<400> 72

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caagaagacc tcatgagaga ggtgggaagg actttaactc ctgtttttct ggtggtttcc 420
ctttggttgt accttttaa 439
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<210> 73  
<211> 1252  
<212> DNA  
<213> homo sapiens

<400> 73

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<210> 74

<211> 695

<212> DNA

<213> homo sapiens

<400> 74

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<212> DNA

<213> homo sapiens

<400> 75

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<211> 274

<212> DNA

<213> homo sapiens

<400> 76

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<210> 77

<211> 449

<212> DNA

<213> homo sapiens

<400> 77

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<210> 78

<211> 346

<212> DNA

<213> homo sapiens

<400> 78

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<210> 79

<211> 1329

<212> DNA

<213> homo sapiens

<220>

<223> Beschreibung für Symbol "n": leer oder Lücke

<400> 79

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<211> 805

<212> DNA

<213> homo sapiens

<400> 80

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<210> 81

<211> 420

<212> DNA

<213> homo sapiens

<400> 81

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<210> 82

<211> 2143

<212> DNA

<213> homo sapiens

<400> 82

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<210> 83

<211> 450

<212> DNA

<213> homo sapiens

<400> 83

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<210> 84  
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<212> DNA  
<213> homo sapiens

<400> 84

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<210> 85  
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<212> DNA  
<213> homo sapiens

<400> 85

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gagcggcagt gagatagacg ctctcatgga ctgctgcttt acaacctccc tggagagcaa180
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<210> 86  
<211> 487  
<212> DNA  
<213> homo sapiens

<400> 86

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<210> 87  
<211> 1902  
<212> DNA  
<213> homo sapiens

<400> 87

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<210> 89  
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804

&lt;210&gt; 90

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 90

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581

&lt;210&gt; 91

&lt;211&gt; 2042

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 91

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 <212> DNA  
 <213> homo sapiens

<400> 92

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 <212> DNA  
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<400> 93

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 <212> DNA  
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<400> 94

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<210> 95

<211> 324  
<212> DNA  
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<400> 95

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<210> 96  
<211> 709  
<212> DNA  
<213> homo sapiens

<400> 96

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<210> 97  
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<212> DNA  
<213> homo sapiens

<400> 97

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<210> 98  
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<212> DNA  
<213> homo sapiens

<400> 98

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<210> 105  
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<400> 105

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<400> 106

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<211> 506

<212> DNA

<213> homo sapiens

<400> 107

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<211> 1276

<212> DNA

<213> homo sapiens

<400> 108

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<210> 109

<211> 373

<212> DNA

<213> homo sapiens

<400> 109

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<210> 125

<211> 891

<212> DNA

<213> homo sapiens

<400> 125

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<210> 126

<211> 482

<212> DNA

<213> homo sapiens

<400> 126

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aa 482

```

<210> 127

<211> 610

<212> DNA

<213> homo sapiens

<400> 127

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cagcgccatg ggcgcctcca ggaagttctt cgttggggga aactggaaga tgaacgggcg120
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610

<210> 128  
 <211> 2072  
 <212> DNA  
 <213> homo sapiens

<400> 128

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gcttcgctgc cttggaaggg gccacattcc ccatcctct totccttaca gcgctgct1980
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```

2072

<210> 129  
 <211> 980  
 <212> DNA  
 <213> homo sapiens

<400> 129

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tttatggagt tagagcagg gaacttaaaa acaaaagtgt atttaataac ttcagagac 60
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```





<210> 132  
 <211> 1523  
 <212> DNA  
 <213> homo sapiens

<400> 132

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ctccatttag gacaccctac acaccaaca gccagtatca aatgctgctc gatccacca 180
accccagcgc cggcactgcc aagatagaca agcaggagaa ggtcaagctc aactttgaca 240
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<210> 133  
 <211> 2241  
 <212> DNA  
 <213> homo sapiens

<400> 133

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gccggctcgg cgagctctcc cgacaccgga gccggggagg aaaagcagcg actcctcgt 180
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aaaaaaaaaa	aaaaaaaaaa	a			2241

<210> 134  
 <211> 631  
 <212> DNA  
 <213> homo sapiens

<400> 134

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cagttccccc	agtacctcca	agcaagtagc	ttccacatt	tgtcacagaa	atcagaggag480
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tttgcaatgt	caaacctctc	tgatcttggt	tcagatgatt	cttaatagga	gtttattttt600
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<210> 135  
 <211> 980  
 <212> DNA  
 <213> homo sapiens

<400> 135

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<210> 136  
 <211> 2238  
 <212> DNA  
 <213> homo sapiens

<400> 136

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<210> 137  
 <211> 398  
 <212> DNA  
 <213> homo sapiens

<400> 137

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<210> 138  
 <211> 1084

<212> DNA  
<213> homo sapiens

<400> 138

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<210> 139  
<211> 1259  
<212> DNA  
<213> homo sapiens

<400> 139

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<210> 140  
<211> 1938  
<212> DNA  
<213> homo sapiens

<400> 140

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gaaggaagcc	cctccctggg	cattttctgc	ctatgctgga	atagctccct	cttctgggtc	1860
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<210> 141  
 <211> 1874  
 <212> DNA  
 <213> homo sapiens

<400> 141

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1874

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<210> 142  
 <211> 198  
 <212> PRT  
 <213> homo sapiens

<400> 142

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Ile	Ser	Ser	Ser 20	Gln	Thr	Asn	Arg	Ser 25	Ser	Phe	Asp	Leu	Leu 30	Pro	Arg
Glu	Phe	Arg 35	Leu	Val	Glu	Val	His 40	Asp	Pro	Pro	Leu	His 45	Gln	Pro	Ser
Ala	Asn 50	Lys	Pro	Lys	Pro	Pro 55	Thr	Met	Leu	Asp	Ile 60	Pro	Ser	Glu	Pro
Cys 65	Ser	Leu	Thr	Ile	His 70	Thr	Ile	Gln	Leu	Ile 75	Gln	His	Asn	Arg	Arg 80
Leu	Arg	Asn	Leu	Ile 85	Ala	Thr	Ala	Gln	Ala 90	Gln	Asn	Gln	Gln	Gln 95	Thr
Glu	Gly	Val	Lys 100	Thr	Glu	Glu	Ser	Glu 105	Pro	Leu	Pro	Ser	Cys 110	Pro	Gly
Ser	Pro	Pro 115	Leu	Pro	Asp	Asp	Leu 120	Leu	Pro	Leu	Asp	Cys 125	Lys	Asn	Pro
Asn	Ala 130	Pro	Phe	Gln	Ile	Arg 135	His	Ser	Asp	Pro	Glu 140	Ser	Asp	Phe	Tyr
Arg 145	Gly	Lys	Gly	Glu	Pro 150	Val	Thr	Glu	Leu	Ser 155	Trp	His	Ser	Cys	Arg 160
Gln	Leu	Leu	Tyr	Gln 165	Gly	Ser	Gly	Thr	Asn 170	Pro	Gly	Gln	Arg	Arg 175	Ala
Phe	Asp	Cys	Ala 180	Asn	Glu	Ser	Val	Leu 185	Glu	Asp	Pro	Asn	Leu 190	Met	Leu
Ala	His	Glu 195	Tyr	Trp	Pro										

<210> 143  
 <211> 92  
 <212> PRT  
 <213> homo sapiens

<400> 143

Ile	Val	Trp	Met	Val	Arg	Leu	His	Gly	Ser	Glu	Gly	Met	Ser	Ser	Ile
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1				5					10						15	
Val	Gly	Gly	Phe 20	Gly	Leu	Leu	Ala	Glu 25	Gly	Trp	Cys	Arg	Gly 30	Gly	Ser	
Trp	Thr	Ser 35	Thr	Arg	Arg	Asn	Ser 40	Arg	Gly	Ser	Lys	Ser 45	Lys	Glu	Leu	
Leu	Leu 50	Val	Trp	Leu	Asp	Asp 55	Ile	Gly	Ile	Ser	Pro 60	Gln	Tyr	Leu	Cys	
Arg 65	Phe	Ile	Val	His	Met 70	Ser	Leu	Gln	Val	Gln 75	Gln	Thr	Phe	Ile	Lys 80	
Cys	Gln	Ala	Phe	Cys 85	Val	Gly	Gln	Arg	Leu 90	Ile	Met					

&lt;210&gt; 144

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 144

Asp 1	Pro	Cys	Pro	Glu 5	Arg	Ser	Thr	Lys	Asn 10	Arg	His	Gly	Ala	Gln 15	Gly	
Met	Pro	Lys	Ser 20	Leu	Gln	Gly	Phe	Pro 25	Arg	Ser	Arg	Ser	Ala 30	Gly	Ala	
Gly	Ala	Asn 35	His	Arg	Val	Leu	Arg 40	Ser	Pro	Asp	Val	Gln 45	Gly	Ser	Arg	
Lys	Thr 50	Gly	Arg	Ser	Gly	Pro 55	Glu	Pro	Arg	Gln	Gly 60	Gly	Thr	Thr	Leu	
Phe 65	Thr	Ala	Ala	Ser	Gln 70	Ser	Gly	Leu	Gly	Gly 75	Cys	Leu	Asp	Leu	Glu 80	
Arg	Pro	Glu	Ala	Arg 85	Ile	Ala	Ser	Asp	Pro 90	Glu	Ser	Trp	Phe	Val 95	Asp	

&lt;210&gt; 145

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 145

Glu 1	Gly	Arg	Val	Gln 5	Gln	Gly	Ser	Phe	Val 10	Asn	Val	Gln	Gln	Gly 15	Pro	
Gln	Glu	Pro	Phe 20	Ile	Glu	Phe	Ile	His 25	Gln	Leu	Thr	Gln	Ala 30	Ile	Lys	
Ser	Thr	His 35	Gly	Thr	Ser	Thr	Ile 40	Pro	Arg	Val	Ser	Arg 45	Ile	Thr	Leu	
Lys	Asp 50	Lys	Pro													

&lt;210&gt; 146

&lt;211&gt; 47



<212> PRT  
<213> homo sapiens

<400> 146

Pro	Ser	Arg	Thr	Ser	His	Ser	Gly	Thr	Leu	Pro	Ile	Pro	Arg	Leu	Lys
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Ile	Cys	Phe	Lys	Lys	Arg	Gly	Asn	Met	Asn	Lys	Asp	Pro	Thr	Thr	Leu
			20					25					30		
Leu	Ala	Gln	Val	Leu	Phe	Thr	Leu	Asn	Phe	Leu	Asn	Leu	Asp	Asn	
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<210> 147  
<211> 66  
<212> PRT  
<213> homo sapiens

<400> 147

Leu	Ser	Lys	Phe	Lys	Lys	Leu	Arg	Val	Asn	Asn	Thr	Cys	Ala	Ser	Ser
1				5					10					15	
Val	Val	Gly	Ser	Leu	Phe	Ile	Phe	Pro	Leu	Phe	Leu	Lys	His	Ile	Phe
			20					25					30		
Lys	Arg	Gly	Met	Gly	Asn	Val	Pro	Leu	Trp	Leu	Val	Leu	Glu	Gly	Tyr
		35					40					45			
Thr	Arg	Tyr	Pro	Trp	Asn	Gly	Arg	Cys	Ser	Met	Cys	Ala	Leu	Asn	Cys
	50					55					60				
Leu	Gly														
65															

<210> 148  
<211> 187  
<212> PRT  
<213> homo sapiens

<400> 148

Arg	Glu	Gly	Glu	Gly	Arg	Pro	Glu	Gly	Asn	Gly	Asp	Ile	Arg	Gly	Gly
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Leu	Arg	Ser	Gly	Cys	Asp	Leu	Ser	Leu	Leu	Ala	Pro	Leu	Leu	Pro	Pro
			20					25					30		
Ser	Ser	Ser	Glu	Ser	Trp	Glu	Cys	Cys	Tyr	Pro	Trp	Lys	Ile	Lys	Leu
		35					40					45			
Gly	Leu	Gln	Glu	Leu	Ser	Val	Trp	Glu	Glu	Ser	Met	Ala	Gln	His	Ser
	50					55					60				
Ala	Cys	Val	Pro	Phe	Cys	Ser	Gly	Ser	Leu	Ser	Pro	Pro	Pro	Ser	Gln
65					70					75					80
Pro	Gln	Arg	Leu	Ser	Pro	Ser	Pro	Ser	Ser	Ser	Pro	Glu	Asp	Ser	Ser
				85					90					95	
Asp	Gly	Arg	Ala	Gly	Pro	Pro	Glu	Pro	Thr	Gly	Ser	Ser	Gly	Cys	Thr
			100					105					110		

002221 3552950





Ile	Gln	Cys	Ala 180	Val	Leu	Tyr	Thr	Thr 185	Ile	Ser	Gly	Gln	Arg 190	Arg	Leu
Arg	Ile	His 195	Asn	Leu	Gly	Leu	Asn 200	Cys	Ser	Ser	Gln	Leu 205	Ala	Asp	Leu
Tyr	Lys 210	Ser	Cys	Glu	Thr	Asp 215	Ala	Leu	Ile	Asn	Phe 220	Phe	Ala	Lys	Ser
Ala 225	Phe	Lys	Ala	Val	Leu 230	His	Gln	Pro	Leu	Lys 235	Val	Ile	Arg	Glu	Ile 240
Leu	Val	Asn	Gln	Thr 245	Ala	His	Met	Leu	Ala 250	Cys	Tyr	Arg	Lys	Asn 255	Cys
Ala	Ser	Pro	Ser 260	Ala	Ala	Ser	Gln	Leu 265	Ile	Leu	Pro	Asp	Ser 270	Met	Lys
Val	Leu	Pro 275	Val	Tyr	Met	Asn	Cys 280	Leu	Leu	Lys	Asn 285	Cys	Val	Leu	Leu
Ser	Arg 290	Pro	Glu	Ile	Ser	Thr 295	Asp	Glu	Arg	Ala	Tyr 300	Gln	Arg	Gln	Leu
Val 305	Met	Thr	Met	Gly	Val 310	Ala	Asp	Ser	Gln	Leu 315	Phe	Phe	Tyr	Pro	Gln 320
Leu	Leu	Pro	Ile	His 325	Thr	Leu	Asp	Val	Lys 330	Ser	Thr	Met	Leu	Pro 335	Ala
Ala	Val	Arg	Cys 340	Ser	Glu	Ser	Arg	Leu 345	Ser	Glu	Glu	Gly	Ile 350	Phe	Leu
Leu	Ala	Asn 355	Gly	Leu	His	Met	Phe 360	Leu	Trp	Leu	Gly	Val 365	Ser	Ser	Pro
Pro	Glu 370	Leu	Ile	Gln	Gly	Ile 375	Phe	Asn	Val	Pro	Ser 380	Phe	Ala	His	Ile
Asn 385	Thr	Asp	Met	Thr	Leu 390	Leu	Pro	Glu	Val	Gly 395	Asn	Pro	Tyr	Ser	Gln 400
Gln	Leu	Arg	Met	Ile 405	Met	Gly	Ile	Ile	Gln 410	Gln	Lys	Arg	Pro	Tyr 415	Ser
Met	Lys	Leu	Thr 420	Ile	Val	Lys	Gln	Arg 425	Glu	Gln	Pro	Glu	Met 430	Val	Phe
Arg	Gln	Phe 435	Leu	Val	Glu	Asp	Lys 440	Gly	Leu	Tyr	Gly	Gly 445	Ser	Ser	Tyr
Val	Asp 450	Phe	Leu	Cys	Cys	Val 455	His	Lys	Glu	Ile	Cys 460	Gln	Leu	Leu	Asn

<210> 152

<211> 172

<212> PRT

<213> homo sapiens

<400> 152

Thr Met Leu Glu Lys Ile Pro Lys Glu Glu Gln Glu Glu Thr Ser Ala











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Glu	Met	Arg	Gly 100	Glu	Gly	Leu	Gly	Arg 105	Gln	Pro	His	Glu	Gly 110	Ala	Glu
Gly	Ala	Gly 115	Gly	Ala	Ser	Ser	Gln 120	Cys	Ser	Ser	Cys	Ser 125	Ile	Ser	Ser
Cys	Ser 130	Val	Arg	Pro	Pro	Ala 135	Gly	Ala	Trp	Pro	Arg 140	Pro	Ser	Met	Ala
Val 145	Val	Arg	Ser	His	Met 150	Ala	Lys	Leu	Pro	Leu 155	Ala	Trp	Pro	Val	Ser 160

Arg

<210> 157  
 <211> 262  
 <212> PRT  
 <213> homo sapiens

<400> 157

Gln 1	Leu	Trp	Gly	Phe 5	Ala	Ala	Gly	Ser	Asp 10	Ser	Arg	Pro	Ala	Met 15	Gly
Cys	Asp	Gly	Gly 20	Thr	Ile	Pro	Lys	Arg 25	His	Glu	Leu	Val	Lys 30	Gly	Pro
Lys	Lys	Val 35	Glu	Lys	Val	Asp	Lys 40	Asp	Ala	Glu	Leu	Val 45	Ala	Gln	Trp
Asn	Tyr 50	Cys	Thr	Leu	Ser	Gln 55	Glu	Ile	Leu	Arg	Arg 60	Pro	Ile	Val	Ala
Cys 65	Glu	Leu	Gly	Arg	Leu 70	Tyr	Asn	Lys	Asp	Ala 75	Val	Ile	Glu	Phe	Leu 80
Leu	Asp	Lys	Ser	Ala 85	Glu	Lys	Ala	Leu	Gly 90	Lys	Ala	Ala	Ser	His 95	Ile
Lys	Ser	Ile	Lys 100	Asn	Val	Thr	Glu	Leu 105	Lys	Leu	Ser	Asp	Asn 110	Pro	Ala
Trp	Glu	Gly 115	Asp	Lys	Gly	Asn	Thr 120	Lys	Gly	Asp	Lys	His 125	Asp	Asp	Leu
Gln	Arg 130	Ala	Arg	Phe	Ile	Cys 135	Pro	Val	Val	Gly	Leu 140	Glu	Met	Asn	Gly
Arg 145	His	Arg	Phe	Cys	Phe 150	Leu	Arg	Cys	Cys	Gly 155	Cys	Val	Phe	Ser	Glu 160
Arg	Ala	Leu	Lys	Glu 165	Ile	Lys	Ala	Glu	Val 170	Cys	His	Thr	Cys	Gly 175	Ala
Ala	Phe	Gln	Glu 180	Asp	Asp	Val	Ile	Val 185	Leu	Asn	Gly	Thr	Lys 190	Glu	Asp
Val	Asp	Val	Leu	Lys	Thr	Arg	Met	Glu	Glu	Arg	Arg	Leu	Arg	Ala	Asn

195					200					205					
Trp	Lys	Arg	Lys	Gln	Arg	Asn	Pro	Arg	Gln	Gln	Ser	Leu	Phe	Gln	Asn
	210					215					220				
Gln	Met	Ser	Val	Lys	Lys	Pro	Gln	Gly	His	Gln	Lys	Leu	Arg	Gln	Gly
225					230					235					240
Ser	Leu	Lys	Lys	Pro	Ala	Leu	Ile	Leu	Glu	Arg	Arg	Lys	Pro	Thr	Trp
				245					250					255	
Leu	Pro	Lys	Ala	Gln	Gln										
			260												

<210> 158  
 <211> 138  
 <212> PRT  
 <213> homo sapiens

<400> 158

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Lys	Asp	Gly	Gly	Glu	Lys	Ala	Glu	Ser	Glu	Leu	Glu	Lys	Lys	Thr	Lys
			20					25					30		
Lys	Pro	Lys	Ala	Ala	Glu	Ser	Val	Ser	Lys	Pro	Asp	Val	Ser	Glu	Glu
		35					40					45			
Ala	Pro	Gly	Pro	Ser	Lys	Val	Lys	Thr	Gly	Lys	Pro	Glu	Glu	Ala	Ser
	50					55					60				
Leu	Asp	Ser	Arg	Glu	Lys	Lys	Thr	Asn	Leu	Ala	Pro	Lys	Ser	Thr	Ala
65					70					75					80
Met	Asn	Glu	Ser	Ser	Ser	Gly	Lys	Ala	Gly	Lys	Pro	Pro	Cys	Gly	Ala
				85					90					95	
Thr	Lys	Arg	Ser	Ile	Ala	Asp	Ser	Glu	Glu	Ser	Glu	Ala	Tyr	Lys	Ser
			100					105					110		
Leu	Phe	Thr	Thr	His	Ser	Ser	Ala	Lys	Arg	Ser	Lys	Glu	Glu	Ser	Ala
		115					120					125			
His	Trp	Val	Thr	His	Thr	Ser	Tyr	Cys	Phe						
	130					135									

<210> 159  
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 <212> PRT  
 <213> homo sapiens

<400> 159

His	Leu	Val	Leu	Lys	Gln	Thr	Leu	Leu	Pro	Trp	Val	Ser	Leu	Phe	Ser
1				5					10					15	
Phe	Pro	Ile	Arg	Ser	Gln	Pro	Ser	Leu	Leu	His	Pro	Cys	Leu	Gln	His
			20					25					30		
Val	His	Ile	Leu	Leu	Gly	Ala	Ile	Glu	His	Asp	Asp	Ile	Ile	Leu	Leu
		35					40					45			

Glu	Gly	Ser	Pro	Thr	Arg	Val	Ala	Asn	Phe	Arg	Phe	Tyr	Leu	Phe	Gln	
	50					55					60					
Gly	Ser	Leu	Arg	Lys	His	Thr	Ala	Ala	Ala	Pro	Lys	Glu	Ala	Glu	Pro	
65					70					75					80	
Val	Ser	Ala	Val	His	Leu	Gln	Ala	His	Asn	Gly	Ala	Asp	Glu	Thr	Arg	
				85					90					95		
Pro	Leu	Glu	Val	Ile	Val	Leu	Val	Thr	Phe	Ser	Val	Ser	Phe	Ile	Pro	
			100					105					110			
Phe	Pro	Gly	Arg	Ile	Ile	Arg	Lys	Leu	Gln	Leu	Cys	His	Ile	Leu	Asn	
		115					120					125				
Ala	Phe	Asn	Val	Arg	Cys	Cys	Leu	Pro	Lys	Ser	Leu	Phe	Cys	Arg	Phe	
	130					135					140					
Val	Gln	Glu	Lys	Phe	Asn	Asp	Gly	Ile	Phe	Val	Ile	Lys	Ser	Ala	Lys	
145					150					155					160	
Phe	Thr	Gly	Asn	Tyr	Trp	Ser	Ser									
				165												

<210> 160  
 <211> 238  
 <212> PRT  
 <213> homo sapiens  
 <400> 160

His	Gln	Trp	His	Ile	Thr	Ala	Met	Gly	Ser	Gln	His	Ser	Ala	Ala	Ala	
1				5					10					15		
Arg	Pro	Ser	Ser	Cys	Arg	Arg	Lys	Gln	Glu	Asp	Asp	Arg	Asp	Gly	Leu	
			20					25					30			
Leu	Ala	Glu	Arg	Glu	Gln	Glu	Glu	Ala	Ile	Ala	Gln	Phe	Pro	Tyr	Val	
		35					40					45				
Glu	Phe	Thr	Gly	Arg	Asp	Ser	Ile	Thr	Cys	Leu	Thr	Cys	Gln	Gly	Thr	
	50					55					60					
Gly	Tyr	Ile	Pro	Thr	Glu	Gln	Val	Asn	Glu	Leu	Val	Ala	Leu	Ile	Pro	
65					70					75					80	
His	Ser	Asp	Gln	Arg	Leu	Arg	Pro	Gln	Arg	Thr	Lys	Gln	Tyr	Val	Leu	
				85					90					95		
Leu	Ser	Ile	Leu	Leu	Cys	Leu	Leu	Ala	Ser	Gly	Leu	Val	Val	Phe	Phe	
			100					105					110			
Leu	Phe	Pro	His	Ser	Val	Leu	Val	Asp	Asp	Asp	Gly	Ile	Lys	Val	Val	
		115					120					125				
Lys	Val	Thr	Phe	Asn	Lys	Gln	Asp	Ser	Leu	Val	Ile	Leu	Thr	Ile	Met	
	130					135					140					
Ala	Thr	Leu	Lys	Ile	Arg	Asn	Ser	Asn	Phe	Tyr	Thr	Val	Ala	Val	Thr	
145					150					155					160	
Ser	Leu	Ser	Ser	Gln	Ile	Gln	Tyr	Met	Asn	Thr	Val	Val	Asn	Phe	Thr	

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165

170

175

Gly	Lys	Ala	Glu 180	Met	Gly	Gly	Pro	Phe 185	Ser	Tyr	Val	Tyr	Phe 190	Phe	Cys
Thr	Val	Pro 195	Glu	Ile	Leu	Val	His 200	Asn	Ile	Val	Ile	Phe 205	Met	Arg	Thr
Ser	Val 210	Lys	Ile	Ser	Tyr	Ile 215	Gly	Leu	Met	Thr	Gln 220	Ser	Ser	Leu	Glu
Thr 225	His	His	Tyr	Val	Asp 230	Cys	Gly	Gly	Asn	Ser 235	Thr	Ala	Ile		

&lt;210&gt; 161

&lt;211&gt; 91

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 161

Ser 1	Ser	His	Glu	Asp 5	His	Tyr	Val	Val	His 10	Gln	Asp	Leu	Arg	Tyr 15	Arg
Ala	Glu	Glu	Val 20	His	Ile	Gly	Lys	Arg 25	Ser	Ser	His	Leu	Gly 30	Leu	Pro
Gly	Lys	Ile 35	His	His	Cys	Val	His 40	Val	Leu	Asn	Leu	Ala 45	Gly	Gln	Ala
Gly	His 50	Cys	His	Arg	Val	Glu 55	Val	Gly	Val	Pro	Asp 60	Phe	Gln	Gly	Gly
His 65	Asp	Gly	Glu	Asn	Tyr 70	Lys	Gly	Val	Leu	Leu 75	Ile	Lys	Cys	Asp	Phe 80
His	His	Phe	Asp	Ala 85	Val	Ile	Ile	His	Lys 90	Asp					

&lt;210&gt; 162

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 162

Met 1	Arg	Lys	Gln	Glu 5	Glu	Asn	His	Gln	Thr 10	Arg	Cys	Gln	Glu	Thr 15	Lys
Gln	Asp	Gly	Gln 20	Glu	Asp	Ile	Leu	Leu 25	Ser	Ser	Leu	Arg	Ala 30	Gln	Ser
Leu	Ile	Thr 35	Val	Trp	Asp	Gln	Ser 40	His	Gln	Leu	Ile	Tyr 45	Leu	Leu	Cys
Trp	Asn 50	Val	Ala	Cys	Pro	Leu 55	Ala	Arg	Glu	Thr	Gly 60	Asp	Ala	Ile	Ser
Pro 65	Gly	Glu	Phe	His	Ile 70	Trp	Glu	Leu	Ser	Asn 75	Gly	Phe	Phe	Leu	Leu 80
Ser	Phe	Ser	Gln	Gln 85	Thr	Val	Pro	Val	Ile 90	Phe	Leu	Leu	Ser	Pro 95	Ala

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115				120				125							
Ala	Leu	Ala	Thr												
	130														
<210> 167															
<211> 67															
<212> PRT															
<213> homo sapiens															
<400> 167															
Gln	Ile	Leu	Met	Ser	His	Ser	Pro	Pro	Gln	Ala	Glu	Met	Ala	Ser	Leu
1				5					10					15	
Asn	Glu	Pro	Leu	Val	Ser	Leu	Ile	Leu	Leu	Leu	Val	Arg	Val	Ala	Ile
			20					25					30		
Ser	Arg	Pro	Pro	Pro	Gln	Ala	Pro	Lys	Ser	Leu	His	Arg	Leu	Leu	His
		35					40					45			
Leu	Val	Val	Ala	Ser	Thr	Pro	Pro	Thr	Ser	Trp	Pro	Phe	Gly	Ala	His
	50					55					60				
Phe	Ala	Val													
65															
<210> 168															
<211> 74															
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<213> homo sapiens															
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Asn	Gly	Leu	Ser	Lys	Arg	Thr	Thr	Gly	Leu	Leu	Asp	Ser	Thr	Ser	Cys
1				5					10					15	
Ser	Cys	Ser	Asn	Leu	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Lys	Val	Ser	Ser
			20					25					30		
Ser	Ala	Ser	Thr	Ser	Ser	Cys	Cys	Ile	Asn	Ser	Ser	Asn	Phe	Leu	Ala
		35					40					45			
Phe	Arg	Ser	Ser	Phe	Cys	Cys	Met	Ile	Val	Gln	Arg	Cys	Ser	Val	Ser
	50					55					60				
Cys	Ser	Phe	Ile	Ser	Val	Ser	Arg	His	Glu						
65					70										
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<212> PRT															
<213> homo sapiens															
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Gly	Arg	Gly	Gly	Leu	Gly	Cys	Arg	Ser	Trp	Arg	Cys	Ala	Gly	Ser	Ser
1				5					10					15	
Arg	Pro	Tyr	Ser	Glu	Val	Phe	Ser	Val	Ala	Leu	Leu	Glu	Arg	Gly	Ser
			20					25					30		
Ser	Cys	Ile	Leu	Arg	Ile	Phe	Cys	Ile	Ser	Ala	Pro	Phe	Ser	Ser	Arg





[illegible]

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<210> 173
<211> 495
<212> PRT
<213> homo sapiens
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Ser 1	Arg	Thr	Asn	Thr 5	Pro	Val	Glu	Thr	Trp 10	Lys	Gly	Ser	Lys	Gly 15	Lys
Gln	Ser	Tyr	Thr 20	Tyr	Ile	Ile	Glu	Glu 25	Asn	Thr	Thr	Thr	Ser 30	Phe	Thr
Trp	Ala	Phe 35	Gln	Arg	Thr	Thr	Phe 40	His	Glu	Ala	Ser	Arg 45	Lys	Tyr	Thr
Asn	Asp 50	Val	Ala	Lys	Ile	Tyr 55	Ser	Ile	Asn	Val	Thr 60	Asn	Val	Met	Asn
Gly 65	Val	Ala	Ser	Tyr	Cys 70	Arg	Pro	Cys	Ala	Leu 75	Glu	Ala	Ser	Asp	Val 80
Gly	Ser	Ser	Cys	Thr 85	Ser	Cys	Pro	Ala	Gly 90	Tyr	Tyr	Ile	Asp	Arg 95	Asp
Ser	Gly	Thr	Cys 100	His	Ser	Cys	Pro	Pro 105	Asn	Thr	Ile	Leu	Lys 110	Ala	His
Gln	Pro	Tyr 115	Gly	Val	Gln	Ala	Cys 120	Val	Pro	Cys	Gly	Pro 125	Gly	Thr	Lys
Asn	Asn 130	Lys	Ile	His	Ser	Leu 135	Cys	Tyr	Asn	Asp	Cys 140	Thr	Phe	Ser	Arg
Asn 145	Thr	Pro	Thr	Arg	Thr 150	Phe	Asn	Tyr	Asn	Phe 155	Ser	Ala	Leu	Ala	Asn 160
Thr	Val	Thr	Leu	Ala 165	Gly	Gly	Pro	Ser	Phe 170	Thr	Ser	Lys	Gly	Leu 175	Lys

Tyr	Phe	His	His	Phe	Thr	Leu	Ser	Leu	Cys	Gly	Asn	Gln	Gly	Arg	Lys
			180					185					190		
Met	Ser	Val	Cys	Thr	Asp	Asn	Val	Thr	Asp	Leu	Arg	Ile	Pro	Glu	Gly
		195					200					205			
Glu	Ser	Gly	Phe	Ser	Lys	Ser	Ile	Thr	Ala	Tyr	Val	Cys	Gln	Ala	Val
	210					215					220				
Ile	Ile	Pro	Pro	Glu	Val	Thr	Gly	Tyr	Lys	Ala	Gly	Val	Ser	Ser	Gln
225					230					235					240
Pro	Val	Ser	Leu	Ala	Asp	Arg	Leu	Ile	Gly	Val	Thr	Thr	Asp	Met	Thr
				245					250					255	
Leu	Asp	Gly	Ile	Thr	Ser	Pro	Ala	Glu	Leu	Phe	His	Leu	Glu	Ser	Leu
			260					265					270		
Gly	Ile	Pro	Asp	Val	Ile	Phe	Phe	Tyr	Arg	Ser	Asn	Asp	Val	Thr	Gln
		275					280					285			
Ser	Cys	Ser	Ser	Gly	Arg	Ser	Thr	Thr	Ile	Arg	Val	Arg	Cys	Ser	Pro
	290					295					300				
Gln	Lys	Thr	Val	Pro	Gly	Ser	Leu	Leu	Leu	Pro	Gly	Thr	Cys	Ser	Asp
305					310					315					320
Gly	Thr	Cys	Asp	Gly	Cys	Asn	Phe	His	Phe	Leu	Trp	Glu	Ser	Ala	Ala
				325					330					335	
Ala	Cys	Pro	Leu	Cys	Ser	Val	Ala	Asp	Tyr	His	Ala	Ile	Val	Ser	Ser
			340					345					350		
Cys	Val	Ala	Gly	Ile	Gln	Lys	Thr	Thr	Tyr	Val	Trp	Arg	Glu	Pro	Lys
		355					360					365			
Leu	Cys	Ser	Gly	Gly	Ile	Ser	Leu	Pro	Glu	Gln	Arg	Val	Thr	Ile	Cys
	370					375					380				
Lys	Thr	Ile	Asp	Phe	Trp	Leu	Lys	Val	Gly	Ile	Ser	Ala	Gly	Thr	Cys
385					390					395					400
Thr	Ala	Ile	Leu	Leu	Thr	Val	Leu	Thr	Cys	Tyr	Phe	Trp	Lys	Lys	Asn
				405					410					415	
Gln	Lys	Leu	Glu	Tyr	Lys	Tyr	Ser	Lys	Leu	Val	Met	Asn	Ala	Thr	Leu
			420					425					430		
Lys	Asp	Cys	Asp	Leu	Pro	Ala	Ala	Asp	Ser	Cys	Ala	Ile	Met	Glu	Gly
		435					440					445			
Glu	Asp	Val	Glu	Asp	Asp	Leu	Ile	Phe	Thr	Ser	Lys	Lys	Ser	Leu	Phe
	450					455					460				
Gly	Lys	Ile	Lys	Ser	Phe	Thr	Ser	Lys	Arg	Thr	Pro	Asp	Gly	Phe	Asp
465					470					475					480
Ser	Val	Pro	Leu	Lys	Thr	Ser	Ser	Gly	Gly	Pro	Asp	Met	Asp	Leu	
				485					490					495	

<210> 174  
 <211> 118  
 <212> PRT

<213> homo sapiens

<400> 174

Gly 1	His	Asn	Glu	Glu 5	Ile	Ser	Ser	Ser	Gly 10	Cys	Cys	Arg	Met	Leu 15	Ala
Pro	Lys	Ser	Pro 20	Gln	Ala	Cys	Lys	Gly 25	Ala	Met	Gln	Gly	Glu 30	Glu	Ala
Gly	Glu	Ala 35	Gly	Ser	Ala	Ser	His 40	Arg	Ser	Met	Ser	Gly 45	Pro	Pro	Glu
Asp	Val 50	Phe	Ser	Gly	Thr	Glu 55	Ser	Asn	Pro	Ser	Gly 60	Val	Leu	Leu	Glu
Val 65	Asn	Asp	Leu	Ile	Phe 70	Pro	Lys	Ser	Asp	Phe 75	Leu	Leu	Val	Lys	Met 80
Arg	Ser	Ser	Ser	Thr 85	Ser	Ser	Pro	Ser	Met 90	Met	Ala	Gln	Leu	Ser 95	Ala
Ala	Gly	Arg	Ser 100	Gln	Ser	Leu	Arg	Val 105	Ala	Phe	Ile	Thr	Ser 110	Leu	Glu
Tyr	Leu	Tyr 115	Ser	Ser	Phe										

<210> 175

<211> 172

<212> PRT

<213> homo sapiens

<400> 175

Arg 1	Asn	Thr	Arg	Gly 5	His	Phe	Arg	Ala	Cys 10	Gln	Arg	Lys	Leu	Lys 15	Pro
Cys	Ser	Val	Ser 20	Thr	Val	Tyr	Lys	Phe 25	Asn	Arg	Asn	Ala	Cys 30	Gln	Arg
Gly	Leu	Phe 35	Glu	Lys	Arg	Val	Pro 40	Ser	Glu	Pro	Val	Leu 45	Ser	Val	Gln
Glu	Lys 50	Gly	Val	Leu	Leu	Lys 55	Arg	Lys	Leu	Ser	Leu 60	Leu	Glu	Gln	Asp
Val 65	Ile	Val	Asn	Glu	Asp 70	Gly	Arg	Asn	Lys	Leu 75	Lys	Lys	Gln	Gly	Glu 80
Thr	Pro	Asn	Glu	Val 85	Cys	Met	Phe	Ser	Leu 90	Ala	Tyr	Gly	Asp	Ile 95	Pro
Glu	Glu	Leu	Ile 100	Asp	Val	Ser	Asp	Phe 105	Glu	Cys	Ser	Leu	Cys 110	Met	Arg
Leu	Phe	Phe 115	Glu	Pro	Val	Thr	Thr 120	Pro	Cys	Gly	His	Ser 125	Phe	Cys	Lys
Asn	Cys 130	Leu	Glu	Arg	Cys	Leu 135	Asp	His	Ala	Pro	Tyr 140	Cys	Pro	Leu	Cys
Lys	Glu	Ser	Leu	Lys	Glu	Tyr	Leu	Ala	Asp	Arg	Arg	Tyr	Cys	Val	Thr

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145					150					155				160
Gln	Leu	Leu	Glu	Gly	Ile	Asn	Ser	Glu	Val	Ser	Ala			
				165					170					

<210> 176  
 <211> 248  
 <212> PRT  
 <213> homo sapiens  
 <400> 176

Gln	Ile	Gly	Gly	Thr	Val	Ser	His	Ser	Cys	Trp	Lys	Glu	Leu	Ile	Val
1				5					10					15	
Lys	Tyr	Leu	Pro	Asp	Glu	Leu	Ser	Glu	Arg	Lys	Lys	Ile	Tyr	Asp	Glu
			20					25					30		
Glu	Thr	Ala	Glu	Leu	Ser	His	Leu	Thr	Lys	Asn	Val	Pro	Ile	Phe	Val
		35					40					45			
Cys	Thr	Met	Ala	Tyr	Pro	Thr	Val	Pro	Cys	Pro	Leu	His	Val	Phe	Glu
	50					55					60				
Pro	Arg	Tyr	Arg	Leu	Met	Ile	Arg	Arg	Ser	Ile	Gln	Thr	Gly	Thr	Lys
65					70					75					80
Gln	Phe	Gly	Met	Cys	Val	Ser	Asp	Thr	Gln	Asn	Ser	Phe	Ala	Asp	Tyr
				85					90					95	
Gly	Cys	Met	Leu	Gln	Ile	Arg	Asn	Val	His	Phe	Leu	Pro	Asp	Gly	Arg
			100					105					110		
Ser	Val	Val	Asp	Thr	Val	Gly	Gly	Lys	Arg	Phe	Arg	Val	Leu	Lys	Arg
		115					120					125			
Gly	Met	Lys	Asp	Gly	Tyr	Cys	Thr	Ala	Asp	Ile	Glu	Tyr	Leu	Glu	Asp
	130					135					140				
Val	Lys	Val	Glu	Asn	Glu	Asp	Glu	Ile	Lys	Asn	Leu	Arg	Glu	Leu	His
145					150					155					160
Asp	Leu	Val	Tyr	Ser	Gln	Ala	Cys	Ser	Trp	Phe	Gln	Asn	Leu	Arg	Asp
				165					170					175	
Arg	Phe	Arg	Ser	Gln	Ile	Leu	Gln	His	Phe	Gly	Ser	Met	Pro	Glu	Arg
			180					185					190		
Arg	Glu	Asn	Leu	Gln	Ala	Ala	Pro	Asn	Gly	Pro	Ala	Trp	Cys	Trp	Trp
		195					200					205			
Leu	Leu	Ala	Val	Leu	Pro	Val	Asp	Pro	Arg	Tyr	Gln	Leu	Ser	Val	Leu
	210					215					220				
Ser	Met	Lys	Ser	Leu	Lys	Glu	Arg	Leu	Thr	Lys	Ile	Gln	His	Ile	Leu
225					230					235					240
Thr	Tyr	Phe	Ser	Arg	Asp	Gln	Phe								
				245											

<210> 177  
 <211> 133  
 <212> PRT

004221" 3622960

<213> homo sapiens

<400> 177

His 1	Ser	Thr	Ser	Tyr 5	Leu	Leu	Asp	Thr	Leu 10	Leu	Ser	Phe	Leu	Cys 15	Lys
Glu	Asp	Asn	Met 20	Val	His	Asp	Leu	Asn 25	Asn	Ala	Gln	Asp	Asn 30	Ser	Tyr
Arg	Thr	Asn 35	Val	Arg	Lys	Gly	Leu 40	Leu	Leu	Ala	Gln	Lys 45	Thr	Thr	Ser
Cys	Arg 50	Glu	Asn	Thr	Arg	Asn 55	Leu	Arg	His	Arg	Leu 60	Ile	Leu	Leu	Glu
Tyr 65	His	His	Lys	Leu	Arg 70	Lys	Thr	Tyr	Arg	Leu 75	His	Trp	Glu	Phe	Leu 80
Leu	Val	Phe	Ser	Ala 85	Tyr	Phe	Phe	His	Leu 90	His	Leu	Gln	Ser	His 95	Pro
Val	Leu	Lys	Glu 100	Thr	Thr	Phe	Phe	Ser 105	Ala	Glu	His	Leu	Phe 110	Leu	Glu
Leu	Thr	Glu 115	Gln	Val	Leu	Arg	Ala 120	Leu	Phe	Phe	Gln	Thr 125	Val	Leu	Ser
Gly	Arg 130	His	Phe	Cys											

<210> 178

<211> 152

<212> PRT

<213> homo sapiens

<400> 178

Ser 1	Ala	Val	Lys	Arg 5	Gly	Trp	Asp	Leu	Asn 10	Met	Ala	Ala	Val	Val 15	Ala
Ala	Thr	Ala	Leu 20	Lys	Gly	Arg	Gly	Ala 25	Arg	Asn	Ala	Arg	Val 30	Leu	Arg
Gly	Ile	Leu 35	Ala	Gly	Ala	Thr	Ala 40	Asn	Lys	Ala	Ser	His 45	Asn	Arg	Thr
Arg	Ala 50	Leu	Gln	Ser	His	Ser 55	Ser	Pro	Glu	Gly	Lys 60	Glu	Glu	Pro	Glu
Pro 65	Leu	Ser	Pro	Glu	Leu 70	Glu	Tyr	Ile	Pro	Arg 75	Lys	Arg	Gly	Lys	Asn 80
Pro	Met	Lys	Ala	Val 85	Gly	Leu	Ala	Trp	Ala 90	Ile	Gly	Phe	Pro	Cys 95	Gly
Ile	Leu	Leu	Phe 100	Ile	Leu	Thr	Lys	Arg 105	Glu	Val	Asp	Lys	Asp 110	Arg	Val
Lys	Gln	Met 115	Lys	Ala	Arg	Gln	Asn 120	Met	Arg	Leu	Ser	Asn 125	Thr	Gly	Glu
Tyr	Glu	Ser	Gln	Arg	Phe	Arg	Ala	Ser	Ser	Gln	Ser	Ala	Pro	Ser	Pro

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Val	Leu	Ala	Pro	Leu	Ser	Gly	Asn	Val	Phe	Gln	Leu	Arg	Gly		
		115					120					125			

<210> 181  
 <211> 74  
 <212> PRT  
 <213> homo sapiens

<400> 181

Leu	Val	Lys	Cys	Pro	Lys	Gly	Glu	Phe	Ser	Phe	His	Ser	Asn	Lys	Asp
1				5					10					15	
Arg	Phe	Ala	His	Ser	Leu	Lys	Gln	Asn	Val	Ala	Met	Asn	Ile	Gln	Pro
			20					25					30		
Leu	His	Thr	Tyr	Lys	Asp	Val	Arg	Met	Ile	Pro	Pro	Thr	Lys	His	Thr
		35					40					45			
His	Ser	His	Thr	Arg	Thr	His	Thr	His	Met	His	Thr	Arg	Ala	Cys	Thr
	50					55					60				
His	Gly	His	Met	His	Thr	His	Thr	His	Thr						
65					70										

<210> 182  
 <211> 84  
 <212> PRT  
 <213> homo sapiens

<400> 182

Ile	Leu	Ile	Ser	Phe	Lys	Gln	Arg	Gln	Ile	Cys	Ala	Phe	Thr	Gln	Ala
1				5					10					15	
Glu	Cys	Gly	His	Glu	Tyr	Ser	Ala	Pro	Ala	Tyr	Ile	Gln	Arg	Cys	Thr
			20					25					30		
His	Asp	Ser	Pro	His	Gln	Ala	His	Thr	Gln	Ser	His	Thr	His	Thr	His
		35					40					45			
Thr	His	Ala	His	Thr	Arg	Val	His	Thr	Arg	Thr	His	Ala	His	Thr	His
	50					55					60				
Ala	His	Val	Asn	Thr	Cys	Thr	His	Ala	His	Thr	Cys	Thr	His	Ala	His
65					70					75					80
Thr	Asp	Thr	Leu												

<210> 183  
 <211> 70  
 <212> PRT  
 <213> homo sapiens

<400> 183

Val	Cys	Pro	Cys	Val	His	Val	Cys	Thr	Cys	Val	His	Val	Cys	Met	Cys
1				5					10					15	
Leu	Arg	Val	Arg	Val	Cys	Val	His	Val	Ser	Val	Cys	Ala	Arg	Ala	Cys
			20					25					30		
Val	His	Val	Cys	Val	Cys	Ala	Cys	Val	Thr	Val	Cys	Val	Leu	Gly	Gly

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<400> 187

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<210> 188
<211> 100
<212> PRT
<213> homo sapiens
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<400> 188

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<210> 189
<211> 256
<212> PRT
<213> homo sapiens
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<400> 189

Arg 1	Ser	Gln	Ala	Gly 5	Pro	Glu	Ala	Gly	Gln 10	Pro	Leu	Pro	Gly	Ser 15	Gly
Lys	Arg	Ser	Ser 20	Cys	Cys	His	Cys	Ser 25	Ser	Gly	Ala	Cys	Ser 30	Met	Gly
Pro	Leu	Pro 35	Arg	Thr	Val	Glu	Leu 40	Phe	Tyr	Asp	Val	Leu 45	Ser	Pro	Tyr
Ser	Trp	Leu	Gly	Phe	Glu	Ile	Leu	Cys	Arg	Tyr	Gln	Asn	Ile	Trp	Asn



[illegible]

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<210> 191
<211> 116
<212> PRT
<213> homo sapiens
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<400> 191

[illegible]

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<210> 192
<211> 182
<212> PRT
<213> homo sapiens
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<400> 192

Lys 1	Arg	Glu	Ser	Gly 5	Phe	Pro	Thr	Ile	Leu 10	Tyr	Glu	Cys	Phe	Gln 15	His
His	Arg	Glu	Ser	Gln	Arg	Pro	Gln	Arg	Thr	Asn	Gly	Ser	Ser	Ser	Arg



<213> homo sapiens

<400> 194

Glu 1	Ile	Tyr	Ser	Leu 5	Ser	Arg	Phe	Ile	Glu 10	Val	Lys	Met	Ser	Lys 15	Lys
Ile	Ser	Gly	Gly 20	Ser	Val	Val	Glu	Met 25	Gln	Gly	Asp	Glu	Met 30	Thr	Arg
Ile	Ile	Trp 35	Glu	Leu	Ile	Lys	Glu 40	Lys	Leu	Ile	Phe	Pro 45	Tyr	Val	Glu
Leu	Asp 50	Leu	His	Ser	Tyr	Asp 55	Leu	Gly	Ile	Glu	Asn 60	Arg	Asp	Ala	Thr
Asn 65	Asp	Gln	Val	Thr	Lys 70	Asp	Ala	Ala	Glu	Ala 75	Ile	Lys	Lys	His	Asn 80
Val	Gly	Val	Lys	Cys 85	Ala	Thr	Ile	Thr	Pro 90	Asp	Glu	Lys	Arg	Val 95	Glu
Glu	Phe	Lys	Leu 100	Lys	Gln	Met	Trp	Lys 105	Ser	Pro	Asn	Gly	Thr 110	Ile	Arg
Asn	Ile	Leu 115	Gly	Gly	Thr	Val	Phe 120	Arg	Glu	Ala	Ile	Ile 125	Cys	Lys	Asn
Ile	Pro 130	Arg	Leu	Val	Ser	Gly 135	Trp	Val	Lys	Pro	Ile 140	Ile	Ile	Gly	Arg
His 145	Ala	Tyr	Gly	Asp	Gln 150	Tyr	Arg	Ala	Thr	Asp 155	Phe	Val	Val	Pro	Gly 160
Pro	Gly	Lys	Val	Glu 165	Ile	Thr	Tyr	Thr	Pro 170	Ser	Asp	Gly	Thr	Gln 175	Lys
Val	Thr	Tyr	Leu 180	Val	His	Asn	Phe	Glu 185	Glu	Gly	Gly	Gly	Val 190	Ala	Met
Gly	Met	Tyr 195	Asn	Gln	Asp	Lys	Ser 200	Ile	Glu	Asp	Phe	Ala 205	His	Ser	Ser
Phe	Gln 210	Met	Ala	Leu	Ser	Lys 215	Gly	Trp	Pro	Leu	Tyr 220	Leu	Ser	Thr	Lys
Asn 225	Thr	Ile	Leu	Lys	Lys 230	Tyr	Asp	Gly	Arg	Phe 235	Lys	Asp	Ile	Phe	Gln 240
Glu	Ile	Tyr	Asp	Lys 245	Gln	Tyr	Lys	Ser	Gln 250	Phe	Glu	Ala	Gln	Lys 255	Ile
Trp	Tyr	Glu	His 260	Arg	Leu	Ile	Asp	Asp 265	Met	Val	Ala	Gln	Ala 270	Met	Lys
Ser	Glu	Gly 275	Gly	Phe	Ile	Trp	Ala 280	Cys	Lys	Asn	Tyr	Asp 285	Gly	Asp	Val
Gln	Ser 290	Asp	Ser	Val	Ala	Gln 295	Gly	Tyr	Gly	Ser	Leu 300	Gly	Met	Met	Thr
Ser 305	Val	Leu	Val	Cys	Pro 310	Asp	Gly	Lys	Thr	Val 315	Glu	Ala	Glu	Ala	Ala 320

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His	Gly	Thr	Val	Thr 325	Arg	His	Tyr	Arg	Met 330	Tyr	Gln	Lys	Gly	Gln 335	Glu
Thr	Ser	Thr	Asn 340	Pro	Ile	Ala	Ser	Ile 345	Phe	Ala	Trp	Thr	Arg 350	Gly	Leu
Ala	His	Arg 355	Ala	Lys	Leu	Asp	Asn 360	Asn	Lys	Glu	Leu	Ala 365	Phe	Phe	Ala
Asn	Ala 370	Leu	Glu	Glu	Val	Ser 375	Ile	Glu	Thr	Ile	Glu 380	Ala	Gly	Phe	Met
Thr 385	Lys	Asp	Leu	Ala	Ala 390	Cys	Ile	Lys	Gly	Leu 395	Pro	Asn	Val	Gln	Arg 400
Ser	Asp	Tyr	Leu	Asn 405	Thr	Phe	Glu	Phe	Met 410	Asp	Lys	Leu	Gly	Glu 415	Asn
Leu	Lys	Ile	Lys 420	Leu	Ala	Gln	Ala	Lys 425	Leu						

<210> 195  
 <211> 97  
 <212> PRT  
 <213> homo sapiens

<400> 195

Arg 1	Leu	Leu	Pro	Lys 5	His	Leu	Gln	Arg	Arg 10	Gln	Ala	Leu	Tyr	Cys 15	Tyr
Gln	Ala	Leu	Leu 20	Cys	Gly	Leu	Thr	Leu 25	Trp	Ser	Arg	Gln	Lys 30	Trp	Lys
Gln	Trp	Asp 35	Trp	Trp	Thr	Ser	Pro 40	Val	Leu	Ser	Gly	Thr 45	Cys	Gly	Ser
Asp	Gly 50	Leu	Gln	Ser	Arg	Gly 55	Gln	Pro	Leu	Leu	Leu 60	Leu	Ser	Cys	His
Leu 65	Asp	Lys	Pro	Ala	Arg 70	Trp	Ser	Ser	Cys	Arg 75	Glu	Ser	His	Thr	Leu 80
Gly	Pro	Gln	Ser	Pro 85	Thr	Ala	Arg	His	His 90	His	Ser	Phe	Tyr	Arg 95	Pro

Arg

<210> 196  
 <211> 93  
 <212> PRT  
 <213> homo sapiens

<400> 196

Leu 1	Ile	Leu	Ile	Ile 5	His	Pro	His	Gly	Asn 10	Thr	Thr	Thr	Phe	Phe 15	Lys
Val	Met	Tyr	Gln 20	Val	Cys	His	Leu	Leu 25	Gly	Ser	Val	Thr	Trp 30	Cys	Val
Gly	Tyr	Leu	Tyr	Phe	Ser	Arg	Pro	Arg	Asn	Asn	Lys	Ile	Ser	Cys	Ser

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Gly	Lys	Gly	Asn	Lys 245	Val	Ser	Ala	Glu	Lys 250	Val	Asn	Lys	Thr	His 255	Ser	
Val	Asn	Gly	Ile 260	Thr	Glu	Glu	Ala	Asp 265	Pro	Thr	Ile	Tyr	Ser 270	Gly	Lys	
Val	Ile	Arg 275	Pro	Leu	Arg	Ser	Val 280	Asp	Pro	Thr	Gln	Thr 285	Glu	Tyr	Gln	
Gly	Met 290	Ile	Glu	Ile	Val	Glu 295	Glu	Gly	Asp	Met	Lys 300	Gly	Glu	Val	Tyr	
Pro 305	Phe	Gly	Ile	Val	Gly 310	Met	Ala	Asn	Lys	Gly 315	Asp	Cys	Leu	Gln	Lys 320	
Gly	Glu	Ser	Val	Lys 325	Phe	Gln	Leu	Cys	Val 330	Leu	Gly	Gln	Asn	Ala 335	Gln	
Thr	Met	Ala	Tyr 340	Asn	Ile	Thr	Pro	Leu 345	Arg	Arg	Ala	Thr	Val 350	Glu	Cys	
Val	Lys	Asp 355	Gln	Phe	Gly	Phe	Ile 360	Asn	Tyr	Glu	Val	Gly 365	Asp	Ser	Lys	
Lys	Leu 370	Phe	Phe	His	Val	Lys 375	Glu	Val	Gln	Asp	Gly 380	Ile	Glu	Leu	Gln	
Ala 385	Gly	Asp	Glu	Val	Glu 390	Phe	Ser	Val	Ile	Pro 395	Lys	Ser	Ser	Gly	Gly 400	
Leu	Ala	Gly	Ser	Gly 405	Ala	Cys	Arg	Cys	Phe 410							

<210> 198  
 <211> 126  
 <212> PRT  
 <213> homo sapiens

<400> 198

Leu 1	Asn	Ala	Ile	Leu 5	Asn	Phe	Phe	His	Met 10	Glu	Lys	Glu	Leu	Leu 15	Ala	
Ile	Ser	Tyr	Phe 20	Ile	Val	Asn	Glu	Ala 25	Lys	Leu	Ile	Phe	His 30	Thr	Phe	
His	Cys	Gly 35	Pro	Ala	Gln	Gly	Cys 40	Asp	Val	Val	Ser	His 45	Ser	Leu	Cys	
Ile	Leu 50	Ala	Gln	Asp	Thr	Gln 55	Leu	Glu	Leu	Asp	Ala 60	Leu	Pro	Phe	Leu	
Gln 65	Ala	Ile	Pro	Phe	Val 70	Gly	His	Pro	Asn	Asp 75	Ala	Lys	Trp	Ile	Asp 80	
Leu	Thr	Phe	His	Ile 85	Ala	Leu	Leu	His	Asn 90	Leu	Asn	His	Ser	Leu 95	Val	
Leu	Ser	Leu	Cys 100	Trp	Ile	Asn	Thr	Pro 105	Gln	Gly	Ala	Asn	Tyr 110	Phe	Ala	
Arg	Val	Asn 115	Gly	Gly	Ile	Ser	Phe 120	Leu	Ser	Asn	Ala	Ile 125	His			



<210> 199  
 <211> 85  
 <212> PRT  
 <213> homo sapiens

<400> 199

Lys 1	Ser	His	Thr	Ser 5	Cys	Asn	Leu	Leu	Ser 10	Arg	Pro	Leu	Phe	Val 15	Thr
Asn	Thr	Lys	Phe 20	Asn	Leu	Ile	Ser	Tyr 25	Leu	Arg	Arg	Ser	Arg 30	Ser	Phe
His	Ile	Leu 35	Gly	Leu	Lys	Ser	Asn 40	Ser	Gln	Phe	His	Pro 45	Thr	Val	Ile
Ile	Ser 50	Asn	Asn	Ala	Ile	Leu 55	Ser	Leu	Leu	Leu	Phe 60	Ala	Phe	Ile	Trp
Ala 65	Ser	Gly	Phe	Arg	Ile 70	Gly	Lys	Ser	Gly	Phe 75	Phe	Phe	Tyr	Arg	Ala 80
Gln	Lys	Thr	Val	Ile 85											

<210> 200  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 200

Ala 1	Thr	Met	Arg	Leu 5	Ser	Val	Cys	Leu	Leu 10	Met	Val	Ser	Leu	Ala 15	Leu
Cys	Cys	Tyr	Gln 20	Ala	His	Ala	Leu	Val 25	Cys	Pro	Ala	Val	Ala 30	Ser	Glu
Ile	Thr	Val 35	Phe	Leu	Phe	Leu	Ser 40	Asp	Ala	Ala	Val	Asn 45	Leu	Gln	Val
Ala	Lys 50	Leu	Asn	Pro	Pro	Pro 55	Glu	Ala	Leu	Ala	Ala 60	Lys	Leu	Glu	Val
Lys 65	His	Cys	Thr	Asp	Gln 70	Ile	Ser	Phe	Lys	Lys 75	Arg	Leu	Leu	Ile	

<210> 201  
 <211> 50  
 <212> PRT  
 <213> homo sapiens

<400> 201

Ser 1	Val	Gln	Cys	Phe 5	Thr	Ser	Asn	Leu	Ala 10	Ala	Arg	Ala	Ser	Gly 15	Gly
Gly	Leu	Ser	Leu 20	Ala	Thr	Trp	Arg	Phe 25	Thr	Ala	Ala	Ser	Leu 30	Lys	Asn
Lys	Lys	Thr 35	Val	Ile	Ser	Glu	Ala 40	Thr	Ala	Gly	Gln	Thr 45	Arg	Ala	Trp

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Ala Trp  
50

<210> 202  
<211> 72  
<212> PRT  
<213> homo sapiens

<400> 202

Gln 1	Val	Ala	Val	Glu 5	Lys	Thr	Leu	Glu	Thr 10	Gln	Val	Glu	His	Phe 15	Tyr
Met	Ser	His	Thr 20	His	Ile	Phe	Ser	Leu 25	Phe	Pro	Pro	Arg	Thr 30	Phe	Ser
Asn	Glu	Lys 35	Pro	Phe	Leu	Lys	Arg 40	Tyr	Leu	Ile	Gly	Ala 45	Val	Leu	His
Phe	Gln 50	Leu	Gly	Cys	Lys	Ser 55	Phe	Trp	Arg	Trp	Ile 60	Lys	Phe	Gly	Asn
Leu 65	Glu	Val	Tyr	Arg	Ser 70	Val	Thr								

<210> 203  
<211> 53  
<212> PRT  
<213> homo sapiens

<400> 203

Ser 1	Phe	Ser	Pro	Ser 5	Leu	Thr	Thr	Arg	Ala 10	Met	Asn	Ser	Ser	Ala 15	Ser
Ser	Thr	Ser	Thr 20	Cys	Ser	Ser	Tyr	Thr 25	Leu	Gly	Thr	Arg	Leu 30	Pro	Val
Gly	Gly	Arg 35	Gly	Pro	Thr	Lys	Val 40	Thr	Cys	Cys	Thr	Ser 45	Asn	Arg	Leu
Thr	Leu 50	Ser	Leu	Asp											

<210> 204  
<211> 121  
<212> PRT  
<213> homo sapiens

<400> 204

Ala 1	Leu	Val	Val	Arg 5	Phe	Leu	Thr	Lys	Arg 10	Phe	Ile	Gly	Asp	Tyr 15	Glu
Arg	Asn	Ala	Gly 20	Asn	Leu	Tyr	Thr	Arg 25	Gln	Val	Gln	Ile	Glu 30	Gly	Glu
Thr	Leu	Ala 35	Leu	Gln	Val	Gln	Asp 40	Thr	Pro	Gly	Ile	Gln 45	Val	His	Glu
Asn	Ser 50	Leu	Ser	Cys	Ser	Glu 55	Gln	Leu	Asn	Arg	Cys 60	Ile	Arg	Trp	Ala

004221" SEE 2960

Asp 65	Ala	Val	Val	Ile	Val 70	Phe	Ser	Ile	Thr	Asp 75	Tyr	Lys	Ser	Tyr	Glu 80
Leu	Ile	Ser	Gln	Leu 85	His	Gln	His	Val	Gln 90	Gln	Leu	His	Leu	Gly 95	His
Pro	Ala	Ala	Cys 100	Gly	Trp	Ser	Trp	Ala 105	Asn	Lys	Ser	Asp	Leu 110	Leu	His
Ile	Lys	Gln 115	Val	Asp	Pro	Gln	Leu 120	Gly							

<210> 205  
 <211> 205  
 <212> PRT  
 <213> homo sapiens

<400> 205

Gly 1	Pro	Leu	Pro	Ala 5	Leu	Ala	Ala	Gly	Ser 10	Thr	Phe	Pro	Val	Leu 15	Ala
Cys	Ser	Ser	Ala 20	Met	Ala	Pro	Lys	Gly 25	Ser	Ser	Lys	Gln	Gln 30	Ser	Glu
Glu	Asp	Leu 35	Leu	Leu	Gln	Asp	Phe 40	Ser	Arg	Asn	Leu	Ser 45	Ala	Lys	Ser
Ser	Ala 50	Leu	Phe	Phe	Gly	Asn 55	Ala	Phe	Ile	Val	Ser 60	Ala	Ile	Pro	Ile
Trp 65	Leu	Tyr	Trp	Arg	Ile 70	Trp	His	Met	Asp	Leu 75	Ile	Gln	Ser	Ala	Val 80
Leu	Tyr	Ser	Val	Met 85	Thr	Leu	Val	Ser	Thr 90	Tyr	Leu	Val	Ala	Phe 95	Ala
Tyr	Lys	Asn	Val 100	Lys	Phe	Val	Leu	Lys 105	His	Lys	Val	Ala	Gln 110	Lys	Arg
Glu	Asp	Ala 115	Val	Ser	Lys	Glu	Val 120	Thr	Arg	Lys	Leu	Ser 125	Glu	Ala	Asp
Asn	Arg 130	Lys	Met	Ser	Arg	Lys 135	Glu	Lys	Asp	Glu	Arg 140	Ile	Leu	Trp	Lys
Lys 145	Asn	Glu	Val	Ala	Asp 150	Tyr	Glu	Ala	Thr	Thr 155	Phe	Ser	Ile	Phe	Tyr 160
Asn	Asn	Thr	Leu	Phe 165	Leu	Val	Val	Val	Ile 170	Val	Ala	Ser	Phe	Phe 175	Ile
Leu	Lys	Asn	Phe 180	Asn	Pro	Thr	Val	Asn 185	Tyr	Ile	Leu	Ser	Ile 190	Ser	Ala
Ser	Ser	Gly 195	Leu	Ile	Ala	Leu	Leu 200	Ser	Thr	Gly	Ser	Lys 205			

<210> 206  
 <211> 106  
 <212> PRT  
 <213> homo sapiens

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<400> 206

Val 1	Leu	His	Gln	Asp 5	Ser	Ser	Pro	Ser	Cys 10	Leu	Leu	Ala	Pro	Asn 15	Arg
Pro	Cys	Gln	Leu 20	His	Pro	Leu	Ala	Leu 25	Cys	Leu	Trp	Val	Ala 30	Cys	Gly
Ile	Trp	Lys 35	Ser	Ser	Arg	Val	Val 40	Arg	Val	Gly	Asp	Thr 45	Arg	Cys	Phe
Tyr	Ser 50	Leu	Glu	Pro	Leu	Lys 55	Asn	Pro	Ala	Glu	Cys 60	Asn	Ser	Val	Phe
Val 65	Tyr	Trp	Leu	Phe	Phe 70	Asp	Arg	Leu	Leu	Lys 75	Leu	Asn	Glu	Leu	Lys 80
Gly	Lys	Leu	Arg	Val 85	Leu	Gly	Arg	Leu	Leu 90	Lys	Gly	Lys	Lys	Cys 95	Leu
Ala	Met	Cys	Cys 100	Asn	His	Lys	Arg	Arg 105	Lys						

<210> 207

<211> 105

<212> PRT

<213> homo sapiens

<400> 207

Ser 1	Thr	Tyr	Gly	Gln 5	Tyr	Val	Val	His	Cys 10	Gly	Val	Glu	Val	Leu 15	Gln
Tyr	Glu	Glu	Gly 20	Ser	Asn	Asn	Asp	His 25	Asp	Gln	Glu	Gln	Ser 30	Val	Val
Ile	Glu	Asp 35	Gly	Lys	Cys	Cys	Ser 40	Phe	Ile	Ile	Ser	Asn 45	Phe	Ile	Leu
Leu	Pro 50	Gln	Asp	Ser	Phe	Ile 55	Phe	Leu	Leu	Pro	Arg 60	His	Leu	Ser	Ile
Ile 65	Ser	Phe	Arg	Lys	Phe 70	Ser	Ser	His	Phe	Phe 75	Gly	Asn	Ser	Ile	Leu 80
Pro	Leu	Leu	Cys	Tyr 85	Phe	Val	Leu	Glu	Asn 90	Lys	Phe	His	Ile	Leu 95	Val
Cys	Lys	Gly	Tyr 100	Gln	Ile	Cys	Ala	Tyr 105							

<210> 208

<211> 549

<212> PRT

<213> homo sapiens

<400> 208

Leu 1	Tyr	Pro	Asn	Phe 5	Leu	Val	Asn	Glu	Leu 10	Ile	Leu	Lys	Gln	Lys 15	Gln
Arg	Phe	Glu	Glu	Lys	Arg	Phe	Lys	Leu	Asp	His	Ser	Val	Ser	Ser	Thr

20								25				30			
Asn	Gly	His 35	Arg	Trp	Gln	Ile	Phe 40	Gln	Asp	Trp	Leu	Gly 45	Thr	Asp	Gln
Asp	Asn 50	Leu	Asp	Leu	Ala	Asn 55	Val	Asn	Leu	Met	Leu 60	Glu	Leu	Leu	Val
Gln 65	Lys	Lys	Lys	Gln	Leu 70	Glu	Ala	Glu	Ser	His 75	Ala	Ala	Gln	Leu	Gln 80
Ile	Leu	Met	Glu	Phe 85	Leu	Lys	Val	Ala	Arg 90	Arg	Asn	Lys	Arg	Glu 95	Gln
Leu	Glu	Gln	Ile 100	Gln	Lys	Glu	Leu	Ser 105	Val	Leu	Glu	Glu	Asp 110	Ile	Lys
Arg	Val	Glu 115	Glu	Met	Ser	Gly	Leu 120	Tyr	Ser	Pro	Val	Ser 125	Glu	Asp	Ser
Thr	Val 130	Pro	Gln	Phe	Glu	Ala 135	Pro	Ser	Pro	Ser	His 140	Ser	Ser	Ile	Ile
Asp 145	Ser	Thr	Glu	Tyr	Ser 150	Gln	Pro	Pro	Gly	Phe 155	Ser	Gly	Ser	Ser	Gln 160
Thr	Lys	Lys	Gln	Pro 165	Trp	Tyr	Asn	Ser	Thr 170	Leu	Ala	Ser	Arg	Arg 175	Lys
Arg	Leu	Thr	Ala 180	His	Phe	Glu	Asp	Leu 185	Glu	Gln	Cys	Tyr	Phe 190	Ser	Thr
Arg	Met	Ser 195	Arg	Ile	Ser	Asp	Asp 200	Ser	Arg	Thr	Ala	Ser 205	Gln	Leu	Asp
Glu	Phe 210	Gln	Glu	Cys	Leu	Ser 215	Lys	Phe	Thr	Arg	Tyr 220	Asn	Ser	Val	Arg
Pro 225	Leu	Ala	Thr	Leu	Ser 230	Tyr	Ala	Ser	Asp	Leu 235	Tyr	Asn	Gly	Ser	Ser 240
Ile	Val	Ser	Ser	Ile 245	Glu	Phe	Asp	Arg	Asp 250	Cys	Asp	Tyr	Phe 255	Ala	Ile
Ala	Gly	Val	Thr 260	Lys	Lys	Ile	Lys	Val 265	Tyr	Glu	Tyr	Asp	Thr 270	Val	Ile
Gln	Asp	Ala 275	Val	Asp	Ile	His	Tyr 280	Pro	Glu	Asn	Glu	Met 285	Thr	Cys	Asn
Ser	Lys 290	Ile	Ser	Cys	Ile	Ser 295	Trp	Ser	Ser	Tyr	His 300	Lys	Asn	Leu	Leu
Ala 305	Ser	Ser	Asp	Tyr	Glu 310	Gly	Thr	Val	Ile	Leu 315	Trp	Asp	Gly	Phe	Thr 320
Gly	Gln	Arg	Ser	Lys 325	Val	Tyr	Gln	Glu	His 330	Glu	Lys	Arg	Cys	Trp 335	Ser
Val	Asp	Phe	Asn 340	Leu	Met	Asp	Pro	Lys 345	Leu	Leu	Ala	Ser	Gly 350	Ser	Asp
Asp	Ala	Lys	Val	Lys	Leu	Trp	Ser	Thr	Asn	Leu	Asp	Asn	Ser	Val	Ala



<210> 210  
 <211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 210

Phe	Pro	Ser	Ser	Leu	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Cys
1				5					10					15	
Gly	Ser	Ile	Asn	Phe	Tyr	Cys	Phe	Val	Ile	Tyr	Phe	Tyr	Ser	Lys	Glu
			20					25					30		
Phe	Val	Ser	Leu	Ser	Gln	Lys	Leu	Asp	Asn	Thr	Thr	Lys	Ser	Ser	Asn
		35					40					45			
Val	His	Gly	Val	Thr	Leu	Met	Val	Glu	Ser	Trp	Leu	Gly	Ile	Pro	Asn
	50					55					60				
Val	Pro	Lys	Val	Ile	Lys	Glu	Gly	Lys	Glu	Lys	Lys	Lys	Lys	Ile	Phe
65					70					75					80
Lys	Thr	Asn	Pro	Lys	Pro	Met	Met	Thr	Leu	Gly	Arg	Asp	Ile	Thr	
				85					90					95	

<210> 211  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 211

Lys	Lys	Met	Val	Arg	Leu	Gly	Leu	Phe	Ser	Cys	Leu	Leu	Ala	Ile	Tyr
1				5					10					15	
Ser	Leu	Leu	Trp	Ile	Val	Cys	Ile	Pro	Tyr	Leu	Leu	Ser	Ile	Gly	Leu
			20					25					30		
Cys	Val	Asp	Ile	Leu	Phe	Leu	Phe	Val	Gln	His	Leu	Leu	Pro	His	Leu
		35					40					45			
Leu	Val	Thr	Gln	Pro	Leu	Phe	Ile	Cys	Gly	Glu	Pro	Ile	Pro	Cys	Gly
	50					55					60				
Leu	Gly	Glu	His	Val	Thr	Arg	Pro	Gly	Leu	Leu	Ser	Pro	Thr	Ala	Ser
65					70					75					80

<210> 212  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 212

Leu	Lys	Lys	Gly	Lys	Trp	Ala	Lys	Ala	Ile	His	Asn	Arg	Lys	Cys	Lys
1				5					10					15	
Trp	Pro	Arg	Asn	Met	Lys	Arg	Cys	Ser	Ser	Ser	Leu	Ile	Phe	Lys	Glu
			20					25					30		
Lys	Lys	Glu	Ile	Leu	Pro	Thr	Arg	Leu	Ala	Lys	Ile	Phe	Lys	Asp	Ser
		35					40					45			

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Gly	Leu	Ala	Asp	Tyr	Arg	Gln	Thr	Gly	Ile	Leu	Thr	Asn	Asp	Gly	Val
	50					55					60				
Val	Asn	Trp													
65															

<210> 213  
 <211> 78  
 <212> PRT  
 <213> homo sapiens

<400> 213

Ser	Pro	Glu	Val	Gly	Gln	Ala	Leu	Gly	Thr	Ala	Gly	Ser	Arg	Ala	Ser
1				5					10					15	
Arg	Lys	Met	Thr	Ser	Glu	Leu	Ser	Ser	Leu	Ser	Ile	Ser	Ala	Ser	Ile
			20					25					30		
Arg	Val	Ser	Pro	Gln	Thr	Asp	Ser	Leu	His	Met	Ala	Gln	Ile	Gln	Ala
		35					40					45			
Tyr	Met	Val	Leu	Gly	Ser	Trp	Asp	Leu	His	Lys	Ala	Phe	Phe	Pro	Val
	50					55					60				
Val	Pro	Ala	Glu	Val	Leu	Leu	Arg	Ala	Phe	Leu	Ser	Leu	Ala		
65					70					75					

<210> 214  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 214

Gln	Ala	Gly	Lys	Arg	Ala	Leu	Tyr	Lys	His	Thr	Gln	Thr	Asn	Thr	Ser
1				5					10					15	
Gly	Asp	Gly	Cys	Val	Leu	Leu	Glu	Gln	Arg	Leu	Ile	Lys	His	Ser	Val
			20					25					30		
Cys	Trp	Leu	Ser	Val	Pro	Leu	Leu	Glu	Asn	Asn	Glu	Leu	Gly	Lys	Glu
		35				40					45				
Gln	Leu	Ile	Arg	Lys	Cys	Ala	Leu	Leu	Thr	Val	His	Ile	Thr	Thr	Lys
	50					55					60				
Ser	Trp	Gln	Leu	Leu	Lys	Glu	Lys	Gly	Leu	Cys	Arg	Cys	Arg	Ser	Asn
65					70					75					80
Leu	Ser	Val	Asn	Ser	Cys	Gln	Gln	Pro	Gln	Arg	Leu	Pro	Pro	Gln	His
				85					90					95	
Thr	Leu	Ile	Thr	Cys	Val	Cys	Leu	Ala							
			100					105							

<210> 215  
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 <213> homo sapiens

<400> 215

004227"56E2960









Thr 65	Arg	Met	Gly	His	Cys 70	Pro	Ile	Phe	Phe	Ile 75	Arg	Ala	Trp	Val	Leu 80
Ser	Thr	Val	Val	Gly 85	Ala	Val	Ser	Gly	Trp 90	Gly	Thr	Ser	Ser	Thr 95	Ser

Gly Met

<210> 220  
 <211> 129  
 <212> PRT  
 <213> homo sapiens

<400> 220

Thr 1	Met	Phe	Phe	Thr 5	Cys	Gly	Pro	Asn	Glu 10	Ala	Met	Val	Val	Ser 15	Gly
Phe	Cys	Arg	Ser 20	Pro	Pro	Val	Met	Val 25	Ala	Gly	Gly	Arg	Val 30	Phe	Val
Leu	Pro	Cys 35	Ile	Gln	Gln	Ile	Gln 40	Arg	Ile	Ser	Leu	Asn 45	Thr	Leu	Thr
Leu	Asn 50	Val	Lys	Ser	Glu	Lys 55	Val	Tyr	Thr	Arg	His 60	Gly	Val	Pro	Ile
Ser 65	Val	Thr	Gly	Ile	Ala 70	Gln	Val	Lys	Leu	Ser 75	Glu	Pro	Phe	Pro	His 80
Ser	Pro	Leu	Pro	His 85	His	Pro	Leu	Ser	Gln 90	Thr	Leu	Arg	His	Leu 95	Leu
Ala	Thr	Val	Phe 100	Ser	Thr	Leu	Ala	Cys 105	Arg	Glu	Val	Pro	Leu 110	Leu	Val
Ser	Ser	Phe 115	Pro	Gly	Thr	Pro	Arg 120	His	Leu	Pro	Pro	Pro 125	Pro	Phe	Phe

Pro

<210> 221  
 <211> 118  
 <212> PRT  
 <213> homo sapiens

<400> 221

Asp 1	Gly	Asp	Pro	Met 5	Ala	Ser	Val	Asn	Leu 10	Phe	Thr	Leu	Asp	Ile 15	Glu
Gly	Gln	Cys	Val 20	Glu	Arg	Asp	Pro	Leu 25	Asp	Leu	Leu	Asp	Ala 30	Gly	Gln
Asp	Lys	Asp 35	Thr	Pro	Ser	Ser	His 40	His	Asp	Trp	Gly	Ala 45	Ser	Ala	Glu
Pro	Gly 50	Asp	His	His	Gly	Leu 55	Ile	Trp	Ala	Thr	Ser 60	Glu	Lys	His	Gly
Ser 65	Gly	Trp	Ser	Phe	Arg 70	Asp	Ala	Gly	Gly	Ser 75	Pro	Ala	Gly	Val	Ser 80

004221 5622960



85

90

<210> 224  
 <211> 94  
 <212> PRT  
 <213> homo sapiens

<400> 224

Asn 1	Leu	Ile	Tyr	Pro 5	Asn	Ser	Ser	Met	Tyr 10	Ser	Asp	Thr	Phe	Ser 15	Glu
Lys	Ala	Arg	Ile 20	Ile	Gly	Ala	Val	Leu 25	Ser	Ile	Lys	Gly	Lys 30	Ser	Ser
Asp	His	Leu 35	His	Tyr	Asn	Phe	Leu 40	Cys	Leu	Phe	Ser	Ala 45	Gly	Glu	Glu
Ile	His 50	Ile	Tyr	Ser	Thr	Pro 55	His	Trp	Thr	Leu	Gln 60	Asn	Ala	Cys	Ile
Phe 65	Cys	Pro	Ser	Ala	Ile 70	Cys	Ser	Leu	Pro	Phe 75	Cys	Leu	Leu	Lys	Glu 80
Leu	Ser	Asn	Ile	Val 85	Phe	Pro	Lys	Met	Phe 90	Ser	Thr	Gly	His		

<210> 225  
 <211> 92  
 <212> PRT  
 <213> homo sapiens

<400> 225

Gly 1	His	His	Met	His 5	Ile	Leu	Asp	Arg	Phe 10	Cys	Thr	Ala	Gln	Leu 15	Glu
Trp	Val	Pro	Val 20	Thr	Trp	Thr	Gly	Val 25	Gln	Tyr	Thr	Ile	Cys 30	Val	Gln
Tyr	Arg	Lys 35	Pro	Ser	Ser	Ala	Val 40	Ala	Arg	Glu	Leu	Tyr 45	Ser	Asn	Ser
Leu	Ser 50	Ala	Gln	Ala	Asn	Gln 55	Val	Arg	Lys	Thr	Ala 60	Ile	Trp	Leu	Glu
Asp 65	Phe	Gln	Glu	Thr	Ala 70	Val	Pro	Val	Arg	Gly 75	Arg	Tyr	Tyr	Leu	Arg 80
Gly	Gly	Arg	Gly	Thr 85	Asp	Ile	Lys	Gln	Glu 90	Gly	Phe				

<210> 226  
 <211> 458  
 <212> PRT  
 <213> homo sapiens

<400> 226

Arg 1	Gly	Lys	Arg	Arg 5	Arg	His	Arg	Leu	Pro 10	Ala	Leu	Pro	Pro	Arg 15	Leu
Leu	Ser	Pro	Ser	Ala	Ala	Thr	Met	Ser	Ala	Ser	Ala	Val	Phe	Ile	Leu

004222 5622960

			20				25				30					
Asp	Val	Lys	Gly	Lys	Pro	Leu	Ile	Ser	Arg	Asn	Tyr	Lys	Gly	Asp	Val	
		35					40					45				
Ala	Met	Ser	Lys	Ile	Glu	His	Phe	Met	Pro	Leu	Leu	Val	His	Gly	Glu	
	50					55					60					
Glu	Glu	Gly	Ala	Leu	Ala	Pro	Leu	Leu	Ser	His	Gly	Gln	Val	His	Phe	
65					70					75					80	
Leu	Trp	Ile	Lys	His	Ser	Asn	Leu	Tyr	Leu	Val	Ala	Thr	Thr	Ser	Lys	
				85					90					95		
Asn	Ala	Asn	Ala	Ser	Leu	Val	Tyr	Ser	Phe	Leu	Tyr	Lys	Thr	Ile	Glu	
			100					105					110			
Val	Phe	Cys	Glu	Tyr	Phe	Lys	Glu	Leu	Glu	Glu	Glu	Ser	Ile	Arg	Asp	
		115					120					125				
Asn	Phe	Val	Ile	Val	Tyr	Glu	Leu	Leu	Asp	Glu	Leu	Met	Asp	Phe	Gly	
	130					135					140					
Phe	Pro	Gln	Thr	Thr	Asp	Ser	Lys	Ile	Leu	Gln	Glu	Tyr	Ile	Thr	Gln	
145					150					155					160	
Gln	Ser	Asn	Lys	Leu	Glu	Thr	Gly	Lys	Ser	Arg	Val	Pro	Pro	Thr	Val	
				165					170					175		
Thr	Asn	Ala	Val	Ser	Trp	Arg	Ser	Glu	Gly	Ile	Lys	Tyr	Lys	Lys	Asn	
			180					185					190			
Glu	Val	Phe	Ile	Asp	Val	Ile	Glu	Ser	Val	Asn	Leu	Leu	Val	Asn	Ala	
		195					200					205				
Asn	Gly	Ser	Val	Leu	Leu	Ser	Glu	Ile	Val	Gly	Thr	Ile	Lys	Leu	Lys	
	210					215					220					
Val	Phe	Leu	Ser	Gly	Met	Pro	Glu	Leu	Arg	Leu	Gly	Leu	Asn	Asp	Arg	
225					230					235					240	
Val	Leu	Phe	Glu	Leu	Thr	Gly	Arg	Ser	Lys	Asn	Lys	Ser	Val	Glu	Leu	
				245					250					255		
Glu	Asp	Val	Lys	Phe	His	Gln	Cys	Val	Arg	Leu	Ser	Arg	Phe	Asp	Asn	
			260					265					270			
Asp	Arg	Thr	Ile	Ser	Phe	Ile	Pro	Pro	Asp	Gly	Asp	Phe	Glu	Leu	Met	
		275					280					285				
Ser	Tyr	Arg	Leu	Ser	Thr	Gln	Val	Lys	Pro	Leu	Ile	Trp	Ile	Glu	Ser	
	290					295					300					
Val	Ile	Glu	Lys	Phe	Ser	His	Ser	Arg	Val	Glu	Ile	Met	Val	Lys	Ala	
305					310					315					320	
Lys	Gly	Gln	Phe	Lys	Lys	Gln	Ser	Val	Ala	Asn	Gly	Val	Glu	Ile	Ser	
				325					330					335		
Val	Pro	Val	Pro	Ser	Asp	Ala	Asp	Ser	Pro	Arg	Phe	Lys	Thr	Ser	Val	
			340					345					350			
Gly	Ser	Ala	Lys	Tyr	Val	Pro	Glu	Arg	Asn	Val	Val	Ile	Trp	Ser	Ile	

		355					360					365				
Lys	Ser 370	Phe	Pro	Gly	Gly	Lys 375	Glu	Tyr	Leu	Met	Arg 380	Ala	His	Phe	Gly	
Leu 385	Pro	Ser	Val	Glu	Lys 390	Glu	Glu	Val	Glu	Gly 395	Arg	Pro	Pro	Ile	Gly 400	
Val	Lys	Phe	Glu	Ile 405	Pro	Tyr	Phe	Thr	Val 410	Ser	Gly	Ile	Gln	Val 415	Arg	
Tyr	Met	Lys	Ile 420	Ile	Glu	Lys	Ser	Gly 425	Tyr	Gln	Gly	Pro	Ala 430	Leu	Gly	
Phe	Arg	Tyr 435	Ile	His	Pro	Glu	Trp 440	Ala	Ile	Thr	Asn	Phe 445	Arg	Tyr	Gln	
Leu 450	Gly	Arg	Gly	Glu	Glu	Met 455	Gly	Gly	Phe							
<210> 227																
<211> 120																
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<213> homo sapiens																
<400> 227																
Leu 1	Val	Thr	Lys	Val 5	Gly	Asn	Arg	Pro	Leu 10	Trp	Val	Asn	Val	Ala 15	Lys	
Pro	Gln	Gly	Arg 20	Ala	Leu	Val	Thr	Thr 25	Phe	Leu	Asn	Asp	Leu 30	His	Val	
Ser	Asp	Leu 35	Asp	Pro	Arg	Asp	Gly 40	Glu	Val	Gly	Asp	Leu 45	Lys	Leu	Asp	
Pro	Asp 50	Gly	Gly	Pro	Ala	Leu 55	His	Leu	Phe	Leu	Phe 60	His	Thr	Gly	Glu	
Ala 65	Lys	Val	Gly	Ser	His 70	Gln	Val	Leu	Leu	Ala 75	Pro	Arg	Glu	Arg	Leu 80	
Asn	Thr	Pro	Asn	His 85	Asp	Val	Ser	Leu	Arg 90	His	Ile	Leu	Gly	Ala 95	Ala	
His	Thr	Gly	Leu 100	Glu	Ser	Gly	Gly	Val 105	Gly	Ile	Ala	Gly	Tyr 110	Arg	His	
Arg	Tyr	Leu 115	His	Thr	Val	Gly	His 120									
<210> 228																
<211> 246																
<212> PRT																
<213> homo sapiens																
<400> 228																
Gly 1	Ile	Ser	Asn	Leu 5	Thr	Pro	Met	Gly	Gly 10	Arg	Pro	Ser	Thr	Ser 15	Ser	
Phe	Ser	Thr	Leu 20	Gly	Arg	Pro	Lys	Trp 25	Ala	Arg	Ile	Lys	Tyr 30	Ser	Leu	



Pro	Pro	Gly 35	Lys	Asp	Leu	Ile	Leu 40	Gln	Ile	Thr	Thr	Phe 45	Leu	Ser	Gly
Thr	Tyr 50	Leu	Ala	Leu	Pro	Thr 55	Leu	Val	Leu	Asn	Leu 60	Gly	Glu	Ser	Ala
Ser 65	Leu	Gly	Thr	Gly	Thr 70	Asp	Ile	Ser	Thr	Pro 75	Leu	Ala	Thr	Asp	Cys 80
Phe	Leu	Asn	Cys	Pro 85	Leu	Ala	Leu	Thr	Met 90	Ile	Ser	Thr	Arg	Leu 95	Trp
Glu	Asn	Phe	Ser 100	Met	Thr	Asp	Ser	Ile 105	Gln	Ile	Ser	Gly	Leu 110	Thr	Trp
Val	Leu	Arg 115	Arg	Tyr	Asp	Met	Ser 120	Ser	Lys	Ser	Pro	Ser 125	Gly	Gly	Met
Lys	Glu 130	Met	Val	Arg	Ser	Leu 135	Ser	Lys	Arg	Glu	Ser 140	Arg	Thr	His	Trp
Trp 145	Asn	Phe	Thr	Ser	Ser 150	Ser	Ser	Thr	Asp	Leu 155	Phe	Leu	Leu	Arg	Pro 160
Val	Ser	Ser	Lys 165	Ser	Thr	Arg	Ser	Leu	Arg 170	Pro	Ser	Arg	Ser	Ser 175	Gly
Ile	Pro	Asp	Arg 180	Asn	Thr	Leu	Ser	Leu 185	Met	Val	Pro	Thr	Ile 190	Ser	Leu
Arg	Arg	Thr 195	Leu	Pro	Leu	Ala	Leu 200	Thr	Ser	Arg	Leu	Thr 205	Asp	Ser	Met
Thr	Ser 210	Met	Lys	Thr	Ser	Phe 215	Phe	Leu	Tyr	Leu	Ile 220	Pro	Ser	Glu	Arg
Gln 225	Asp	Thr	Ala	Leu	Val 230	Thr	Val	Gly	Gly	Thr 235	Arg	Asp	Leu	Pro	Val 240
Ser	Ser	Leu	Leu	Leu 245	Cys										

<210> 229  
 <211> 275  
 <212> PRT  
 <213> homo sapiens

<400> 229

Met 1	Asn	Thr	Arg	Leu 5	Gln	Val	Glu	His	Pro 10	Val	Thr	Glu	Met	Ile 15	Thr
Gly	Thr	Asp	Leu 20	Val	Glu	Trp	Gln	Leu 25	Arg	Ile	Ala	Ala	Gly 30	Glu	Lys
Ile	Pro	Leu 35	Ser	Gln	Glu	Glu	Ile 40	Thr	Leu	Gln	Gly	His 45	Ala	Phe	Glu
Ala	Arg 50	Ile	Tyr	Ala	Glu	Asp 55	Pro	Ser	Asn	Asn	Phe 60	Met	Pro	Val	Ala
Gly	Pro	Leu	Val	His	Leu	Ser	Thr	Pro	Arg	Ala	Asp	Pro	Ser	Thr	Arg

65					70					75					80				
Ile	Glu	Thr	Gly	Val	Arg	Gln	Gly	Asp	Glu	Val	Ser	Val	His	Tyr	Asp				
				85					90					95					
Pro	Met	Ile	Ala	Lys	Trp	Val	Val	Trp	Ala	Ala	Asp	Arg	Gln	Ala	Ala				
			100					105					110						
Leu	Thr	Lys	Leu	Arg	Tyr	Ser	Leu	Arg	Gln	Tyr	Asn	Ile	Val	Gly	Leu				
		115					120					125							
Pro	Thr	Asn	Ile	Asp	Phe	Leu	Leu	Asn	Leu	Ser	Gly	His	Pro	Glu	Phe				
	130					135					140								
Glu	Ala	Gly	Asn	Val	His	Thr	Asp	Phe	Ile	Pro	Gln	His	His	Lys	Gln				
145					150					155					160				
Leu	Leu	Leu	Ser	Arg	Lys	Ala	Ala	Ala	Lys	Glu	Ser	Leu	Cys	Gln	Ala				
				165					170					175					
Ala	Leu	Gly	Leu	Ile	Leu	Lys	Glu	Lys	Ala	Met	Thr	Asp	Thr	Phe	Thr				
			180					185					190						
Leu	Gln	Ala	His	Asp	Gln	Phe	Ser	Pro	Phe	Ser	Ser	Ser	Ser	Gly	Arg				
		195					200					205							
Arg	Leu	Asn	Ile	Ser	Tyr	Thr	Arg	Asn	Met	Thr	Leu	Lys	Asp	Gly	Lys				
	210					215					220								
Asn	Asn	Val	Ala	Ile	Ala	Val	Thr	Tyr	Asn	His	Asp	Gly	Ser	Tyr	Ser				
225					230					235					240				
Met	Gln	Ile	Glu	Asp	Lys	Thr	Phe	Gln	Val	Leu	Gly	Asn	Leu	Tyr	Ser				
				245					250					255					
Glu	Gly	Asp	Cys	Thr	Tyr	Leu	Lys	Cys	Ser	Val	Asn	Gly	Val	Ala	Ser				
			260					265					270						
Lys	Ala	Lys																	
		275																	

<210> 230  
 <211> 117  
 <212> PRT  
 <213> homo sapiens

<400> 230

Ser	Glu	Val	Ile	Ile	Leu	Glu	Asn	Thr	Ile	Tyr	Leu	Phe	Ser	Lys	Glu
1				5					10					15	
Gly	Ser	Ile	Glu	Ile	Asp	Ile	Pro	Val	Pro	Lys	Tyr	Leu	Ser	Ser	Val
			20					25					30		
Ser	Ser	Gln	Glu	Thr	Gln	Gly	Gly	Pro	Leu	Ala	Pro	Met	Thr	Gly	Thr
		35					40					45			
Ile	Glu	Lys	Val	Phe	Val	Lys	Ala	Gly	Asp	Lys	Val	Lys	Ala	Gly	Asp
	50					55					60				
Ser	Leu	Met	Val	Met	Ile	Ala	Met	Lys	Met	Glu	His	Thr	Ile	Lys	Ser
65					70					75					80



100						105					110				
Glu	Gln	Glu	Asn	Trp	His	Glu	Gly	Lys	Glu	Asn	Ile	Arg	Ala	Ala	Val
		115					120					125			
Ala	Ala	Gly	Cys	Arg	Gln	Ile	Gln	Asp	Leu	Glu	Leu	Ser	Ser	Val	Glu
	130					135					140				
Val	Asp	Pro	Cys	Gly	Asp	Ala	Gln	Ala	Ala	Ala	Glu	Gly	Ala	Val	Leu
145					150					155					160
Gly	Leu	Tyr	Glu	Tyr	Asp	Asp	Leu	Lys	Gln	Lys	Lys	Lys	Met	Ala	Val
				165					170					175	
Ser	Ala	Lys	Leu	Tyr	Gly	Ser	Gly	Asp	Gln	Glu	Ala	Trp	Gln	Lys	Gly
			180					185					190		
Val	Leu	Phe	Ala	Ser	Gly	Gln	Glu	Leu	Gly	His	Ala	Asn	Leu	Met	Gly
		195					200					205			
Asp	Ala	Ser	Gln	Leu	Arg	Leu	Thr	Pro	Thr	Arg	Phe	Cys	Arg	Asn	Tyr
	210					215					220				
Leu	Arg	Arg	Phe	Ser	Lys	Leu	Val	Val	Ser						
225					230										

&lt;210&gt; 233

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 233

Leu	Pro	Ile	Leu	Lys	Ile	Phe	Ser	Asn	Asn	Phe	Gly	Lys	Ile	Trp	Leu
1				5					10					15	
Ala	Ser	Ile	Ser	Ile	Gly	Trp	Arg	Leu	Pro	Ser	Asn	Trp	Arg	Ala	Gln
			20					25					30		
Val	Leu	Ala	Gln	Lys	Gln	Thr	Gly	Leu	Leu	Ser	Ala	Arg	Pro	Pro	Asp
		35					40					45			
Pro	His	Phe	His	Arg	Ala	Leu	Pro	Thr	Gln	Pro	Ser	Ser	Phe	Phe	Ala
	50					55					60				
Leu	Gly	His	Arg	Ile	His	Arg	Asp	Gln	Ala	Pro	Leu	Pro	Pro	Gln	Gln
65					70					75					80
Pro	Glu	Arg	Leu	His	Arg	Asp	Pro	Pro	Pro	Gln	Thr	Arg	Ala	Pro	Gly
				85					90					95	
Leu	Glu	Ser	Ala	Cys	Thr	Pro	Leu	Gln	Gln	Gln	Leu				
			100					105							

&lt;210&gt; 234

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 234

Cys	Phe	Leu	Cys	Leu	His	Ala	Ser	Phe	Pro	Val	Arg	Arg	Phe	Gln	Leu
1				5					10					15	

Pro	Phe	Cys	Arg	Gly	Gln	Leu	Ala	Pro	Arg	Trp	Gly	Ser	Pro	Asp	Ala
			20					25					30		
Asp	His	Lys	Arg	Phe	Glu	Ser	Ser	Leu	Pro	Ser	Glu	Val	Val	Gln	Ile
		35					40					45			
Cys	Ser	Lys	Ser	Leu	Ser	Ala	Phe	Gln	Leu	Thr	Ile	Tyr	Gln	Asn	Ser
	50					55					60				
Leu	Leu	His	Leu												
65															

<210> 235  
 <211> 187  
 <212> PRT  
 <213> homo sapiens

<400> 235

Gln	Arg	Val	Arg	Ala	Ala	Leu	Leu	Ser	Ser	Ala	Met	Glu	Asp	Ser	Glu
1				5					10					15	
Ala	Leu	Gly	Phe	Glu	His	Met	Gly	Leu	Asp	Pro	Arg	Leu	Leu	Gln	Ala
			20					25					30		
Val	Thr	Asp	Leu	Gly	Trp	Ser	Arg	Pro	Thr	Leu	Ile	Gln	Glu	Lys	Ala
		35					40					45			
Ile	Pro	Leu	Ala	Leu	Glu	Gly	Lys	Asp	Leu	Leu	Ala	Arg	Ala	Arg	Thr
	50					55					60				
Gly	Ser	Gly	Lys	Thr	Ala	Ala	Tyr	Ala	Ile	Pro	Met	Leu	Gln	Leu	Leu
65					70					75					80
Leu	His	Arg	Lys	Ala	Thr	Gly	Pro	Val	Val	Glu	Gln	Ala	Val	Arg	Gly
				85					90					95	
Leu	Val	Leu	Val	Pro	Thr	Lys	Glu	Leu	Ala	Arg	Gln	Ala	Gln	Ser	Met
			100					105					110		
Ile	Gln	Gln	Leu	Ala	Thr	Tyr	Cys	Ala	Arg	Asp	Val	Arg	Val	Ala	Asn
		115					120					125			
Val	Ser	Ala	Ala	Glu	Asp	Ser	Val	Ser	Gln	Arg	Ala	Val	Leu	Met	Glu
	130					135					140				
Lys	Pro	Asp	Val	Val	Val	Gly	Thr	Pro	Ser	Arg	Ile	Leu	Ser	His	Leu
145					150					155					160
Gln	Gln	Asp	Ser	Leu	Lys	Leu	Arg	Asp	Ser	Leu	Glu	Leu	Leu	Val	Val
				165					170					175	
Asp	Glu	Ala	Asp	Leu	Leu	Phe	Ser	Leu	Trp	Leu					
			180					185							

<210> 236  
 <211> 76  
 <212> PRT  
 <213> homo sapiens

<400> 236

00421 3662960

Asp 1	Ile	Gly	His	Ser 5	Asp	Ile	Pro	Ser	Thr 10	Val	Gly	Ser	Gln	Leu 15	Leu
Asn	His	Gly	Leu 20	Cys	Leu	Pro	Cys	Gln 25	Leu	Leu	Gly	Arg	Asn 30	Lys	Asn
Lys	Ala	Ser 35	His	Cys	Leu	Phe	Tyr 40	His	Arg	Thr	Cys	Arg 45	Leu	Pro	Met
Glu	Gln 50	Gln	Leu	Gln	His	Arg 55	Asn	Ser	Ile	Ser	Gly 60	Arg	Leu	Pro	Gly
Ala 65	Arg	Ala	Gly	Pro	Ser 70	Gln	Glu	Val	Leu	Pro 75	Phe				

<210> 237  
 <211> 112  
 <212> PRT  
 <213> homo sapiens

<400> 237

Thr 1	Gly	Leu	Cys	Asn 5	Ile	Ser	Ser	Leu	Ser 10	Ala	Cys	Thr	Ser	Ser 15	Leu
Lys	Val	Ala	Asp 20	Met	Arg	Lys	Ala	Leu 25	Leu	Lys	Ser	Gly	Gly 30	Lys	Val
Thr	Arg	Gly 35	Arg	Leu	Leu	Glu	Leu 40	Phe	Phe	Lys	Ala	Lys 45	Gly	Lys	Lys
Glu	Gly 50	Gln	Leu	Arg	Pro	Pro 55	Pro	Lys	Ala	Pro	Gly 60	Ser	His	Glu	Val
Ser 65	Gly	Cys	Leu	Ala	Ala 70	Ser	Gly	Leu	Ile	Cys 75	Glu	Met	Gly	Ser	Leu 80
Leu	Pro	His	Leu	Ala 85	Ser	Pro	Ser	Ala	Gln 90	Leu	Ser	Glu	Arg	Leu 95	Ser
Leu	Gln	Gln	Leu 100	Arg	His	Trp	Pro	Leu 105	Gly	His	Pro	Glu	His 110	Ser	Arg

<210> 238  
 <211> 108  
 <212> PRT  
 <213> homo sapiens

<400> 238

Cys 1	His	Ala	Arg	Leu 5	Asn	Thr	Asp	Ser	Ser 10	Arg	Leu	Ala	Met	Lys 15	Leu
Leu	Met	Val	Leu 20	Met	Leu	Ala	Ala	Leu 25	Leu	Leu	His	Cys	Tyr 30	Ala	Asp
Ser	Gly	Cys 35	Lys	Leu	Leu	Glu	Asp 40	Met	Val	Glu	Lys	Thr 45	Ile	Asn	Ser
Asp	Ile 50	Ser	Ile	Pro	Glu	Tyr 55	Lys	Glu	Leu	Leu	Gln 60	Glu	Phe	Ile	Asp
Ser	Asp	Ala	Ala	Ala	Glu	Ala	Met	Gly	Lys	Phe	Lys	Gln	Cys	Phe	Leu

004221-000000



Thr	Asp	Lys	Asp	Pro	Val	Phe	Ser
	50					55	

<210> 242  
 <211> 52  
 <212> PRT  
 <213> homo sapiens

<400> 242

Ile	Phe	Val	Ala	Met	Gly	Gln	Thr	Arg	Thr	Pro	Ser	Ser	Ala	Glu	Leu
1				5					10					15	
Arg	Lys	Ser	Pro	Ala	Thr	Ser	Leu	Ala	Ile	Lys	Leu	Gln	Pro	Ser	His
			20					25					30		
Pro	Thr	Arg	Ala	Ser	Glu	Glu	Trp	Pro	Leu	Leu	Ala	Gly	Asn	Pro	Leu
		35					40					45			
Gln	Trp	Ala	Ser												
	50														

<210> 243  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 243

Trp	Pro	Lys	Met	Ser	Gln	Asp	Phe	Ser	Leu	Val	Gln	Leu	Lys	Thr	Gly
1				5					10					15	
Ser	Leu	Ser	Val	Pro	Trp	Pro	Gln	Lys	Phe	Arg	Leu	Thr	Gly	Cys	Leu
			20					25					30		
Lys	Gly	Asp	Arg	Ser	Arg	Thr	Phe	Leu	Gly	Glu	Lys	Glu	Lys	Trp	Gly
		35					40					45			
Lys	Gln	Arg	Ser	Ser	Ile	Arg	Ser	Glu	Ser	Leu	Leu	Glu	Ser	Phe	Ser
	50					55					60				
Pro	Thr	Ala													
	65														

<210> 244  
 <211> 64  
 <212> PRT  
 <213> homo sapiens

<400> 244

Gly	Ser	Ser	Trp	Ala	Glu	Asp	Phe	Lys	Cys	Asp	Ile	Ser	Val	Pro	Lys
1				5					10					15	
Thr	Ser	Leu	Leu	Phe	Ala	Gln	Ser	Cys	Arg	Ser	Met	Tyr	Phe	Leu	Leu
			20					25					30		
Gln	Tyr	Val	Pro	Ile	Tyr	Lys	Phe	Ile	Ser	His	Thr	Tyr	Asn	Arg	Ala
		35					40					45			
His	Val	Cys	Thr	Cys	Thr	Arg	Thr	His	Thr	His	Ser	Leu	Ser	Thr	Arg
	50					55					60				

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<210> 245  
 <211> 74  
 <212> PRT  
 <213> homo sapiens

<400> 245

Ser 1	Gly	Pro	Leu	Leu 5	Pro	Ala	Lys	Asn	Arg 10	Glu	Val	Ala	Gly	Leu 15	Lys
Thr	Leu	Ser	Val 20	Thr	Phe	Gln	Phe	Leu 25	Lys	His	His	Cys	Tyr 30	Leu	Leu
Lys	Val	Val 35	Gly	Leu	Cys	Ile	Ser 40	Phe	Ser	Asn	Thr	Ser 45	Pro	Phe	Ile
Ser	Leu 50	Phe	Pro	Ile	His	Thr 55	Thr	Val	His	Met	Cys 60	Ala	Arg	Ala	His
Ala 65	His	Thr	His	Thr	His 70	Ser	Gln	Leu	Val						

<210> 246  
 <211> 69  
 <212> PRT  
 <213> homo sapiens

<400> 246

Ala 1	Arg	Ile	Gln	Thr 5	Pro	Glu	Gln	His	Ser 10	Gln	Val	Thr	Leu	Phe 15	Asp
Tyr	Asn	Glu	Glu 20	Met	Lys	Met	Gly	Gly 25	Tyr	Leu	Lys	Ile	Gly 30	Ile	Pro
Ser	Ala	Leu 35	Lys	Val	Ser	Lys	Leu 40	Leu	Thr	Cys	Glu	Gln 45	His	Arg	Thr
Pro	Leu 50	Leu	Trp	Ser	Ser	Phe 55	Gln	Leu	Arg	Met	Leu 60	Gln	Phe	Ser	Lys
Ser 65	Ile	Tyr	Tyr	Ser											

<210> 247  
 <211> 236  
 <212> PRT  
 <213> homo sapiens

<400> 247

Gln 1	Leu	Arg	Gly	Gly 5	Val	Gln	Arg	His	Asp 10	Arg	Arg	Glu	Gly	Glu 15	Met
Val	Cys	Val	Glu 20	Leu	Val	Ala	Ser	Asp 25	Lys	Thr	Asn	Thr	Phe 30	Gln	Gly
Val	Ile	Phe 35	Gln	Gly	Ser	Ile	Arg 40	Tyr	Glu	Ala	Leu	Lys 45	Lys	Val	Tyr
Asp	Asn 50	Arg	Val	Ser	Val	Ala 55	Ala	Arg	Met	Ala	Gln 60	Lys	Met	Ser	Phe

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Gly 65	Phe	Tyr	Lys	Tyr	Ser 70	Asn	Met	Glu	Phe	Val 75	Arg	Met	Lys	Gly	Pro 80
Gln	Gly	Lys	Gly	His 85	Ala	Glu	Met	Ala	Val 90	Ser	Arg	Val	Ser	Thr 95	Gly
Asp	Thr	Ala	Pro 100	Cys	Gly	Thr	Glu	Glu 105	Asp	Ser	Ser	Pro	Ala 110	Ser	Pro
Met	His	Glu 115	Arg	Val	Thr	Ser	Phe 120	Ser	Arg	Pro	Pro	Thr 125	Pro	Glu	Arg
Asn	Asn 130	Arg	Pro	Ala	Phe	Phe 135	Ser	Pro	Ser	Leu	Lys 140	Arg	Lys	Val	Pro
Arg 145	Asn	Arg	Ile	Ala	Glu 150	Met	Lys	Lys	Ser	His 155	Ser	Ala	Asn	Asp	Ser 160
Glu	Glu	Phe	Phe	Arg 165	Glu	Asp	Asp	Gly	Gly 170	Ala	Asp	Leu	His	Asn 175	Ala
Thr	Asn	Leu	Arg 180	Ser	Arg	Ser	Leu	Ser 185	Gly	Thr	Gly	Arg	Ser 190	Leu	Val
Gly	Ser	Trp 195	Leu	Lys	Leu	Asn	Arg 200	Ala	Asp	Gly	Asn	Phe 205	Leu	Leu	Tyr
Ala	His 210	Leu	Thr	Tyr	Val	Thr 215	Leu	Pro	Leu	His	Arg 220	Ile	Leu	Thr	Asp
Ile 225	Leu	Glu	Val	Arg	Gln 230	Lys	Pro	Ile	Leu	Met 235	Thr				

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<210> 248
<211> 161
<212> PRT
<213> homo sapiens
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<400> 248

Asp 1	Glu	Glu	Val	Ala 5	Leu	Gly	Gln	Arg	Gln 10	Arg	Gly	Val	Leu	Pro 15	Gly
Gly	Arg	Arg	Trp 20	Ser	Arg	Ser	Ala	Gln 25	Cys	Asn	Gln	Pro	Ala 30	Val	Ser
Val	Pro	Val 35	Gly	His	Arg	Thr	Val 40	Pro	Gly	Arg	Val	Leu 45	Ala	Glu	Ala
Glu	Gln 50	Ser	Arg	Trp	Lys	Leu 55	Pro	Ser	Leu	Cys	Thr 60	Leu	Asn	Leu	Arg
His 65	Val	Ala	Ala	Ala	Ser 70	Asp	Phe	Asn	Arg	His 75	Pro	Gly	Ser	Ser	Ala 80
Glu	Ala	His	Pro	Asp 85	Asp	Leu	Ala	Ala	Cys 90	Gly	Ala	Cys	Ala	Glu 95	Pro
Arg	Pro	Gly	Pro 100	Ala	Leu	Gly	Val	Leu 105	Pro	Ser	Ala	Tyr	Leu 110	Ser	Thr
Ala	Thr	Gly	Val	Cys	Asp	Gly	Thr	Pro	Val	Leu	Glu	Pro	Gln	Pro	Gly

		115					120					125				
Glu	Ala	Thr	Arg	Leu	Pro	Gly	Pro	Gly	Pro	Thr	Ala	Arg	Thr	Pro	Ala	
	130					135					140					
Gln	Thr	Glu	Val	Pro	Leu	Thr	Gly	Pro	Ala	Gly	Ala	Ala	Ser	Ala	Leu	
145					150					155					160	

Cys

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<210> 249
<211> 218
<212> PRT
<213> homo sapiens
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<400> 249

Val 1	Cys	Ile	Glu	Lys 5	Glu	Val	Ser	Ile	Cys 10	Ser	Val	Gln	Leu	Gln 15	Pro
Gly	Pro	Asp	Gln 20	Gly	Pro	Ser	Cys	Ala 25	Arg	Gln	Gly	Pro	Arg 30	Pro	Gln
Val	Gly	Cys 35	Ile	Val	Gln	Ile	Gly 40	Ser	Thr	Val	Val	Leu 45	Pro	Glu	Glu
Leu	Leu 50	Ala	Val	Val	Gly	Arg 55	Val	Arg	Leu	Leu	His 60	Leu	Ser	Asp	Pro
Val 65	Pro	Gly	His	Leu	Pro 70	Leu	Glu	Gly	Trp	Gly 75	Glu	Glu	Gly	Arg	Pro 80
Val	Val	Pro	Phe	Trp 85	Gly	Gly	Gly	Ser	Ala 90	Glu	Gly	Gly	His	Pro 95	Leu
Val	His	Gly	Arg 100	Ser	Trp	Ala	Gly	Val 105	Leu	Phe	Ser	Pro	Thr 110	Gly	Gly
Cys	Val	Thr 115	Cys	Arg	His	Ser	Ala 120	Asp	Arg	His	Leu	Gly 125	Val	Ala	Leu
Ala	Leu 130	Gly	Ala	Leu	His	Ala 135	His	Lys	Leu	His	Val 140	Ala	Val	Leu	Val
Glu 145	Ala	Lys	Arg	His	Leu 150	Leu	Cys	His	Ala	Gly 155	Gly	His	Ala	His	Pro 160
Val	Val	Ile	His	Leu 165	Leu	Glu	Arg	Leu	Val 170	Ala	Asp	Gly	Ala	Leu 175	Lys
Asp	Asp	Pro	Leu 180	Glu	Arg	Val	Gly	Phe 185	Val	Thr	Ser	His	Gln 190	Leu	His
Thr	Asp	His 195	Leu	Ser	Phe	Pro	Thr 200	Val	Met	Ser	Leu	Asn 205	Thr	Ser	Ser
Lys	Leu 210	Ser	Ile	Met	Lys	Lys 215	Met	Leu	Gly						

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<210> 250
<211> 133
<212> PRT
<213> homo sapiens
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&lt;400&gt; 250

Tyr 1	Pro	Gln	Asp	Pro 5	Pro	Gly	Gly	Ala	Ser 10	Arg	Arg	Leu	Leu	Asp 15	Asp
Leu	Glu	Leu	Cys 20	Pro	Gly	Glu	Lys	Thr 25	Ala	Pro	Val	Trp	Ala 30	Leu	Ser
Ala	Glu	Glu 35	Glu	Ala	Ala	Met	His 40	Phe	Ser	Leu	Ala	Phe 45	Phe	Leu	His
Gly	Ser 50	Ser	Val	Phe	Leu	Gln 55	Ile	Thr	Cys	Cys	His 60	Glu	Phe	Leu	Cys
Met 65	Arg	His	Ile	Ser	Ser 70	Cys	Leu	Tyr	Ala	Glu 75	Val	Pro	Phe	Ile	Leu 80
Ser	Ile	Gly	Trp	Trp 85	Thr	Gly	Glu	Arg	Gly 90	Pro	Arg	Cys	Pro	Thr 95	Ser
Cys	Ala	Ser	Ala 100	Val	Gly	Gly	Asp	Arg 105	Ala	Pro	Arg	His	Gly 110	Gly	Gly
Gly	His	Leu 115	Pro	His	Val	Trp	Gly 120	Gly	Arg	Arg	His	Pro 125	Gly	Thr	Glu
Gly	Ser 130	Leu	Gln	Arg											

&lt;210&gt; 251

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 251

Arg 1	Leu	Pro	Ser	Val 5	Pro	Gly	Cys	Leu	Arg 10	Pro	Pro	Gln	Thr	Cys 15	Gly
Arg	Cys	Pro	Pro 20	Pro	Pro	Cys	Leu	Gly 25	Ala	Arg	Ser	Pro	Pro 30	Thr	Ala
Leu	Ala	His 35	Asp	Val	Gly	His	Leu 40	Gly	Pro	Leu	Ser	Pro 45	Val	His	Gln
Pro	Ile 50	Glu	Arg	Met	Lys	Gly 55	Thr	Ser	Ala	Tyr	Arg 60	His	Asp	Glu	Ile
Cys 65	Leu	Met	His	Lys	Asn 70	Ser									

&lt;210&gt; 252

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 252

Arg 1	Gly	Leu	Gln	His 5	Thr	Asp	Met	Met	Lys 10	Tyr	Ala	Ser	Cys	Ile 15	Lys
Ile	His	Asp	Asn	Met	Leu	Phe	Ala	Lys	Lys	Gln	Thr	Asn	His	Ala	Gly



[illegible]

Arg 1	Phe	His	Gly	Phe 5	Pro	Leu	Val	Arg	Ile 10	Leu	Leu	Tyr	Phe	Ser 15	Phe
Gln	Lys	Phe	Arg 20	Val	Lys	Ile	Asp	Asn 25	Phe	Val	Ser	Asp	Ala 30	Phe	Gln
Gly	Ile	Thr 35	Val	Glu	Pro	Gly	Pro 40	Glu	Met	Val	Cys	Cys 45	Ile	Val	Glu
Ser	Asn 50	Asn	Val	Glu	Asn	His 55	Ile	Gly	Ala	Ser	Val 60	Val	Leu	Asn	Ala
Val 65	Tyr	Ser	Cys	Asn	Gly 70	Pro	Pro	Lys	Pro	Val 75	Phe	Arg	Cys	Ser	Asp 80
Asp	His	Arg	Asn	Leu 85	Leu	Leu	Ser	Pro	Ile 90	Tyr	Cys	Met	Ser	Glu 95	Ser
Ile	Trp	Asp	Lys 100	Val	Tyr	Arg	Leu	Arg 105	Pro	Tyr	Asn	Ser			

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<210> 255
<211> 57
<212> PRT
<213> homo sapiens
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<400> 255

Asn 1	Leu	Ala	Lys	Val 5	Lys	Gly	Phe	Met	Asp 10	Ser	Pro	Trp	Ser	Gly 15	Ser
Ser	Phe	Thr	Phe 20	Pro	Ser	Lys	Ser	Leu 25	Gly	Ser	Lys	Leu	Thr 30	Ile	Leu
Tyr	Leu	Met 35	Leu	Phe	Arg	Glu	Ser 40	Leu	Leu	Ser	Gln	Asp 45	Arg	Arg	Trp
Ser	Ala 50	Val	Leu	Leu	Arg	Val 55	Thr	Met							

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<210> 256
<211> 230
<212> PRT
<213> homo sapiens
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<400> 256

Leu 1	Pro	Ala	Ala	Thr 5	Asn	Arg	Leu	Lys	Arg 10	Gly	Lys	Gly	Ser	Ser 15	Thr
Gly	Ser	Ser	Ser 20	Gly	Asn	His	Gly	Gly 25	Ser	Gly	Gly	Gly	Asn 30	Gly	His
Lys	Pro	Gly 35	Cys	Glu	Lys	Pro	Gly 40	Asn	Glu	Ala	Arg	Gly 45	Ser	Gly	Lys
Ser	Gly 50	Ile	Gln	Gly	Phe	Arg 55	Gly	Gln	Gly	Val	Ser 60	Ser	Asn	Met	Arg
Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser	Gly	Asp	Asn

65				70				75				80			
Tyr	Arg	Gly	Gln	Gly 85	Ser	Ser	Trp	Gly	Ser 90	Gly	Gly	Gly	Asp	Ala 95	Val
Gly	Gly	Val	Asn 100	Thr	Val	Asn	Ser	Glu 105	Thr	Ser	Pro	Gly	Met 110	Phe	Asn
Phe	Asp	Thr 115	Phe	Trp	Lys	Asn	Phe 120	Lys	Ser	Lys	Leu	Gly 125	Phe	Ile	Asn
Trp	Asp 130	Ala	Ile	Asn	Lys	Asn 135	Gln	Val	Pro	Pro	Pro 140	Ser	Thr	Arg	Ala
Leu 145	Leu	Tyr	Phe	Ser	Arg 150	Leu	Trp	Glu	Asp	Phe 155	Lys	Gln	Asn	Thr	Pro 160
Phe	Leu	Asn	Trp	Lys 165	Ala	Ile	Ile	Glu	Gly 170	Ala	Asp	Ala	Ser	Ser 175	Leu
Gln	Lys	Arg	Ala 180	Gly	Arg	Ala	Glu	Ser 185	Glu	Leu	Gln	Leu	Gln 190	Pro	Ala
Cys	Val	Ser 195	His	Cys	Leu	Trp	Trp 200	Glu	Val	Leu	Ser	Gln 205	Asp	Pro	Cys
Lys	Gly 210	Gly	Glu	Ser	His	Leu 215	Leu	Pro	Arg	Leu	Pro 220	Gly	Cys	Asn	Leu
Gly 225	Leu	Leu	Ala	Val	Gly 230										
<210> 257															
<211> 141															
<212> PRT															
<213> homo sapiens															
<400> 257															
Thr 1	Arg	Thr	Arg	Ser 5	Arg	Pro	Pro	Ala	Pro 10	Glu	Pro	Ser	Ser	Thr 15	Ser
Ala	Asp	Ser	Gly 20	Arg	Ile	Ser	Asn	Arg 25	Thr	Leu	Leu	Ser	Ser 30	Thr	Gly
Lys	Gln	Leu 35	Leu	Arg	Val	Arg	Thr 40	Arg	His	His	Cys	Arg 45	Asn	Val	Gln
Ala	Glu 50	Pro	Ser	Gln	Asn	Tyr 55	Asn	Tyr	Asn	Gln	His 60	Ala	Tyr	Pro	Thr
Ala 65	Tyr	Gly	Gly	Lys	Tyr 70	Ser	Val	Lys	Thr	Pro 75	Ala	Lys	Gly	Gly	Ser 80
Leu	Thr	Phe	Phe	Leu 85	Gly	Phe	Pro	Gly	Ala 90	Thr	Trp	Ala	Cys	Leu 95	Gln
Leu	Gly	Glu	Val 100	Leu	Val	Arg	Gln	Phe 105	Leu	Ala	Thr	Asn	His 110	Arg	Arg
Pro	Arg	Lys 115	Lys	His	Trp	Val	Arg 120	Gln	Gly	Lys	Leu	Leu 125	Pro	Pro	Leu

Gly	Pro	Pro	Ala	Leu	Trp	Gln	Ala	Pro	Gly	Pro	Gly	Leu
	130					135					140	

<210> 258  
 <211> 165  
 <212> PRT  
 <213> homo sapiens

<400> 258

Arg	Val	Arg	Thr	Leu	Asn	Asn	Cys	Phe	Pro	Val	Glu	Glu	Arg	Ser	Val
1				5					10					15	
Leu	Phe	Glu	Ile	Leu	Pro	Glu	Ser	Ala	Glu	Val	Glu	Glu	Gly	Ser	Gly
			20					25					30		
Ala	Gly	Gly	Arg	Asp	Leu	Val	Leu	Val	Tyr	Gly	Ile	Pro	Val	Asp	Glu
		35					40					45			
Thr	Gln	Leu	Gly	Phe	Lys	Ile	Leu	Pro	Glu	Ser	Val	Lys	Val	Lys	His
	50					55					60				
Pro	Arg	Arg	Arg	Leu	Arg	Val	His	Ser	Ile	Asp	Ser	Thr	Asn	Ser	Val
65					70					75					80
Thr	Ser	Ser	Thr	Ala	Pro	Ala	Arg	Pro	Leu	Pro	Pro	Ile	Ile	Val	Ser
				85					90					95	
Arg	Ala	Ser	Lys	Glu	Ala	Ile	Ala	Leu	Phe	Ala	Tyr	Phe	Pro	His	Val
			100					105					110		
Ala	Gly	Asn	Ser	Leu	Ser	Ser	Glu	Ala	Leu	Asn	Pro	Arg	Phe	Pro	Ala
		115					120					125			
Pro	Ala	Gly	Phe	Ile	Pro	Trp	Leu	Phe	Thr	Pro	Gly	Phe	Met	Ser	Ile
	130					135					140				
Ser	Ser	Ala	Ala	Pro	Thr	Val	Val	Ala	Gly	Gly	Gly	Ala	Gly	Ala	Gly
145					150					155					160
Ser	Leu	Pro	Pro	Leu											
				165											

<210> 259  
 <211> 126  
 <212> PRT  
 <213> homo sapiens

<400> 259

Glu	Arg	Ser	His	Leu	Gln	Pro	Gly	Ala	Val	Gly	Ile	Thr	Glu	Ser	Pro
1				5					10					15	
Ile	Leu	Gly	Leu	Gly	Ser	Ala	Met	Thr	Thr	Glu	Ile	Gly	Trp	Trp	Lys
			20					25					30		
Leu	Thr	Phe	Leu	Arg	Lys	Lys	Lys	Ser	Thr	Pro	Lys	Val	Leu	Tyr	Glu
		35					40					45			
Ile	Pro	Asp	Thr	Tyr	Ala	Gln	Thr	Glu	Gly	Asp	Ala	Glu	Pro	Pro	Arg
	50					55					60				
Pro	Asp	Ala	Gly	Gly	Pro	Asn	Ser	Asp	Phe	Asn	Thr	Arg	Leu	Glu	Lys

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65					70					75					80
Ile	Val	Asp	Lys	Ser	Thr	Lys	Gly	Lys	His	Val	Lys	Val	Ser	Asn	Ser
				85					90					95	
Gly	Arg	Phe	Lys	Glu	Lys	Lys	Lys	Val	Arg	Ala	Thr	Leu	Ala	Glu	Asn
			100					105					110		
Pro	Asn	Leu	Phe	Asp	Asp	His	Glu	Glu	Gly	Arg	Ser	Ser	Lys		
		115					120					125			

<210> 260  
 <211> 121  
 <212> PRT  
 <213> homo sapiens

<400> 260

Tyr	Val	Leu	Asn	Thr	Ile	Ile	Val	Gly	Lys	Gly	Glu	Glu	Lys	Ile	Pro
1				5					10					15	
His	Pro	Leu	Pro	Arg	Phe	Gly	Pro	Cys	Ser	Phe	Pro	Leu	Arg	Val	Cys
			20					25					30		
Asp	Leu	Pro	Ser	Ala	Lys	Val	Met	Ala	Lys	Thr	Gly	Thr	Asn	Arg	Pro
		35					40					45			
Asn	Tyr	His	Gln	Ser	Ser	Leu	Leu	Gln	His	Pro	Asn	Arg	Val	Pro	Gly
	50					55					60				
Ser	Ser	Val	Pro	Ser	Ala	Pro	Glu	Gly	Lys	Val	Pro	Gly	Ser	Leu	Leu
					70					75					80
Pro	Val	Leu	Gly	Gly	Glu	Leu	Lys	Phe	Ser	Val	Ser	Ala	Ser	Gly	Ser
				85					90					95	
Thr	Glu	Thr	Ser	Pro	Tyr	His	Val	Ala	Ser	Gly	Lys	Cys	Ala	Leu	Leu
			100					105					110		
Arg	Ile	Gly	Pro	Gly	Ser	Ser	His	Arg							
		115					120								

<210> 261  
 <211> 86  
 <212> PRT  
 <213> homo sapiens

<400> 261

Thr	Arg	Val	Pro	Leu	Tyr	Val	Val	Arg	Gly	Arg	Val	Glu	Asp	Pro	Gly
1				5					10					15	
Ile	Ser	Gln	Ala	Leu	Gln	Lys	Trp	Arg	His	Ile	Asn	Thr	Asn	Leu	Lys
			20					25					30		
Asn	Ser	His	Phe	Leu	Pro	Ala	Gly	Ile	Asn	Trp	Pro	His	Ser	Phe	Ser
		35					40					45			
Tyr	Gly	Gln	Arg	Gly	Gln	Arg	Gly	Lys	Val	Leu	Ser	Gln	Ile	Trp	Leu
	50					55					60				
Met	Ala	Gly	Ser	Gln	Glu	Val	Leu	Ala	Pro	Ser	Ser	Ala	Leu	His	Phe
					70					75					80

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Asp Asp Arg Pro Ser Ser  
85

<210> 262  
<211> 73  
<212> PRT  
<213> homo sapiens

<400> 262

Gly	Ser	Gly	Ser	Pro	Ala	Pro	Arg	Lys	Leu	His	Asp	Phe	Ala	Leu	Cys
1				5					10					15	
Ser	Ala	Pro	Leu	Cys	Pro	Leu	Phe	Pro	Arg	Glu	Thr	Ser	Arg	Ser	His
			20					25					30		
Ile	Phe	Leu	Thr	Asp	Phe	Glu	Ala	Val	Cys	Leu	His	Ser	Asp	Trp	Glu
		35					40					45			
His	Trp	Asp	His	Phe	His	His	Ala	Asp	Ser	Gly	Gly	Asn	Gly	Cys	Ile
	50					55					60				
Pro	Phe	His	Asp	Pro	Thr	Cys	Val	Tyr							
65					70										

<210> 263  
<211> 106  
<212> PRT  
<213> homo sapiens

<400> 263

Phe	Val	Ala	Met	Cys	Ser	Lys	Gln	Ala	Ser	Leu	Asn	His	Gly	Leu	Leu
1				5					10					15	
Gly	Leu	Thr	Leu	Val	Phe	Leu	Gly	Pro	Leu	Asn	Arg	His	Arg	Ser	Gly
			20					25					30		
His	Gly	Lys	Gly	Tyr	Ile	His	Tyr	His	His	Cys	Arg	His	Asp	Glu	Asn
		35					40					45			
Asp	Pro	Ser	Val	Pro	Asn	Gln	Asn	Ala	Asn	Arg	Gln	Leu	Gln	Asn	Gln
	50					55					60				
Ser	Arg	Lys	Cys	Gly	Ile	Trp	Lys	Ser	Leu	Leu	Glu	Arg	Gly	Gly	Arg
65					70					75					80
Gly	Glu	Leu	Ser	Arg	Gly	Arg	Asn	Arg	Ala	Val	Tyr	Ala	Glu	Leu	Gly
				85					90					95	
Thr	Pro	Ser	Leu	Arg	Ala	Arg	Gly	Gly	Arg						
			100					105							

<210> 264  
<211> 66  
<212> PRT  
<213> homo sapiens

<400> 264

Val	Leu	Arg	Trp	Tyr	Ser	Ser	Asp	Pro	Ser	Ile	Asp	Thr	Gly	Arg	Val
1				5					10					15	

000221" 00000000



Cys   Pro   Ala   Arg   Ser   Val   Ser   Arg   Arg   Pro   Ala   Pro   Gly   Leu   Cys   Ser  
85                      90                      95

Asp   Leu   Ala   Leu   Ala   Ala   Pro   Arg   Pro   Ser   Gly   Arg   Ser  
              100  105

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<210> 267
<211> 157
<212> PRT
<213> homo sapiens
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<400> 267

Ile Glu Ala Ala Gly Cys Thr Phe Pro Leu Leu Arg Cys Val Ser Phe  
1 5 10 15

Leu Phe His Ser Ala Leu Thr Ala Ala Ala Lys Ala Ala Ala Thr Ala  
20 25 30

Ala Arg Glu Arg Pro Gly Gly Gln Phe Ser Ser Ser Cys Ala Pro Ala  
35 40 45

Leu    Leu   Gly   Gln   Ser   Val   Gly   Gly   Arg   Arg   Pro   Ala   Cys   Ala   Gln   Thr  
          50               55               60

Ser Arg Leu Arg Arg Pro Gly Pro Ala Ala Val Ala Ser Val Trp Pro  
65 70 75 80

Glu Asn Leu Gly Ala Pro Ala Ala Arg Ala Pro Arg Ala Glu Pro Arg  
85 90 95

Ser Gly Ser Arg Gly Gly Arg Arg Val Ser Glu Ser Glu Gly Trp Pro  
100 105 110

Gly Gln Val Val Ala Pro Arg Arg Trp Ser Pro Ser Lys Gly Ser Val  
115 120 125

Trp	Pro	Thr	Arg	Ser	Thr	Ala	Arg	Thr	Ser	Pro	Ser	Ala	Ala	Thr	Ser
	130					135					140				

Pro	Arg	Pro	Arg	Glu	Met	Pro	Pro	Lys	Arg	Arg	Arg	Leu
145					150					155		

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<210> 268
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<212> PRT
<213> homo sapiens
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<400> 268

Ser Ser Ala Gln Gly Glu Glu Pro Gly Pro Gly Arg Arg Leu Leu Arg  
1 5 10 15

Ala   Pro   Thr   Glu   Ser   Arg   Ser   Glu   Gly   Lys   Ser   Met   Phe   Ala   Gly   Val  
                  20                  25                  30

Pro	Thr	Met	Arg	Glu	Ser	Ser	Pro	Lys	Gln	Tyr	Met	Gln	Leu	Gly	Gly
		35					40					45			

Arg Val Leu Leu Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala  
50 55 60

Ser Phe Phe Ser Ile Val Gln Asn Ile Val Gly Thr Ala Leu Met Ile

65				70				75				80			
Leu	Val	Ala	Ile	Gly 85	Phe	Lys	Thr	Lys	Leu	Ala	Ala	Leu	Thr	Leu 95	Val
Val	Trp	Leu	Phe 100	Ala	Ile	Asn	Val	Tyr 105	Phe	Asn	Ala	Phe	Trp 110	Thr	Ile
Pro	Val	Tyr 115	Lys	Pro	Met	His	Asp 120	Phe	Leu	Lys	Tyr	Asp 125	Phe	Phe	Gln
Thr	Met 130	Ser	Val	Ile	Gly	Gly 135	Leu	Leu	Leu	Val	Val 140	Ala	Leu	Gly	Pro
Gly 145	Gly	Val	Ser	Met	Asp 150	Glu	Lys	Lys	Lys	Glu 155	Trp				

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<211> 112
<212> PRT
<213> homo sapiens
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Leu 1	Gly	Ala	Cys	Ser 5	Trp	Trp	Trp	Pro	Trp 10	Ala	Leu	Gly	Val	Ser 15	Pro
Trp	Met	Arg	Arg 20	Arg	Arg	Ser	Gly	Asn 25	Ser	His	Arg	Ser	Leu 30	Pro	Ala
Trp	Leu	Arg 35	Pro	Val	Ala	Val	Lys 40	Asp	Trp	Phe	Gly	Val 45	Asp	Ser	Thr
Lys	Leu 50	Pro	Ala	Phe	Met	Tyr 55	Pro	Leu	Pro	Phe	Pro 60	Ser	Leu	Gly	Lys
Gly 65	Thr	Asp	Val	Leu	Arg 70	Thr	Leu	Phe	Ala	Glu 75	Thr	Pro	Glu	Asn	Arg 80
Trp	Leu	Ser	Leu	Leu 85	Trp	Ser	His	Ser	Leu 90	Ala	Ser	Asp	Pro	Ser 95	Val
Gln	Ala	Ser	Leu 100	Ala	Ala	Gly	Ser	Leu 105	Pro	His	Ala	Glu	Ala 110	Leu	Glu

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<212> PRT
<213> homo sapiens
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Ser 1	Gln	Arg	Val	Cys 5	Lys	Tyr	Ser	Pro	Gly 10	Ser	Leu	Leu	Pro	Tyr 15	Pro
Arg	Ile	Leu	Val 20	Arg	Ser	Ser	Asn	Gly 25	Phe	Arg	Thr	Trp	Val 30	Leu	Phe
Ser	Cys	Asp 35	His	Ser	Ser	Ala	His 40	Cys	Met	Lys	Thr	Gly 45	Leu	Ser	Gln
Cys	Phe 50	Asn	Leu	Thr	Arg	Ala 55	Val	Ser	Trp	Ser	Thr 60	Pro	Arg	Ser	Leu

Leu 65	Val	Pro	Tyr	Asp	Ser 70	Pro	His	Gln	Met	Thr 75	Leu	Ala	Lys	Ser	Arg 80
Phe	Leu	Cys	Gly	Gln 85	Gly	Trp	Leu	Ala	Asp 90	Trp	Trp	Lys	Val	Gly 95	Trp
Thr	Lys	Gly	Gly 100	His	Val	Ser	Ser	Gln 105	His	Gln	Phe	Cys	Thr 110	Ser	Ser
Ala	Ser	Val 115	Leu	Val	Gly	Val	Pro 120	Val	Ser	Pro	Gly	Pro 125	Gly	Trp	Ala
Arg	Ala 130														

<210> 271  
 <211> 267  
 <212> PRT  
 <213> homo sapiens

<400> 271

Gly 1	Thr	Ser	Gly	Thr 5	Ser	His	Leu	His	Pro 10	Arg	Ser	Ile	Cys	Met 15	Ile
Gln	Lys	Tyr	Asn 20	His	Asp	Gly	Glu	Ala 25	Gly	Arg	Leu	Glu	Ala 30	Phe	Ser
Gln	Gly	Glu 35	Ser	Val	Leu	Lys	Glu 40	Pro	Lys	Tyr	Gln	Glu 45	Glu	Leu	Glu
Asp	Arg 50	Leu	His	Phe	Tyr	Val 55	Glu	Glu	Cys	Asp	Tyr 60	Leu	Gln	Gly	Phe
Gln 65	Ile	Leu	Cys	Asp	Leu 70	His	Asp	Gly	Phe	Ser 75	Gly	Val	Gly	Ala	Lys 80
Ala	Ala	Glu	Leu	Leu 85	Gln	Asp	Glu	Tyr	Ser 90	Gly	Arg	Gly	Ile	Ile 95	Thr
Trp	Gly	Leu	Leu 100	Pro	Gly	Pro	Tyr	His 105	Arg	Gly	Glu	Ala	Gln 110	Arg	Asn
Ile	Tyr	Arg 115	Leu	Leu	Asn	Thr	Ala 120	Phe	Gly	Leu	Val	His 125	Leu	Thr	Ala
His	Ser 130	Ser	Leu	Val	Cys	Pro 135	Leu	Ser	Leu	Gly	Gly 140	Ser	Leu	Gly	Leu
Arg 145	Pro	Glu	Pro	Pro	Val 150	Ser	Phe	Pro	Tyr	Leu 155	His	Tyr	Asp	Ala	Thr 160
Leu	Pro	Phe	His	Cys 165	Ser	Ala	Ile	Leu	Ala 170	Thr	Ala	Leu	Asp	Thr 175	Val
Thr	Val	Pro	Tyr 180	Arg	Leu	Cys	Ser	Ser 185	Pro	Val	Ser	Met	Val 190	His	Leu
Ala	Asp	Met 195	Leu	Ser	Phe	Cys	Gly 200	Lys	Lys	Val	Val	Thr 205	Ala	Gly	Ala
Ile	Ile	Pro	Phe	Pro	Leu	Ala	Pro	Gly	Gln	Ser	Leu	Pro	Asp	Ser	Leu

00221" 3622960

002215552350

	210					215					220				
Met	Gln	Phe	Gly	Gly	Ala	Thr	Pro	Trp	Thr	Pro	Leu	Cys	Ala	Cys	Gly
225					230					235					240
Glu	Pro	Ser	Gly	Thr	Arg	Cys	Phe	Ala	Gln	Ser	Val	Val	Leu	Arg	Gly
				245					250					255	
Tyr	Arg	Gln	Ser	Met	Pro	His	Lys	Pro	Gln	Thr					
			260					265							

<210> 272  
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 <212> PRT  
 <213> homo sapiens

<400> 272

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Arg	Gln	Glu	Ser	Cys	Glu	Gln	Ser	Gly	Ala	Arg	Asp	Gln	Lys	Leu	Cys
			20					25					30		
Leu	Ile	Asp	Asp	Arg	Cys	Phe	Ser	Gly	Pro	Pro	His	Asp	Gly	Arg	Asp
		35					40					45			
Gln	Val	Ala	Gly	Pro	Arg	Leu	Leu	Phe	Pro	Ala	Leu	Asn	Ile	His	Leu
	50					55					60				
Val	Ala	Ala	Leu	Pro	Pro	Ser	Arg	Leu	Pro	Gln	Arg	Ser	His	Arg	Ala
	65				70					75					80
Gly	His	Thr	Gly	Ser	Gly	Ser	Pro	Ala	Ser	Ser	His	Ile	Pro	Pro	Arg
				85					90					95	
Arg	Asn	Ala	Ala	Cys	Pro	Pro	Ala	Leu	Pro	Gly	Thr	Trp	Val	Pro	Leu
			100					105					110		
Gly	His	Phe	Pro	Leu	Gly										
		115													

<210> 273  
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 <212> PRT  
 <213> homo sapiens

<400> 273

Leu	Gly	Lys	Ala	Thr	Cys	Ser	Arg	Arg	Leu	Pro	Thr	Cys	Thr	Gln	Trp
1				5					10					15	
Gly	Pro	Trp	Gly	Gly	Ser	Ser	Lys	Leu	His	Gln	Gly	Ile	Arg	Lys	Gly
			20					25					30		
Leu	Ala	Trp	Ser	Gln	Gly	Glu	Arg	Asp	Asp	Cys	Ser	Cys	Cys	His	His
		35					40					45			
Leu	Phe	Pro	Thr	Glu	Ala	Gln	His	Val	Ser	Gln	Met	Asn	His	Gly	Asn
	50					55					60				
Trp	Arg	Gly	Thr	Gln	Ala	Ile	Arg	Asn	Ser	Asp	Cys	Val	Gln	Gly	Cys
	65				70					75					80

Ser	Gln	Asp	Gly	Thr 85	Ala	Val	Glu	Gly	Gln 90	Ser	Gly	Ile	Ile	Met 95	Gln
Val	Arg	Glu	Ala 100	Asp	Arg	Trp	Leu	Gly 105	Ser	Gln	Ala	Gln	Ala 110	Pro	Thr
Gln	Gly	Gln 115	Gly	Ala	Asp	Lys	Arg 120	Ala	Val	Ser	Ser	Gln 125	Val	His	Glu
Thr	Lys 130	Ser	Cys	Val											

<210> 274  
 <211> 124  
 <212> PRT  
 <213> homo sapiens

<400> 274

Pro 1	Gln	Ala	Trp	Arg 5	Arg	Leu	Cys	Arg	Cys 10	Cys	Ser	Ala	Arg	Pro 15	Val
Ala	Pro	Gly	Ala 20	Arg	Arg	Leu	Val	Pro 25	Cys	Arg	Thr	Pro	Thr 30	Arg	Gln
Pro	Ala	Gly 35	Gly	Thr	Cys	His	His 40	Pro	Ala	Ala	Phe	Arg 45	Gly	Arg	Ser
Arg	His 50	Ile	Pro	Val	Pro	His 55	Ala	Leu	Gly	Phe	Gly 60	Ala	Ser	Ala	Gly
Arg 65	Ser	Val	Pro	Leu	Gln 70	Ala	Leu	Ser	Gln	Ser 75	Pro	Gly	Ala	Ala	Asp 80
Leu	Gln	Val	Phe	Ser 85	Thr	Gly	Ala	Ala	Pro 90	Val	Ile	His	Thr	Arg 95	Leu
Leu	Glu	Asp	Pro 100	Ile	Leu	Gly	Ala	Thr 105	Leu	Pro	Ala	Gly	Pro 110	Ile	Arg
Cys	Arg	Ala 115	Val	Gly	Leu	Val	Pro 120	Arg	His	Cys	His				

<210> 275  
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 <212> PRT  
 <213> homo sapiens

<400> 275

Gly 1	Ser	Ser	Arg	Arg 5	His	Gly	Gly	Gly	Tyr 10	Ala	Ala	Val	Ala	Leu 15	Leu
Val	Leu	Leu 20	Leu	Leu	Gly	Pro	Gly	Gly 25	Trp	Cys	Leu	Ala	Glu 30	Pro	Pro
Arg	Asp	Ser 35	Leu	Arg	Glu	Glu	Leu 40	Val	Ile	Thr	Pro	Leu 45	Pro	Ser	Gly
Asp	Val 50	Ala	Ala	Thr	Phe	Gln 55	Phe	Arg	Thr	Arg	Trp 60	Asp	Ser	Glu	Leu

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004221 5622960

Gln 65	Arg	Glu	Gly	Val	Ser 70	His	Tyr	Arg	Leu	Phe 75	Pro	Lys	Ala	Leu	Gly 80
Gln	Leu	Ile	Ser	Lys 85	Tyr	Ser	Leu	Arg	Glu 90	Leu	His	Leu	Ser	Phe 95	Thr
Gln	Gly	Phe	Trp 100	Arg	Thr	Arg	Tyr	Trp 105	Gly	Pro	Pro	Phe	Leu 110	Gln	Ala
Pro	Ser	Gly 115	Ala	Glu	Leu	Trp	Val 120	Trp	Phe	Gln	Asp	Thr 125	Val	Thr	Asp
Val	Asp 130	Lys	Ser	Trp	Lys	Glu 135	Leu	Ser	Asn	Val	Leu 140	Ser	Gly	Ile	Phe
Cys 145	Ala	Ser	Leu	Asn	Phe 150	Ile	Asp	Ser	Thr	Asn 155	Thr	Val	Thr	Pro	Thr 160
Ala	Ser	Phe	Lys	Pro 165	Leu	Gly	Leu	Ala	Asn 170	Asp	Thr	Asp	His	Tyr 175	Phe
Leu	Arg	Tyr	Ala 180	Val	Leu	Pro	Arg	Glu 185	Val	Val	Cys	Thr	Glu 190	Asn	Leu
Thr	Pro	Trp 195	Lys	Lys	Leu	Leu	Pro 200	Cys	Ser	Ser	Lys	Ala 205	Gly	Leu	Ser
Val	Leu 210	Leu	Lys	Ala	Asp	Arg 215	Leu	Phe	His	Thr	Ser 220	Tyr	His	Ser	Gln
Ala 225	Val	His	Ile	Arg	Pro 230	Val	Cys	Arg	Asn	Ala 235	Arg	Cys	Thr	Ser	Ile 240
Ser	Trp	Glu	Leu	Arg 245	Gln	Thr	Leu	Ser	Val 250	Val	Phe	Asp	Ala	Phe 255	Ile
Thr	Gly	Gln	Gly 260	Lys	Lys	Asp	Trp	Ser 265	Leu	Phe	Arg	Met	Phe 270	Ser	Arg
Thr	Leu	Thr 275	Glu	Pro	Cys	Pro	Leu 280	Ala	Ser	Glu	Ser	Arg 285	Val	Tyr	Val
Asp	Ile 290	Thr	Thr	Tyr	Asn	Gln 295	Asp	Asn	Glu	Thr	Leu 300	Glu	Val	His	Pro
Pro 305	Pro	Thr	Thr	Thr	Tyr 310	Gln	Asp	Val	Ile	Leu 315	Gly	Thr	Arg	Lys	Thr 320
Tyr	Ala	Ile	Tyr	Asp 325	Leu	Leu	Asp	Thr	Ala 330	Met	Ile	Asn	Asn	Ser 335	Arg
Asn	Leu	Asn	Ile 340	Gln	Leu	Lys	Trp	Lys 345	Arg	Pro	Pro	Glu	Asn 350	Glu	Ala
Pro	Pro	Val 355	Pro	Phe	Leu	His	Ala 360	Gln	Arg	Tyr	Val	Ser 365	Gly	Tyr	Gly
Leu	Gln 370	Lys	Gly	Glu	Leu	Ser 375	Thr	Leu	Leu	Tyr	Asn 380	Thr	His	Pro	Tyr
Arg 385	Ala	Phe	Pro	Val	Leu 390	Leu	Leu	Asp	Thr	Val 395	Pro	Trp	Tyr	Leu	Arg 400

Leu	Leu	His	Pro	Leu 405	Pro	Ala	Cys	Pro	Gly 410	Pro	Ala	Ala	Thr	Pro 415	Pro
Pro	Gly	Asp	Ala 420	Asp	Ser	Ala	Ala	Gly 425	Gln						

<210> 276  
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 <212> PRT  
 <213> homo sapiens

<400> 276

Ser 1	Pro	Ser	Ile	Leu 5	Tyr	Gly	Ser	Cys	Thr 10	Cys	His	Ser	His	Lys 15	Ala
Phe	Gly	Gly	Pro 20	Asp	Thr	Gly	Gly	His 25	Pro	Ser	Cys	Arg	Pro 30	His	Gln
Val	Gln	Ser 35	Cys	Gly	Ser	Gly	Ser 40	Lys	Thr	Leu	Ser	Leu 45	Met	Trp	Ile
Asn	Leu 50	Gly	Arg	Ser	Ser	Val 55	Met	Ser	Ser	Gln	Gly 60	Ser	Ser	Ala	Pro
Leu 65	Ser	Thr	Ser	Ser	Thr 70	Pro	Pro	Thr	Gln	Ser 75	Leu	Pro	Leu	Pro	Pro 80
Ser	Asn	Pro	Trp	Val 85	Trp	Pro	Met	Thr	Leu 90	Thr	Thr	Thr	Phe	Cys 95	Ala
Met	Leu	Cys	Cys 100	Arg	Gly	Arg	Trp	Ser 105	Ala	Pro	Lys	Thr	Ser 110	Pro	Pro
Gly	Arg	Ser 115	Ser	Cys	Pro	Val	Val 120	Pro	Arg	Gln	Ala	Ser 125	Leu	Cys	Cys

<210> 277  
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 <212> PRT  
 <213> homo sapiens

<400> 277

Ala 1	Gln	Asp	Thr	Gly 5	Gly	Pro	Gly	Arg	Gln 10	Ser	Gly	His	Gly	Gly 15	Asp
Leu	Gln	Ile	Pro 20	Ile	Ser	Leu	Phe	Leu 25	Arg	Arg	Leu	Asn	Thr 30	Gln	His
Trp	Arg	Pro 35	Gly	Ser	Arg	Lys	Val 40	Met	Ala	Val	Val	Pro 45	Ala	Ser	Leu
Ser	Gly 50	Gln	Asp	Val	Gly	Ser 55	Phe	Ala	Tyr	Leu	Thr 60	Ile	Lys	Asp	Arg
Ile 65	Pro	Gln	Ile	Leu	Thr 70	Lys	Val	Ile	Asp	Thr 75	Leu	His	Arg	His	Lys 80
Ser	Glu	Phe	Phe	Glu 85	Lys	His	Gly	Glu	Glu 90	Gly	Val	Glu	Ala	Glu 95	Lys
Lys	Ala	Ile	Ser	Leu	Leu	Ser	Lys	Leu	Arg	Asn	Glu	Leu	Gln	Thr	Asp

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004221 555555

		435					440					445				
Val	Gly	Leu	Gln	Pro	Gly	Gln	Gly	Glu	Gln	Leu	Leu	Ala	Ser	Glu	Pro	
	450					455					460					
Ser	Trp	Trp	Thr	Thr	Gly	Lys	Tyr	Gly	Ile	Phe	Gln	Tyr	Asp	Gly	Pro	
465					470					475					480	
Leu																

<210> 278  
 <211> 128  
 <212> PRT  
 <213> homo sapiens

<400> 278

Phe	His	Ile	Ser	Val	Ser	Thr	Asn	Phe	Ser	Thr	Lys	Gly	Ile	Asn	Gly	
1				5					10					15		
Leu	Ser	Val	Cys	Asn	Ser	Phe	Arg	Asn	Leu	Glu	Arg	Arg	Glu	Ile	Ala	
			20					25					30			
Phe	Phe	Ser	Ala	Ser	Thr	Pro	Ser	Ser	Pro	Cys	Phe	Ser	Lys	Asn	Ser	
		35					40					45				
Leu	Leu	Cys	Arg	Cys	Asn	Val	Ser	Ile	Thr	Leu	Val	Lys	Ile	Cys	Gly	
	50					55					60					
Ile	Leu	Ser	Leu	Ile	Val	Arg	Tyr	Ala	Asn	Asp	Pro	Thr	Ser	Cys	Pro	
65					70					75					80	
Glu	Arg	Asp	Ala	Gly	Thr	Thr	Ala	Ile	Thr	Phe	Arg	Asp	Pro	Gly	Arg	
				85					90					95		
Gln	Cys	Trp	Val	Phe	Asn	Arg	Arg	Arg	Asn	Arg	Glu	Ile	Gly	Ile	Cys	
			100					105					110			
Lys	Ser	Pro	Pro	Cys	Pro	Asp	Cys	Arg	Pro	Gly	Pro	Pro	Val	Ser	Cys	
		115					120					125				

<210> 279  
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<400> 279

Glu	Leu	Leu	Asn	Gln	Val	Lys	Gly	Asp	His	Arg	Thr	Glu	Ile	Phe	His	
1				5					10					15		
Ile	Phe	Gln	Trp	Ser	Thr	Ser	Trp	Ala	Gln	Arg	Pro	Gly	Ala	Val	Pro	
			20					25					30			
Leu	Ala	Gln	Ala	Ala	Asp	Gln	Pro	Glu	Phe	Gln	Leu	Leu	Met	Phe	Leu	
		35					40					45				
Trp	Tyr	Arg	Val	Val	Gln	Asp	Gly	Ser	His	Ser	Glu	Pro	Asp	Glu	Met	
	50					55					60					
Glu	Gln	Lys	Thr	Pro	Ile	Phe	Cys	His	Leu	Ser	Thr	Ser	Cys	Asn	Ser	
65					70					75					80	

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 1.5
Gender	Male 50.0%
Education (years)	12.0 ± 1.0
Marital status	Married 70.0%
Income (USD/month)	1,200 ± 200
Health status	Good 60.0%
Smoking status	Smoker 30.0%
Alcohol consumption	Alcohol 20.0%
Exercise frequency	Regular 40.0%
Family size	3.0 ± 0.5
Living arrangement	Alone 10.0%
Religious affiliation	Christian 80.0%
Occupation	Retired 50.0%
Comorbidities	Hypertension 40.0%
Diabetes 20.0%	
Cholesterol 30.0%	
Arthritis 10.0%	
Depression 15.0%	
Other 5.0%	
Medication use	Yes 35.0%
No 65.0%	
Health insurance	Yes 90.0%
No 10.0%	
Healthcare utilization	Regular 70.0%
Emergency 10.0%	
Other 20.0%	
Healthcare satisfaction	Satisfied 60.0%
Dissatisfied 40.0%	
Healthcare access	Easy 70.0%
Difficult 30.0%	
Healthcare cost	Low 50.0%
High 50.0%	
Healthcare quality	Good 60.0%
Poor 40.0%	
Healthcare safety	High 70.0%
Low 30.0%	
Healthcare effectiveness	High 60.0%
Low 40.0%	
Healthcare equity	High 70.0%
Low 30.0%	
Healthcare transparency	High 60.0%
Low 40.0%	
Healthcare accountability	High 70.0%
Low 30.0%	
Healthcare responsiveness	High 60.0%
Low 40.0%	
Healthcare patient-centeredness	High 70.0%
Low 30.0%	
Healthcare community engagement	High 60.0%
Low 40.0%	
Healthcare leadership	High 70.0%
Low 30.0%	
Healthcare governance	High 60.0%
Low 40.0%	
Healthcare innovation	High 70.0%
Low 30.0%	
Healthcare sustainability	High 60.0%
Low 40.0%	
Healthcare resilience	High 70.0%
Low 30.0%	
Healthcare adaptability	High 60.0%
Low 40.0%	
Healthcare inclusivity	High 70.0%
Low 30.0%	
Healthcare diversity	High 60.0%
Low 40.0%	
Healthcare equity	High 70.0%
Low 30.0%	
Healthcare justice	High 60.0%
Low 40.0%	
Healthcare fairness	High 70.0%
Low 30.0%	
Healthcare integrity	High 60.0%
Low 40.0%	
Healthcare honesty	High 70.0%
Low 30.0%	
Healthcare openness	High 60.0%
Low 40.0%	
Healthcare transparency	High 70.0%
Low 30.0%	
Healthcare accountability	High 60.0%
Low 40.0%	
Healthcare responsiveness	High 70.0%
Low 30.0%	
Healthcare patient-centeredness	High 60.0%
Low 40.0%	
Healthcare community engagement	High 70.0%
Low 30.0%	
Healthcare leadership	High 60.0%
Low 40.0%	
Healthcare governance	High 70.0%
Low 30.0%	
Healthcare innovation	High 60.0%
Low 40.0%	
Healthcare sustainability	High 70.0%
Low 30.0%	
Healthcare resilience	High 60.0%
Low 40.0%	
Healthcare adaptability	High 70.0%
Low 30.0%	
Healthcare inclusivity	High 60.0%
Low 40.0%	
Healthcare diversity	High 70.0%
Low 30.0%	
Healthcare equity	High 60.0%
Low 40.0%	
Healthcare justice	High 70.0%
Low 30.0%	
Healthcare fairness	High 60.0%
Low 40.0%	
Healthcare integrity	High 70.0%
Low 30.0%	
Healthcare honesty	High 60.0%
Low 40.0%	
Healthcare openness	High 70.0%
Low 30.0%	
Healthcare transparency	High 60.0%
Low 40.0%	
Healthcare accountability	High 70.0%
Low 30.0%	
Healthcare responsiveness	High 60.0%
Low 40.0%	
Healthcare patient-centeredness	High 70.0%
Low 30.0%	
Healthcare community engagement	High 60.0%
Low 40.0%	
Healthcare leadership	High 70.0%
Low 30.0%	
Healthcare governance	High 60.0%
Low 40.0%	
Healthcare innovation	High 70.0%
Low 30.0%	
Healthcare sustainability	High 60.0%
Low 40.0%	
Healthcare resilience	High 70.0%
Low 30.0%	
Healthcare adaptability	High 60.0%
Low 40.0%	
Healthcare inclusivity	High 70.0%
Low 30.0%	
Healthcare diversity	High 60.0%
Low 40.0%	
Healthcare equity	High 70.0%
Low 30.0%	
Healthcare justice	High 60.0%
Low 40.0%	
Healthcare fairness	High 70.0%
Low 30.0%	
Healthcare integrity	High 60.0%
Low 40.0%	
Healthcare honesty	High 70.0%
Low 30.0%	
Healthcare openness	High 60.0%
Low 40.0%	
Healthcare transparency	High 70.0%
Low 30.0%	
Healthcare accountability	High 60.0%
Low 40.0%	
Healthcare responsiveness	High 70.0%
Low 30.0%	
Healthcare patient-centeredness	High 60.0%
Low 40.0%	
Healthcare community engagement	High 70.0%
Low 30.0%	
Healthcare leadership	High 60.0%
Low 40.0%	
Healthcare governance	High 70.0%
Low 30.0%	
Healthcare innovation	High 60.0%
Low	

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<210> 281
<211> 70
<212> PRT
<213> homo sapiens
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<400> 281

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<210> 282  
 <211> 71  
 <212> PRT  
 <213> homo sapiens

<400> 282

Ile	Asp	Val	Phe	Pro	Leu	Leu	Val	Gly	Phe	Asn	Gln	Leu	Phe	Asn	Asn
1				5					10					15	
Ile	Ser	Tyr	Ser	Gln	His	His	Gln	Leu	Ser	Arg	Ala	Glu	Ile	Ser	Phe
			20					25					30		
Pro	Leu	Leu	Pro	His	Phe	Cys	Ala	Ala	Val	Ala	Glu	Pro	Pro	Glu	Ile
		35					40					45			
Lys	Met	Gln	Pro	Gln	Thr	Gln	Thr	Thr	Glu	Lys	Ala	Asp	Ser	His	Lys
	50					55					60				
Thr	Ile	Pro	Pro	Val	Val	Lys									
65					70										

<210> 283  
 <211> 114  
 <212> PRT  
 <213> homo sapiens

<400> 283

Lys	Pro	Arg	Gln	Leu	Pro	Asn	Met	Ala	Phe	Leu	Pro	Ser	Pro	Ala	Trp
1				5					10					15	
Trp	Ile	Ser	Leu	Leu	Ala	Val	Pro	Pro	Gln	Tyr	Arg	Lys	Val	Leu	Met
			20					25					30		
Pro	Lys	Leu	Lys	Ala	Lys	Pro	Ile	Arg	Thr	Ala	Ser	Gly	Ile	Ala	Val
		35					40					45			
Val	Ala	Val	Met	Cys	Lys	Pro	His	Arg	Cys	Pro	His	Ile	Ser	Phe	Thr
	50					55					60				
Gly	Asn	Ile	Cys	Val	Tyr	Cys	Pro	Gly	Trp	Asp	Leu	Ile	Leu	Ile	Leu
65					70					75					80
Ser	Ile	Pro	Pro	Ser	Leu	Thr	Leu	Gly	Tyr	Glu	Pro	Thr	Ser	Met	Arg
				85					90					95	
Ser	Tyr	Ser	Val	Pro	Asp	Met	Asp	Pro	Phe	Pro	Tyr	Arg	Thr	Arg	Thr
			100					105					110		

Pro Asp

<210> 284  
 <211> 127  
 <212> PRT  
 <213> homo sapiens

<400> 284

Trp	Val	Ser	Pro	Leu	Thr	Trp	Ala	Ser	Arg	Pro	Cys	Asp	Thr	Glu	Glu
1				5					10					15	

004321 00000000

Gly	Arg	Gln	Ala 20	Met	Ile	Ser	Thr	Arg 25	Arg	Gly	Trp	Ala	Glu 30	Arg	Pro
Tyr	Leu	Ala 35	Ala	Val	Leu	Val	Phe 40	Thr	Leu	Phe	Arg	Ser 45	Met	Ser	Phe
Pro	Cys 50	Ser	Trp	Ala	Ser	Ile 55	Ser	Cys	Leu	Ile	Thr 60	Ser	Pro	Ile	Val
Ser 65	Ile	Ile	Ser	Ser	Ala 70	Gly	Leu	Arg	Ser	Pro 75	Asp	Tyr	Gly	Gly	Phe 80
Thr	Thr	Arg	Pro	Gly 85	Ser	Asn	Ile	Leu	Gly 90	Ser	Arg	Val	Gly	His 95	Tyr
Thr	His	Gln	Thr 100	Met	Glu	Asp	Ser	Pro 105	Pro	Asp	Gln	Glu	Ala 110	Thr	Ala
Trp	Ala	Pro 115	Glu	Leu	Ala	Thr	Pro 120	Pro	Cys	Thr	Asp	Glu 125	Asp	Arg	

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<210> 285
<211> 92
<212> PRT
<213> homo sapiens
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<400> 285

Pro 1	His	Thr	Thr	Asn 5	Pro	Thr	Cys	Phe	Lys 10	Leu	Phe	Leu	Ile	Arg 15	Cys
Pro	Cys	Pro	Val 20	Arg	Lys	Arg	Val	His 25	Ile	Trp	His	Gly	Ile 30	Ala	Pro
His	Gly	Gly 35	Trp	Leu	Ile	Ala	Gln 40	Cys	Lys	Thr	Gly	Trp 45	Asn	Thr	Gln
Asn	Gln 50	Asn	Gln	Val	Pro	Pro 55	Arg	Ala	Val	Tyr	Thr 60	Tyr	Ile	Ser	Cys
Lys 65	Thr	Asp	Val	Trp	Thr 70	Ser	Val	Gly	Phe	Ala 75	His	His	Ser	His	Asp 80
Ser	Asn	Pro	Thr	Ser 85	Ser	Ser	Asp	Gly	Phe 90	Arg	Leu				

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<210> 286
<211> 76
<212> PRT
<213> homo sapiens
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<400> 286

Asp 1	Leu	Ser	Arg	Pro 5	Gly	Gly	Thr	Arg	Phe 10	Val	Leu	Thr	Ile	Gln 15	Gln
Thr	Phe	Phe	Ser 20	Lys	Val	Phe	Val	Gln 25	Asp	Asn	Phe	Lys	Asn 30	Asn	Ile
Lys	Ile	Asn 35	Asn	Gly	Phe	Asp	Phe 40	Ser	Leu	Lys	Ile	Glu 45	Lys	Lys	Gly
Val	Gly	Gly	Gly	Val	Asn	His	Trp	Pro	Phe	Phe	Phe	Trp	Arg	Gly	Pro

	50					55					60				
Ile	Gly	Ile	Val	Arg	Pro	Trp	Gly	Ser	Gly	Leu	Ser				
65					70					75					

<210> 287  
 <211> 97  
 <212> PRT  
 <213> homo sapiens

<400> 287

Arg	Thr	Phe	Val	Leu	Phe	Tyr	His	Arg	Leu	Thr	Leu	Gln	Leu	Leu	Ile
1				5					10					15	
Asn	Thr	Ser	Phe	Gly	Asp	Val	Trp	Cys	Lys	Thr	His	Lys	His	Thr	Gln
			20					25					30		
Lys	Ser	Thr	Ser	Pro	Leu	His	Asp	Pro	Ser	Leu	Leu	Ser	Gly	Thr	Ile
		35					40					45			
Ser	Ala	Ala	Ser	Cys	Thr	Leu	Leu	Gly	Pro	Pro	Pro	Ile	His	Arg	Gly
	50					55					60				
Phe	Arg	Gly	Thr	Gln	Ile	Thr	Ala	Gly	Phe	Gln	Phe	Phe	Phe	Asn	Asn
65					70					75					80
Thr	Phe	Leu	Trp	Ser	Val	Pro	Thr	Ala	Leu	Ser	Val	Leu	Leu	Lys	Leu
				85					90					95	

Glu

<210> 288  
 <211> 77  
 <212> PRT  
 <213> homo sapiens

<400> 288

Ile	Leu	His	Leu	Glu	Met	Tyr	Gly	Val	Lys	His	Thr	Asn	Thr	His	Lys
1				5					10					15	
Lys	Ala	Gln	Ala	Arg	Cys	Met	Thr	Arg	Leu	Ser	Phe	Leu	Gly	Leu	Phe
			20					25					30		
Leu	Leu	Arg	Pro	Ala	Pro	Ser	Trp	Ala	His	Leu	Arg	Phe	Thr	Glu	Val
		35					40					45			
Ser	Gly	Gly	Pro	Lys	Ser	Leu	Leu	Val	Phe	Asn	Phe	Phe	Leu	Thr	Ile
	50					55					60				
His	Phe	Cys	Gly	Gln	Phe	Gln	Gln	His	Cys	Pro	Tyr	Phe			
65					70					75					

<210> 289  
 <211> 28  
 <212> PRT  
 <213> homo sapiens

<400> 289

Ile	Leu	Ile	Asp	Gly	Val	Arg	Ala	Ala	Phe	Ile	Pro	Tyr	Arg	Glu	Tyr
1				5					10					15	





<400> 294

Ala	Ile	Asn	Lys	Val	Ser	Ser	Gly	Tyr	Gly	Pro	Leu	Ala	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Val	Ser	Val	Glu	Ala	Ala	Gln	Arg	Ile	Ser	Leu	Asn	Phe	Ser
			20					25					30		
Gln	Lys	Trp	Leu	Leu	Thr										
		35													

<210> 295

<211> 40

<212> PRT

<213> homo sapiens

<400> 295

Phe	Thr	Ser	Phe	Asn	Leu	Leu	Ile	Pro	Arg	Thr	Ile	Leu	Ser	Thr	Thr
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Asn	Arg	Asn	Glu	Ile	Leu	Ile	His	Lys	Arg	Lys	Leu	Lys	Thr	Phe	Ile
			20					25					30		
Ala	Tyr	Val	Gly	Leu	Ser	Asn	Lys								
		35					40								

<210> 296

<211> 71

<212> PRT

<213> homo sapiens

<400> 296

Val	Asn	Leu	Leu	Lys	Tyr	Gly	Gln	Ile	His	Leu	Ala	Val	Lys	Gln	Leu
1				5					10					15	
Asn	Ile	His	Cys	Tyr	Leu	Ile	Lys	Val	Phe	Val	Ser	Val	Leu	Pro	Gly
			20					25					30		
Pro	Asn	Ile	Lys	Thr	Thr	Ser	Val	Gln	Lys	Ile	Asn	Val	Gln	Arg	Ala
		35					40					45			
Val	Cys	Ser	Leu	Phe	Trp	Tyr	Val	His	Phe	Lys	Lys	Thr	Pro	Leu	Ser
	50					55					60				
Ser	Leu	Ala	Asn	Gln	Glu	Tyr									
65					70										

<210> 297

<211> 67

<212> PRT

<213> homo sapiens

<400> 297

Arg	Phe	Tyr	Leu	Tyr	Phe	Ile	Leu	Ser	Arg	Gly	Thr	Asn	Ser	Arg	His
1				5					10					15	
Thr	Phe	Ala	Arg	Pro	Ser	Cys	Arg	Lys	Thr	Gln	Ser	Arg	Lys	Gly	Lys
			20					25					30		
Asn	Lys	Ile	Ala	Ile	Lys	Tyr	Met	Val	Leu	Gly	Ala	Gly	Arg	Thr	Arg



<212> PRT  
 <213> homo sapiens

<400> 300

Gln	Ser	Arg	Ser	Arg	Pro	Arg	Arg	Glu	Gly	Val	Gly	Thr	Gly	Ser	Arg
1				5					10					15	
Ala	Val	Leu	Cys	Ile	Leu	Ala	Thr	Cys	Gly	Ser	Lys	Met	Ser	Asp	Ile
			20					25					30		
Gly	Asp	Trp	Phe	Arg	Ser	Ile	Pro	Ala	Ile	Thr	Arg	Tyr	Trp	Phe	Ala
		35					40					45			
Ala	Thr	Val	Ala	Val	Pro	Leu	Val	Gly	Lys	Leu	Gly	Leu	Ile	Ser	Pro
	50					55					60				
Ala	Tyr	Leu	Phe	Leu	Trp	Pro	Glu	Ala	Phe	Leu	Tyr	Arg	Phe	Gln	Ile
65					70					75					80
Trp	Arg	Pro	Ile	Thr	Ala	Thr	Phe	Tyr	Phe	Pro	Val	Gly	Pro	Gly	Thr
				85					90					95	
Gly	Phe	Leu	Tyr	Leu	Val	Asn	Leu	Tyr	Phe	Leu	Tyr	Gln	Tyr	Ser	Thr
			100					105					110		
Arg	Leu	Glu	Thr	Gly	Ala	Phe	Asp	Gly	Arg	Pro	Ala	Asp	Tyr	Leu	Phe
		115					120					125			
Met	Leu	Leu	Phe	Asn	Trp	Ile	Cys	Ile	Val	Ile	Thr	Gly	Leu	Ala	Met
	130					135					140				
Asp	Met	Gln	Leu	Leu	Met	Ile	Pro	Leu	Ile	Met	Ser	Val	Leu	Tyr	Val
145					150					155					160
Trp	Ala	Gln	Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe	Trp	Phe	Gly	Thr
				165					170					175	
Arg	Phe	Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu	Gly	Phe	Asn	Tyr
			180					185					190		
Ile	Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly	Asn	Leu	Val	Gly
		195					200					205			
His	Leu	Tyr	Phe	Phe	Leu	Met	Phe	Arg	Tyr	Pro	Met	Asp	Leu	Gly	Gly
	210					215					220				
Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg	Trp	Leu	Pro	Ser
225					230					235					240
Arg	Arg	Gly	Gly	Val	Ser	Gly	Phe	Gly	Val	Pro	Pro	Ala	Ser	Met	Arg
				245					250					255	
Arg	Ala	Ala	Asp	Gln	Asn	Gly	Gly	Gly	Gly	Arg	His	Asn	Trp	Gly	Gln
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Gly	Phe	Arg	Leu	Gly	Asp	Gln									
			275												

<210> 301  
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 <212> PRT  
 <213> homo sapiens

000221" 00000000

1. Demographic Data		2. Socioeconomic Data		3. Health Status Data		4. Health Service Utilization Data		5. Health Beliefs and Attitudes Data	
Age	Mean = 45.2	Income	Mean = \$12,500	Cholesterol	Mean = 240	Physician Visits	Mean = 2.5	Health Beliefs	Mean = 3.5
Gender	Male = 55%	Education	Mean = 12 years	Blood Pressure	Mean = 140/90	Hospitalizations	Mean = 1.2	Health Attitudes	Mean = 4.2
Marital Status	Married = 60%	Occupation	Mean = 3.5	Smoking Status	Smoker = 30%	Emergency Room Visits	Mean = 0.8	Health Knowledge	Mean = 2.8
Religion	Protestant = 40%	Health Insurance	Medicaid = 70%	Alcohol Consumption	Mean = 2 drinks/week	Preventive Services	Mean = 1.5	Health Motivation	Mean = 3.8
Employment	Employed = 50%	Home Ownership	Owned = 65%	Diabetes Status	Diabetic = 15%	Immunizations	Mean = 2.0	Health Self-Efficacy	Mean = 3.2
Living Arrangements	Alone = 35%	Neighborhood Safety	Safe = 60%	Hypertension	Mean = 25%	Chronic Disease Management	Mean = 1.8	Health Decision-Making	Mean = 3.0
Transportation	Own Car = 45%	Access to Healthcare	Access = 75%	Heart Disease	Mean = 20%	Medication Adherence	Mean = 2.2	Health Communication	Mean = 2.5
Food Access	Access = 60%	Health Literacy	Mean = 2.5	Stroke	Mean = 10%	Healthcare Satisfaction	Mean = 2.8	Health Information Seeking	Mean = 3.5
Exercise Habits	Exercise = 20%	Stress Levels	Mean = 3.0	Cancer Screening	Mean = 1.0	Healthcare Access Barriers	Mean = 1.5	Health Communication Channels	Mean = 3.0
Substance Use	Alcohol = 15%	Depression	Mean = 1.5	Healthcare Quality	Mean = 2.5	Healthcare Cost Concerns	Mean = 2.0	Health Communication Effectiveness	Mean = 3.2
Healthcare Needs	Need = 30%	Healthcare Satisfaction	Mean = 2.8	Healthcare Access Barriers	Mean = 1.5	Healthcare Cost Concerns	Mean = 2.0	Health Communication Effectiveness	Mean = 3.2
Healthcare Access	Access = 75%	Healthcare Satisfaction	Mean = 2.8	Healthcare Access Barriers	Mean = 1.5	Healthcare Cost Concerns	Mean = 2.0	Health Communication Effectiveness	Mean = 3.2
Healthcare Satisfaction	Mean = 2.8	Healthcare Access Barriers	Mean = 1.5	Healthcare Cost Concerns	Mean = 2.0	Health Communication Effectiveness	Mean = 3.2	Health Communication Effectiveness	Mean = 3.2
Healthcare Access Barriers	Mean = 1.5	Healthcare Cost Concerns	Mean = 2.0	Health Communication Effectiveness	Mean = 3.2	Health Communication Effectiveness	Mean = 3.2	Health Communication Effectiveness	Mean = 3.2
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<212> PRT
<213> homo sapiens
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Thr	Leu	Ser	Asp 20	Ser	Gly	Asp	Lys	Val 25	Ala	Val	Glu	Trp	Asp 30	Lys	Asp
His	Gly	Val 35	Leu	Glu	Ser	His	Leu 40	Ala	Glu	Lys	Gly	Arg 45	Gly	Met	Glu
Leu	Ser 50	Asp	Leu	Ile	Val	Phe 55	Asn	Gly	Lys	Leu	Tyr 60	Ser	Val	Asp	Asp
Arg 65	Thr	Gly	Val	Val	Tyr 70	Gln	Ile	Glu	Gly	Ser 75	Lys	Ala	Val	Pro	Trp 80
Val	Ile	Leu	Ser	Asp 85	Gly	Asp	Gly	Thr	Val 90	Glu	Lys	Gly	Phe	Lys 95	Ala
Glu	Trp	Leu	Ala 100	Val	Lys	Asp	Glu	Arg 105	Leu	Tyr	Val	Gly	Gly 110	Leu	Gly
Lys	Glu	Trp 115	Thr	Thr	Thr	Thr	Gly 120	Asp	Val	Val	Asn	Glu 125	Asn	Pro	Glu
Trp	Val 130	Lys	Val	Val	Gly	Tyr 135	Lys	Gly	Ser	Val	Asp 140	His	Glu	Asn	Trp
Val 145	Ser	Asn	Tyr	Asn	Ala 150	Leu	Arg	Ala	Ala	Ala 155	Gly	Ile	Gln	Pro	Pro 160
Gly	Asn	Leu	Ile	His 165	Glu	Ser	Ala	Cys	Trp 170	Ser	Asp	Thr	Leu	Gln 175	Arg

Trp	Phe	Phe	Leu 180	Pro	Arg	Arg	Ala	Ser 185	Gln	Glu	Arg	Tyr	Ser 190	Glu	Glu
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 <212> PRT  
 <213> homo sapiens

<400> 303

Arg 1	Trp	Trp	Ala	Thr 5	Arg	Ala	Ala	Trp	Thr 10	Thr	Arg	Thr	Gly	Cys 15	Pro
Thr	Thr	Thr	Pro 20	Cys	Gly	Leu	Leu	Pro 25	Ala	Ser	Ser	Arg	Gln 30	Val	Thr
Ser	Ser	Met 35	Ser	Leu	Pro	Ala	Gly 40	Val	Thr	Arg	Cys	Ser 45	Ala	Gly	Ser
Ser	Cys 50	Arg	Ala	Ala	Pro	Ala 55	Arg	Ser	Ala	Thr	Ala 60	Arg	Lys	Asp	Asp
Glu 65	Arg	Lys	Gly	Ala	Asn 70	Leu	Leu	Leu	Ser	Ala 75	Ser	Pro	Asp	Phe	Gly 80
Asp	Ile	Ala	Val	Ser 85	His	Val	Gly	Ala	Val 90	Val	Pro	Thr	His	Gly 95	Phe
Ser	Ser	Phe	Lys 100	Phe	Ile	Pro	Asn	Thr 105	Asp	Asp	Gln	Ile	Ile 110	Val	Ala
Leu	Lys	Ser 115	Glu	Glu	Asp	Ser	Gly 120	Arg	Val	Ala	Ser	Tyr 125	Ile	Met	Ala
Phe	Thr 130	Leu	Asp	Gly	Arg	Phe 135	Leu	Leu	Pro	Glu	Thr 140	Lys	Ile	Gly	Ser
Val 145	Lys	Tyr	Glu	Gly	Ile 150	Glu	Phe	Ile							

<210> 304  
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 <212> PRT  
 <213> homo sapiens

<400> 304

Val 1	Gly	Thr	Thr	Ala 5	Pro	Thr	Trp	Leu	Thr 10	Ala	Met	Ser	Pro	Lys 15	Ser
Gly	Glu	Ala	Leu 20	Ser	Ser	Arg	Leu	Ala 25	Pro	Leu	Arg	Ser	Ser 30	Ser	Phe
Leu	Ala	Val 35	Ala	Leu	Leu	Ala	Gly 40	Ala	Ala	Arg	Gln	Glu 45	Glu	Pro	Ala
Leu	Gln 50	Arg	Val	Thr	Pro	Ala 55	Gly	Arg	Leu	Met	Asp 60	Glu	Val	Thr	Trp

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Arg 65	Leu	Asp	Ala	Gly	Ser 70	Ser	Pro	Gln	Gly	Val 75	Val	Val	Gly	His	Pro 80
Val	Leu	Val	Val	His 85	Ala	Ala	Leu	Val	Ala 90	His	His	Leu	His	Pro 95	Leu
Arg	Val	Leu	Val 100	His	His	Ile	Thr	Arg 105	Ser	Gly	Arg	Pro	Leu 110	Leu	Ala
Gln	Ala	Ala 115	His	Val	Gln	Thr	Leu 120	Val	Leu	His	Cys	Gln 125	Pro	Phe	Gly
Leu	Glu 130	Ala	Phe	Leu	His	Gly 135	Ala	Val	Ala	Val	Gly 140	Gln	Asn	His	Pro
Gly 145	His	Gly	Phe	Ala	Ala 150	Phe	Asp	Leu	Val	Asp 155	Asp	Pro	Arg	Pro	Val 160
Ile	His	Gly	Val	Glu 165	Phe	Pro	Ile	Glu	Asn 170	Asn	Gln	Val	Gly		

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<210> 305
<211> 61
<212> PRT
<213> homo sapiens
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<400> 305

Lys 1	Leu	Val	Cys	Leu 5	Glu	Ala	Asp	Ser	Lys 10	Ser	Ser	Phe	Ser	Ser 15	Glu
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Ser	Cys	Ser 35	Lys	Met	Gly	Asp	Val 40	Lys	Glu	Asn	Tyr	Leu 45	Glu	Thr	Phe
Ile	Ser 50	Ser	Pro	Lys	Trp	Ser 55	Phe	Ile	Leu	Cys	Leu 60	Ser			

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<210> 306
<211> 144
<212> PRT
<213> homo sapiens
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<400> 306

Asn 1	Thr	Met	Ala	Val 5	Ala	Ala	Val	Lys	Trp 10	Val	Met	Ser	Lys	Arg 15	Thr
Ile	Leu	Lys	His 20	Leu	Phe	Pro	Val	Gln 25	Asn	Gly	Ala	Leu	Tyr 30	Cys	Val
Cys	His	Lys 35	Ser	Thr	Tyr	Ser	Pro 40	Leu	Pro	Asp	Asp	Tyr 45	Asn	Cys	Asn
Val	Glu 50	Leu	Ala	Leu	Thr	Ser 55	Asp	Gly	Arg	Thr	Ile 60	Val	Cys	Tyr	His
Pro 65	Ser	Val	Asp	Ile	Pro 70	Tyr	Glu	His	Thr	Lys 75	Pro	Ile	Pro	Arg	Pro 80
Asp	Pro	Val	His	Asn	Asn	Glu	Glu	Thr	His	Asp	Gln	Val	Leu	Lys	Thr





Val	Lys	Asn	Ile	Thr 85	Leu	Asn	Phe	Gly	Pro 90	Gln	His	Pro	Ala	Ala 95	His
Gly	Val	Leu	Arg 100	Leu	Val	Met	Glu	Leu 105	Ser	Gly	Glu	Met	Val 110	Arg	Lys
Cys	Asp	Pro 115	His	Ile	Gly	Leu	Leu 120	His	Arg	Gly	Thr	Glu 125	Lys	Leu	Ile
Glu	Tyr 130	Lys	Thr	Tyr	Leu	Gln 135	Ala	Leu	Pro	Tyr	Phe 140	Asp	Arg	Leu	Asp
Tyr 145	Val	Ser	Met	Met	Cys 150	Asn	Glu	Gln	Ala	Tyr 155	Ser	Leu	Ala	Val	Glu 160
Lys	Leu	Leu	Asn	Ile 165	Arg	Pro	Pro	Pro	Arg 170	Ala	Gln	Trp	Ile	Arg 175	Val
Leu	Phe	Gly	Glu 180	Ile	Thr	Arg	Leu	Leu 185	Asn	His	Ile	Met	Ala 190	Val	Thr
Thr	His	Ala 195	Leu	Asp	Leu	Gly	Ala 200	Met	Thr	Pro	Phe	Phe 205	Trp	Leu	Phe
Glu	Glu 210	Arg	Glu	Lys	Met	Phe 215	Glu	Phe	Tyr	Glu	Arg 220	Val	Ser	Gly	Ala
Arg 225	Met	His	Ala	Ala	Tyr 230	Ile	Arg	Pro	Gly	Gly 235	Val	His	Gln	Asp	Leu 240
Pro	Leu	Gly	Leu	Met 245	Asp	Asp	Ile	Tyr	Gln 250	Phe	Ser	Lys	Asn	Phe 255	Ser
Leu	Arg	Leu	Asp 260	Glu	Leu	Glu	Glu	Leu 265	Leu	Thr	Asn	Asn	Arg 270	Ile	Trp
Arg	Asn	Arg 275	Thr	Ile	Asp	Ile	Gly 280	Val	Val	Thr	Ala	Glu 285	Glu	Ala	Leu
Asn	Tyr 290	Gly	Phe	Ser	Gly	Val 295	Met	Leu	Arg	Gly	Ser 300	Gly	Ile	Gln	Trp
Asp 305	Leu	Arg	Lys	Thr	Gln 310	Pro	Tyr	Asp	Val	Tyr 315	Asp	Gln	Val	Glu	Phe 320
Asp	Val	Pro	Val	Gly 325	Ser	Arg	Gly	Asp	Cys 330	Tyr	Asp	Arg	Tyr	Leu 335	Cys
Arg	Val	Glu	Glu 340	Met	Arg	Gln	Ser	Leu 345	Arg	Ile	Ile	Ala	Gln 350	Cys	Leu
Asn	Lys	Met 355	Pro	Pro	Gly	Glu	Ile 360	Lys	Val	Asp	Asp	Ala 365	Lys	Val	Ser
Pro	Pro 370	Lys	Arg	Ala	Glu	Met 375	Lys	Thr	Ser	Met	Glu 380	Ser	Leu	Ile	His
His 385	Phe	Lys	Leu	Tyr	Thr 390	Glu	Gly	Tyr	Gln	Val 395	Pro	Pro	Gly	Ala	Thr 400
Tyr	Thr	Ala	Ile	Glu 405	Ala	Pro	Lys	Gly	Glu 410	Phe	Gly	Val	Tyr	Leu 415	Val



Pro	Lys	Leu	Leu	Cys	Pro	Phe	His	Ile	Trp	Leu	Pro	Leu	Pro	Asn	Thr
	50					55					60				
Ser	Ala	Gly	Leu	Asn	Arg	Gln	Ser	Asp	Ser	Ser	Pro	Arg	Pro	Gln	His
65					70					75					80
Leu	Gly	Arg	Asp	Ala	Pro	Glu	Ala	Ala	Gln	Ser	Pro	Gln	Arg	Arg	His
				85					90					95	
Leu	Thr	Pro	Ala												
			100												

<210> 311  
 <211> 162  
 <212> PRT  
 <213> homo sapiens

<400> 311

Arg	Arg	Leu	Arg	Gly	Gly	Glu	Pro	Ser	Thr	Asp	Arg	Arg	Arg	Asp	Pro
1				5					10					15	
Glu	Ser	Arg	Thr	Pro	Ala	Pro	Pro	Pro	Thr	Pro	Arg	Ala	Met	Asp	Pro
			20					25					30		
Lys	Asp	Arg	Lys	Lys	Ile	Gln	Phe	Ser	Val	Pro	Ala	Pro	Pro	Ser	Gln
		35					40					45			
Leu	Asp	Pro	Arg	Gln	Val	Glu	Met	Ile	Arg	Arg	Arg	Arg	Pro	Thr	Pro
	50					55					60				
Ala	Met	Leu	Phe	Arg	Leu	Ser	Glu	His	Ser	Ser	Pro	Glu	Glu	Glu	Ala
65					70					75					80
Ser	Pro	His	Gln	Arg	Ala	Ser	Gly	Glu	Gly	His	His	Leu	Lys	Ser	Lys
				85					90					95	
Arg	Pro	Asn	Pro	Cys	Ala	Tyr	Thr	Pro	Pro	Ser	Leu	Lys	Ala	Val	Gln
			100					105					110		
Arg	Ile	Ala	Glu	Ser	His	Leu	Gln	Ser	Ile	Ser	Asn	Leu	Asn	Glu	Asn
		115					120					125			
Gln	Ala	Ser	Glu	Glu	Glu	Asp	Glu	Leu	Gly	Glu	Leu	Arg	Glu	Leu	Gly
	130					135					140				
Tyr	Pro	Arg	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Ala	Arg	Leu
145					150					155					160
Lys	Ser														

<210> 312  
 <211> 154  
 <212> PRT  
 <213> homo sapiens

<400> 312

Val	Ser	Leu	Gly	Arg	Asn	Leu	Ser	Ala	Leu	Pro	Pro	Leu	Ser	Leu	Ala
1				5					10					15	
His	Arg	His	Pro	Ala	Cys	Ile	Ser	Gln	Glu	Glu	Val	Glu	Gly	Thr	Ser
			20					25					30		

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Leu	Phe	Pro 35	Arg	Asn	Pro	Leu	Tyr 40	Pro	His	Pro	Val	Leu 45	Cys	Ser	Ser	.
Pro	Arg 50	Leu	Leu	Gly	Leu	Arg 55	Leu	Leu	Thr	Ser	Arg 60	Arg	Leu	Arg	Leu	
Val 65	Cys	Val	Cys	Leu	Phe 70	Ala	His	Leu	Trp	Leu 75	Ile	Pro	Arg	Glu	Pro 80	
Gly	His	Leu	Leu	Pro 85	Asp	Ala	His	Pro	Cys 90	Gln	Ser	Phe	Leu	His 95	Ser	
Pro	Ser	Gly	Arg 100	Trp	Asp	Val	Arg	Gln 105	Pro	Thr	Leu	Glu	Asn 110	Pro	Glu	
Asn	Arg	Glu 115	Gln	Gly	Phe	Ala	Leu 120	His	Asn	Ser	Thr	Pro 125	Gln	Ile	Leu	
Ser	Pro 130	Gly	His	Arg	Arg	Pro 135	Thr	Gly	Gln	Asp	Pro 140	Lys	Ile	Trp	Gly	
Lys 145	Glu	Val	Leu	Arg	Thr 150	Leu	Arg	Tyr	Pro							

<210> 313  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 313

Ala 1	Gln	Gly	Leu	Gly 5	Leu	Phe	Asp	Leu	Arg 10	Trp	Cys	Pro	Ser	Pro 15	Glu	
Ala	Leu	Trp	Trp 20	Gly	Glu	Ala	Ser	Ser 25	Ser	Gly	Glu	Glu	Cys 30	Ser	Glu	
Ser	Arg	Asn 35	Ser	Met	Ala	Gly	Val 40	Gly	Leu	Leu	Arg	Arg 45	Ile	Ile	Ser	
Thr	Trp 50	Arg	Gly	Ser	Ser	Trp 55	Leu	Gly	Gly	Ala	Gly 60	Thr	Glu	Asn	Trp	
Ile 65	Phe	Leu	Arg	Ser	Leu 70	Gly	Ser	Met	Ala	Arg 75	Gly	Val	Gly	Gly	Gly 80	
Ala	Gly	Val	Arg	Asp 85	Ser	Gly	Ser	Arg	Arg 90	Arg	Ser	Val	Leu	Gly 95	Ser	
Pro	Pro	Arg	Arg 100	Arg												

<210> 314  
 <211> 162  
 <212> PRT  
 <213> homo sapiens

<400> 314

Ser 1	Asp	Arg	Trp	Thr 5	Cys	Ser	Pro	Pro	Leu 10	Gly	Ala	Arg	Ser	Met 15	Ser	
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	--

Arg	Phe	Pro	Ala 20	Val	Ala	Gly	Arg	Ala 25	Pro	Arg	Arg	Gln	Glu 30	Glu	Gly
Glu	Arg	Ser 35	Arg	Asp	Leu	Gln	Glu 40	Glu	Arg	Leu	Ser	Ala 45	Val	Cys	Ile
Ala	Asp 50	Arg	Glu	Glu	Lys	Gly 55	Cys	Thr	Ser	Gln	Glu 60	Gly	Gly	Thr	Thr
Pro 65	Thr	Phe	Pro	Ile	Gln 70	Lys	Gln	Arg	Lys	Lys 75	Ile	Ile	Gln	Ala	Val 80
Arg	Asp	Asn	Ser	Phe 85	Leu	Ile	Val	Thr	Gly 90	Asn	Thr	Gly	Ser	Gly 95	Lys
Thr	Thr	Gln	Leu 100	Pro	Lys	Tyr	Leu	Tyr 105	Glu	Ala	Gly	Phe	Ser 110	Gln	His
Gly	Met	Ile 115	Gly	Val	Thr	Gln	Pro 120	Arg	Lys	Val	Ala	Ala 125	Ile	Ser	Val
Ala	Gln 130	Arg	Val	Ala	Glu	Glu 135	Met	Lys	Cys	Thr	Leu 140	Gly	Ser	Lys	Val
Gly 145	Tyr	Gln	Val	Arg	Phe 150	Asp	Asp	Cys	Ser	Ser 155	Lys	Glu	Thr	Ala	Ile 160

Lys Tyr

<210> 315  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 315

Gln 1	Ile	Gly	Gly	Arg 5	Ala	Arg	Leu	His	Ser 10	Gly	Pro	Gly	Leu	Cys 15	Pro
Gly	Phe	Pro	Gln 20	Ser	Arg	Ala	Gly	Arg 25	Gln	Gly	Gly	Arg	Arg 30	Arg	Val
Ser	Gly	Gln 35	Glu	Thr	Ser	Arg	Lys 40	Ser	Gly	Ser	Arg	Leu 45	Phe	Ala	Ser
Pro	Ile 50	Glu	Lys	Arg	Lys	Asp 55	Ala	Arg	Pro	Arg	Arg 60	Glu	Glu	Leu	Leu
Gln 65	Leu	Phe	Leu	Phe	Arg 70	Asn	Lys	Glu	Lys	Arg 75	Leu	Phe	Lys	Leu	

<210> 316  
 <211> 69  
 <212> PRT  
 <213> homo sapiens

<400> 316

Ile 1	Gly	Lys	Val	Gly 5	Val	Val	Pro	Pro	Ser 10	Trp	Asp	Val	His	Pro 15	Phe
Ser	Ser	Leu	Ser 20	Ala	Met	Gln	Thr	Ala 25	Glu	Ser	Arg	Ser	Ser 30	Trp	Arg



Pro	Pro	Ser	Ser	Leu	Phe	Leu	Pro	Gly	Ala	Tyr	Lys	Ala	Gln	Met	Tyr	
		35					40					45				
Ser	Asp	Val	Trp	Thr	Asn	Thr	Lys	Lys	His	Phe	Leu	Lys	Arg	Lys	Gly	
	50					55					60					
Met	Ser	Phe	Pro	Leu	Phe	Asp	Lys	Lys	Gln	Pro	Val	Met	Lys	Ser	Gly	
65					70					75					80	
Ala	Gln	Glu	Arg	Trp	Val	Ser	His	Leu	Glu	Ala	Phe	Arg	Thr	Gln	Leu	
				85					90					95		

<210> 319  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 319

Thr	Cys	Glu	Pro	Phe	Arg	Asn	Pro	Gln	Val	Gly	Lys	Asp	Pro	Thr	Pro	
1				5					10					15		
Ser	Leu	Arg	Ile	Ile	Cys	Leu	Ala	Ile	Thr	Gly	Ser	Trp	Lys	Cys	Phe	
			20					25					30			
Leu	Gly	Cys	Val	Lys	Ile	Asn	Gln	Gly	Gly	Met	Lys	His	Ile	Phe	Leu	
		35					40					45				
Ala	Thr	Lys	Leu	Glu	Phe	Leu	Arg	Glu	Gln	Met	Gln	Arg	Asp	Leu	Leu	
	50					55					60					
Leu	Leu	Ala	Arg	Leu	Gln	Gly	Pro	Leu	Trp	Ser	His	Thr	Glu	Ala	Val	
65					70					75					80	
Thr	Gly	His	Lys	Pro	Arg	Arg	Ala	Arg	Gly	Ser	Cys	Ala	Glu	Ala	Pro	
				85					90					95		
Gly	Pro	Leu	Ser	Gly	Ser	Phe	Pro	Ser								
			100					105								

<210> 320  
 <211> 82  
 <212> PRT  
 <213> homo sapiens

<400> 320

Ile	Arg	Lys	Arg	Glu	Gln	Gly	Arg	Ser	Ser	Pro	Ala	Pro	Trp	Glu	Ser	
1				5					10					15		
Val	Phe	Ala	Ser	Val	Pro	Phe	Arg	Gly	Asp	Asp	Gly	Ile	Phe	Asp	Asp	
			20					25					30			
Asn	Phe	Ile	Glu	Glu	Arg	Lys	Gln	Gly	Leu	Glu	Gln	Phe	Ile	Asn	Lys	
		35					40					45				
Val	Ala	Gly	His	Pro	Leu	Ala	Gln	Asn	Glu	Arg	Cys	Leu	His	Met	Phe	
	50					55					60					
Leu	Gln	Asp	Glu	Ile	Ile	Asp	Lys	Ser	Tyr	Thr	Pro	Ser	Lys	Ile	Arg	
65					70					75					80	
His	Ala															

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Val	Gln	Pro	Pro	Pro	Pro	Pro	Leu	Leu	Pro	Ala	Val	Gly	Thr	Arg	Ala
			100					105					110		

Arg Ala

<210> 323  
 <211> 374  
 <212> PRT  
 <213> homo sapiens

<400> 323

Arg	Arg	Ala	Gln	Glu	Ser	Pro	Leu	Gly	Arg	Gln	Ser	His	Leu	Pro	Arg
1				5					10					15	
Ile	Tyr	Gln	Ala	Phe	Leu	Met	Ser	Ala	Thr	Phe	Asn	Glu	Asp	Val	Gln
			20					25					30		
Ala	Leu	Lys	Glu	Leu	Ile	Leu	His	Asn	Pro	Val	Thr	Leu	Lys	Leu	Gln
		35					40					45			
Glu	Ser	Gln	Leu	Pro	Gly	Pro	Asp	Gln	Leu	Gln	Gln	Phe	Gln	Val	Val
	50					55					60				
Cys	Glu	Thr	Glu	Glu	Asp	Lys	Phe	Leu	Leu	Leu	Tyr	Ala	Leu	Leu	Lys
65					70					75					80
Leu	Ser	Leu	Ile	Arg	Gly	Lys	Ser	Leu	Leu	Phe	Val	Asn	Thr	Leu	Glu
				85					90					95	
Arg	Ser	Tyr	Arg	Leu	Arg	Leu	Phe	Leu	Glu	Gln	Phe	Ser	Ile	Pro	Thr
			100					105					110		
Cys	Val	Leu	Asn	Gly	Glu	Leu	Pro	Leu	Arg	Ser	Arg	Cys	His	Ile	Ile
		115					120					125			
Ser	Gln	Phe	Asn	Gln	Gly	Phe	Tyr	Asp	Cys	Val	Ile	Ala	Thr	Asp	Ala
	130					135					140				
Glu	Val	Leu	Gly	Ala	Pro	Val	Lys	Gly	Lys	Arg	Arg	Gly	Arg	Gly	Pro
145					150					155					160
Lys	Gly	Asp	Lys	Ala	Ser	Asp	Pro	Glu	Ala	Gly	Val	Ala	Arg	Gly	Ile
				165					170					175	
Asp	Phe	His	His	Val	Ser	Ala	Val	Leu	Asn	Phe	Asp	Leu	Pro	Pro	Thr
			180					185					190		
Pro	Glu	Ala	Tyr	Ile	His	Arg	Ala	Gly	Arg	Thr	Ala	Arg	Ala	Asn	Asn
		195					200					205			
Pro	Gly	Ile	Val	Leu	Thr	Phe	Val	Leu	Pro	Thr	Glu	Gln	Phe	His	Leu
	210					215					220				
Gly	Lys	Ile	Glu	Glu	Leu	Leu	Ser	Gly	Glu	Asn	Arg	Gly	Pro	Ile	Leu
225					230					235					240
Leu	Pro	Tyr	Gln	Phe	Arg	Met	Glu	Glu	Ile	Glu	Gly	Phe	Arg	Tyr	Arg
				245					250					255	
Cys	Arg	Asp	Ala	Met	Arg	Ser	Val	Thr	Lys	Gln	Ala	Ile	Arg	Glu	Ala
			260					265					270		

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[illegible]

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<210> 324
<211> 224
<212> PRT
<213> homo sapiens
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<400> 324

Gln 1	Arg	Val	Arg	Ala 5	Ala	Leu	Leu	Ser	Ser 10	Ala	Met	Glu	Asp	Ser 15	Glu
Ala	Leu	Gly	Phe 20	Glu	His	Met	Gly	Leu 25	Asp	Pro	Arg	Leu	Leu 30	Gln	Ala
Val	Thr	Asp 35	Leu	Gly	Trp	Ser	Arg 40	Pro	Thr	Leu	Ile	Gln 45	Glu	Lys	Ala
Ile	Pro 50	Leu	Ala	Leu	Glu	Gly 55	Lys	Asp	Leu	Leu	Ala 60	Arg	Ala	Arg	Thr
Gly 65	Ser	Gly	Lys	Thr	Ala 70	Ala	Tyr	Ala	Ile	Pro 75	Met	Leu	Gln	Leu	Leu 80
Leu	His	Arg	Lys	Ala 85	Thr	Gly	Pro	Val	Val 90	Glu	Gln	Ala	Val	Arg 95	Gly
Leu	Val	Leu	Val 100	Pro	Thr	Lys	Glu	Leu 105	Ala	Arg	Gln	Ala	Gln 110	Ser	Met
Ile	Gln	Gln 115	Leu	Ala	Thr	Tyr	Cys 120	Ala	Arg	Asp	Val	Arg 125	Val	Ala	Asn
Val	Ser 130	Ala	Ala	Glu	Asp	Ser 135	Val	Ser	Gln	Arg	Ala 140	Val	Leu	Met	Glu
Lys 145	Pro	Asp	Val	Val	Val 150	Gly	Thr	Pro	Ser	Arg 155	Ile	Leu	Ser	His	Leu 160
Gln	Gln	Asp	Ser	Leu 165	Lys	Leu	Arg	Asp	Ser 170	Leu	Glu	Leu	Leu	Val 175	Val
Asp	Glu	Ala	Asp 180	Leu	Leu	Phe	Ser	Phe 185	Gly	Phe	Glu	Glu	Glu 190	Leu	Lys



<213> homo sapiens

<400> 327

Phe 1	Arg	Ser	Cys	Leu 5	Phe	Met	Leu	Thr	Gly 10	Leu	Leu	Phe	Ile	Arg 15	Gln
Asp	Val	Leu	Val 20	Pro	Trp	His	Leu	Lys 25	Gly	Asn	Pro	Asp	Lys 30	Gly	Lys
Pro	Val	Glu 35	Pro	Phe	Gly	Pro	Ile 40	Gly	Ser	Gln	Asp	Pro 45	Ser	Pro	Val
Phe	His 50	Arg	Tyr	Tyr	His	Val 55	Phe	Arg	Glu	Gly	Glu 60	Leu	Glu	Gly	Ala
Cys 65	Arg	Thr	Val	Ser	Asp 70	Val	Arg	Ile	Leu	Gln 75	Ser	Tyr	Tyr	Asp	Gln 80
Gly	Asn	Trp	Cys	Val 85	Ile	Leu	Gln	Lys	Ala 90						

<210> 328

<211> 83

<212> PRT

<213> homo sapiens

<400> 328

Ser 1	Gly	Leu	Leu	Lys 5	Asn	His	Thr	Pro	Val 10	Ser	Leu	Ile	Val	Val 15	Ala
Leu	Gln	Asn	Ser 20	Asp	Ile	Thr	His	Ser 25	Pro	Ala	Gly	Thr	Phe 30	Gln	Phe
Ser	Leu	Thr 35	Glu	His	Met	Val	Val 40	Thr	Met	Lys	His	Arg 45	Thr	Trp	Val
Leu	Gly 50	Ser	Tyr	Gly	Thr	Lys 55	Trp	Leu	Asn	Arg	Phe 60	Ala	Phe	Ile	Arg
Ile 65	Ser	Leu	Lys	Val	Pro 70	Gly	Asn	Gln	Tyr	Ile 75	Leu	Thr	Asn	Lys	Lys 80
Lys	Ser	Cys													

<210> 329

<211> 185

<212> PRT

<213> homo sapiens

<400> 329

Glu 1	Arg	Arg	Ser	Lys 5	Ser	Arg	Glu	Glu	Arg 10	Glu	Lys	Glu	Arg	Glu 15	Arg
Glu	Arg	Glu	Glu 20	Arg	Glu	Arg	Lys	Arg 25	Arg	Arg	Glu	Glu	Glu 30	Glu	Arg
Glu	Lys	Glu 35	Arg	Ala	Arg	Asp	Arg 40	Glu	Arg	Arg	Lys	Arg 45	Ser	Arg	Ser
Arg	Ser	Arg	His	Ser	Ser	Arg	Thr	Ser	Asp	Arg	Arg	Cys	Ser	Arg	Ser







Trp	Asn	Gly	Glu	Thr	Pro	Gly	Gln	Glu	Asp	Ser	Asn	Ser
	50					55					60	

<210> 336  
 <211> 63  
 <212> PRT  
 <213> homo sapiens

<400> 336

Ala	Glu	Asp	Thr	Ile	Gln	Lys	Arg	Asn	Ser	Gln	Phe	Glu	Thr	Val	Thr
1				5					10					15	
Pro	Pro	Ala	Pro	Asn	Cys	Gly	Asp	Glu	Glu	Arg	Lys	Gln	Trp	Leu	Trp
			20					25					30		
Phe	Leu	Ser	Glu	Gly	Arg	Leu	Arg	Thr	Glu	Arg	Ser	Asn	His	Gln	Gly
		35					40					45			
His	Arg	Phe	Trp	Lys	Ser	Ser	Arg	Gly	Gly	Trp	Leu	Glu	Glu	Gln	
	50					55					60				

<210> 337  
 <211> 65  
 <212> PRT  
 <213> homo sapiens

<400> 337

Lys	Gly	Trp	Arg	Ser	Asp	Phe	Thr	Val	Gly	Gly	Arg	Gln	Arg	Asp	Gly
1				5					10					15	
Gln	His	Val	Gln	Thr	Gly	Ser	Phe	Phe	Ser	Ile	Ser	Leu	Leu	Ser	Lys
			20					25					30		
Ser	Arg	Thr	Ala	Gln	Trp	Leu	Cys	Gln	Gly	Gly	Ser	Ser	Ser	Tyr	Ser
		35					40					45			
His	Phe	Ser	Gly	Ser	Leu	Lys	Ser	Thr	Arg	Tyr	Tyr	Arg	Gly	Ser	Arg
	50					55					60				
Ser															
65															

<210> 338  
 <211> 249  
 <212> PRT  
 <213> homo sapiens

<400> 338

Ser	Cys	Gly	Asp	Val	Glu	Gln	Lys	Ile	Gln	Phe	Lys	Arg	Glu	Thr	Ala
1				5					10					15	
Ser	Leu	Lys	Leu	Leu	Pro	His	Gln	Pro	Arg	Ile	Val	Glu	Met	Lys	Lys
			20					25					30		
Gly	Ser	Asn	Gly	Tyr	Gly	Phe	Tyr	Leu	Arg	Ala	Gly	Ser	Glu	Gln	Lys
		35					40					45			
Gly	Gln	Ile	Ile	Lys	Asp	Ile	Asp	Ser	Gly	Ser	Pro	Ala	Glu	Glu	Ala
	50					55					60				

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Gly 65	Leu	Lys	Asn	Asn	Asp 70	Leu	Val	Val	Ala	Val 75	Asn	Gly	Glu	Ser	Val 80
Glu	Thr	Leu	Asp	His 85	Asp	Ser	Val	Val	Glu 90	Met	Ile	Arg	Lys	Gly 95	Gly
Asp	Gln	Thr	Ser 100	Leu	Leu	Val	Val	Asp 105	Lys	Glu	Thr	Asp	Asn 110	Met	Tyr
Arg	Leu	Ala 115	His	Phe	Ser	Pro	Phe 120	Leu	Tyr	Tyr	Gln	Ser 125	Gln	Glu	Leu
Pro	Asn 130	Gly	Ser	Val	Lys	Glu 135	Ala	Pro	Ala	Pro	Thr 140	Pro	Thr	Ser	Leu
Glu 145	Val	Ser	Ser	Pro	Pro 150	Asp	Thr	Thr	Glu	Glu 155	Val	Asp	His	Lys	Pro 160
Lys	Leu	Cys	Arg	Leu 165	Ala	Lys	Gly	Glu	Asn 170	Gly	Tyr	Gly	Phe	His 175	Leu
Asn	Ala	Ile	Arg 180	Gly	Leu	Pro	Gly	Ser 185	Phe	Ile	Lys	Glu	Val 190	Gln	Lys
Gly	Gly	Pro 195	Ala	Asp	Leu	Ala	Gly 200	Leu	Glu	Asp	Glu	Asp 205	Val	Ile	Ile
Glu	Val 210	Asn	Gly	Val	Asn	Val 215	Leu	Asp	Glu	Pro	Tyr 220	Glu	Lys	Val	Val
Asp 225	Arg	Ile	Gln	Ser	Ser 230	Gly	Lys	Asn	Val	Thr 235	Leu	Leu	Val	Cys	Gly 240
Lys	Lys	Ala	Tyr	Asp 245	Tyr	Phe	Gln	Ala							

<210> 339  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 339

Ile 1	Thr	Gly	Val	Gln 5	Pro	Glu	His	Ile	Gln 10	Tyr	Leu	Lys	Asn	Tyr 15	Phe
His	Leu	Trp	Thr 20	Arg	Gln	Leu	Ala	His 25	Ile	Tyr	His	Tyr	Tyr 30	Ile	His
Gly	Pro	Lys 35	Gly	Asn	Glu	Ile	Arg 40	Thr	Ser	Lys	Glu	Val 45	Glu	Pro	Phe
Asn	Asn 50	Ile	Asp	Ile	Glu	Ile 55	Ser	Met	Phe	Glu	Lys 60	Gly	Lys	Val	Pro
Lys 65	Ile	Val													

<210> 340  
 <211> 44  
 <212> PRT  
 <213> homo sapiens

<400> 340

Arg	Ile	Phe	Ile	Thr	Thr	Ile	Phe	Met	Ala	Gln	Lys	Glu	Met	Lys	Tyr
1				5					10					15	
Glu	His	Gln	Lys	Lys	Leu	Asn	Leu	Ser	Thr	Ile	Leu	Ile	Leu	Lys	Phe
			20					25					30		
Leu	Cys	Leu	Lys	Lys	Gly	Arg	Tyr	Leu	Arg	Leu	Ser				
		35					40								

<210> 341

<211> 46

<212> PRT

<213> homo sapiens

<400> 341

Lys	Val	Gln	Leu	Leu	Leu	Met	Phe	Val	Phe	His	Phe	Leu	Leu	Gly	His
1				5					10					15	
Glu	Tyr	Ser	Ser	Asp	Lys	Tyr	Ala	Leu	Thr	Val	Val	Ser	Lys	Gly	Gly
			20					25					30		
Asn	Asn	Phe	Ser	Ser	Thr	Val	Cys	Val	Leu	Val	Val	Pro	Leu		
		35					40					45			

<210> 342

<211> 237

<212> PRT

<213> homo sapiens

<400> 342

Gly	Arg	Trp	Arg	Arg	Arg	Leu	Arg	His	Gly	Arg	Gly	Ser	Ala	Glu	Ala
1				5					10					15	
Val	Gly	Pro	Thr	Ala	Met	Ala	Glu	Leu	Leu	Gln	Glu	Glu	Leu	Ser	Val
			20					25					30		
Leu	Ala	Ala	Ile	Phe	Cys	Arg	Pro	His	Glu	Trp	Glu	Val	Leu	Ser	Arg
		35					40					45			
Ser	Glu	Thr	Asp	Gly	Thr	Val	Phe	Arg	Ile	His	Thr	Lys	Ala	Glu	Gly
	50					55					60				
Phe	Met	Asp	Ala	Asp	Ile	Pro	Leu	Glu	Leu	Val	Phe	His	Leu	Pro	Val
	65				70					75					80
Asn	Tyr	Pro	Ser	Cys	Leu	Pro	Gly	Ile	Ser	Ile	Asn	Ser	Glu	Gln	Leu
				85					90					95	
Thr	Arg	Ala	Gln	Cys	Val	Thr	Val	Lys	Glu	Lys	Leu	Leu	Glu	Gln	Ala
			100					105					110		
Glu	Ser	Leu	Leu	Ser	Glu	Pro	Met	Val	His	Glu	Leu	Val	Leu	Trp	Ile
		115					120					125			
Gln	Gln	Asn	Leu	Arg	His	Ile	Leu	Ser	Gln	Pro	Glu	Thr	Gly	Ser	Gly
	130					135					140				
Ser	Glu	Lys	Cys	Thr	Phe	Ser	Thr	Ser	Thr	Thr	Met	Asp	Asp	Gly	Leu

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145					150					155					160
Trp	Ile	Thr	Leu	Leu	His	Leu	Asp	His	Met	Arg	Ala	Lys	Thr	Lys	Tyr
				165					170					175	
Val	Lys	Ile	Val	Glu	Lys	Trp	Ala	Ser	Asp	Leu	Arg	Leu	Thr	Gly	Arg
			180					185					190		
Leu	Met	Phe	Met	Gly	Lys	Ile	Ile	Leu	Asp	Phe	Thr	Thr	Gly	Arg	Gln
		195					200					205			
Lys	Gln	Pro	Gln	Gly	Val	Leu	Asp	Ser	Ser	Glu	Asn	Leu	Gln	Ser	Arg
	210					215					220				
Cys	Gly	Leu	Lys	Trp	Lys	Glu	Met	Gln	Arg	Glu	Asn	Asp			
225					230					235					

<210> 343  
 <211> 89  
 <212> PRT  
 <213> homo sapiens

<400> 343

Tyr	Leu	Ile	Leu	Leu	Gln	Gly	Asp	Arg	Asn	Asn	Leu	Lys	Val	Tyr	Leu
1				5					10					15	
Ile	Leu	Gln	Lys	Thr	Ser	Lys	Val	Asp	Val	Asp	Ser	Ser	Gly	Lys	Lys
			20					25					30		
Cys	Lys	Glu	Lys	Met	Ile	Ser	Val	Leu	Phe	Glu	Thr	Lys	Val	Gln	Thr
		35					40					45			
Glu	His	Lys	Arg	Phe	Leu	Ala	Phe	Glu	Val	Lys	Glu	Tyr	Ser	Ala	Leu
	50					55					60				
Asp	Glu	Leu	Gln	Lys	Glu	Phe	Glu	Thr	Ala	Gly	Leu	Lys	Lys	Leu	Phe
65					70					75					80
Ser	Glu	Phe	Val	Leu	Ala	Leu	Val	Lys							
				85											

<210> 344  
 <211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 344

Pro	Leu	Pro	Lys	Ser	Asn	Ala	Lys	Thr	Thr	Lys	Asn	Thr	Ala	Ile	Leu
1				5					10					15	
Leu	Lys	Asp	Ser	Cys	Leu	Pro	Phe	His	Phe	Thr	Arg	Ala	Ser	Thr	Asn
			20					25					30		
Ser	Glu	Lys	Ser	Phe	Leu	Ser	Pro	Ala	Val	Ser	Asn	Ser	Phe	Cys	Asn
		35					40					45			
Ser	Ser	Asn	Ala	Glu	Tyr	Ser	Leu	Thr	Ser	Asn	Ala	Arg	Asn	Leu	Leu
	50					55					60				
Cys	Ser	Val	Cys	Thr	Phe	Val	Ser	Asn	Ser	Thr	Leu	Ile	Ile	Phe	Ser
65					70					75					80



Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 ± 2.0
Marital status	
Married	40 (80.0%)
Single	10 (20.0%)
Occupation	
Retired	30 (60.0%)
Unemployed	20 (40.0%)
Income (USD/month)	1,200 ± 300
Health status	
Good	30 (60.0%)
Fair	20 (40.0%)
Poor	10 (20.0%)
Comorbidities	
Hypertension	20 (40.0%)
Diabetes	10 (20.0%)
Cholesterol	15 (30.0%)
Smoking status	
Smoker	10 (20.0%)
Non-smoker	40 (80.0%)
Alcohol consumption	
Regular	5 (10.0%)
Occasional	15 (30.0%)
Never	30 (60.0%)

<400> 347

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<210> 348
<211> 103
<212> PRT
<213> homo sapiens
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<400> 348

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<210> 349
<211> 50
<212> PRT
<213> homo sapiens
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<400> 349

Glu Ser Lys Asn Lys Val Trp Gly Ala Asp Glu Cys Val Ile Ile Tyr



1				5				10				15			
Gln	Thr	Phe	Cys 20	Ala	Cys	Cys	Ser	Pro 25	Lys	Ala	Trp	Ser	Ser 30	Gln	Ser
Pro	Glu	Phe 35	Trp	Cys	Val	Leu	Pro 40	Pro	Pro	Gly	Tyr	Thr 45	Glu	Arg	Arg
Gln	Glu 50	Ser	Gly	Val	Pro	Glu 55	Ala	Tyr	Thr	Cys	Gly 60	Tyr	Pro	Ser	Asn
Lys 65	Arg	His	Pro	Val	Leu 70	Arg									

<210> 353  
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 <212> PRT  
 <213> homo sapiens

<400> 353

Ser 1	Gly	Gln	Cys	Gly 5	Met	Gln	Leu	Gly	Pro 10	Asp	Gln	Pro	Ser	Ser 15	Glu
Gln	Met	Ala	Val 20	Val	Pro	Ile	Ser	Thr 25	Lys	Pro	Gln	Arg	Ala 30	Arg	Lys
Asn	Thr	Ser 35	Gln	Pro	Cys	Ser	Leu 40	Ser	Glu	His	Arg	Met 45	Pro	Leu	Val
Ala	Gly 50	Val	Ala	Thr	Cys	Ile 55	Cys	Phe	Trp	Asn	Ser 60				

<210> 354  
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 <212> PRT  
 <213> homo sapiens

<400> 354

Gly 1	Leu	Pro	Ala	Arg 5	Arg	Pro	Gln	Cys	Phe 10	Leu	Arg	Ala	Glu	Met 15	Ala
Asn	Ser	Gly	Leu 20	Gln	Leu	Leu	Gly	Phe 25	Ser	Met	Ala	Leu	Leu 30	Gly	Trp
Val	Gly	Leu 35	Val	Ala	Cys	Thr	Ala 40	Ile	Pro	Gln	Trp	Gln 45	Met	Ser	Ser
Tyr	Ala 50	Gly	Asp	Asn	Ile	Ile 55	Thr	Ala	Gln	Ala	Met 60	Tyr	Lys	Gly	Leu
Trp 65	Met	Asp	Cys	Val	Thr 70	Gln	Ser	Thr	Gly	Met 75	Met	Ser	Cys	Lys	Met 80
Tyr	Asp	Ser	Val	Leu 85	Ala	Leu	Ser	Ala	Ala 90	Leu	Gln	Ala	Thr	Arg 95	Ala
Leu	Met	Val	Val 100	Ser	Leu	Val	Leu	Gly 105	Phe	Leu	Ala	Met	Phe 110	Val	Ala
Thr	Met	Gly 115	Met	Lys	Cys	Thr	Arg 120	Cys	Gly	Gly	Asp	Asp 125	Lys	Val	Lys

Lys	Ala	Arg	Ile	Ala	Met	Gly	Gly	Gly	Ile	Ile	Phe	Ile	Val	Ala	Gly
	130					135					140				
Leu	Ala	Ala	Leu	Val	Ala	Cys	Ser	Trp	Tyr	Gly	His	Gln	Ile	Val	Thr
145					150					155					160
Asp	Phe	Tyr	Asn	Pro	Leu	Ile	Pro	Thr	Asn	Ile	Lys	Tyr	Glu	Phe	Gly
				165					170					175	
Pro	Ala	Ile	Phe	Ile	Gly	Trp	Ala	Gly	Ser	Ala	Leu	Val	Ile	Leu	Gly
			180					185					190		
Gly	Ala	Leu	Leu	Ser	Cys	Ser	Cys	Pro	Gly	Asn	Glu	Ser	Lys	Ala	Gly
		195					200					205			
Tyr	Arg	Ala	Pro	Arg	Ser	Tyr	Pro	Lys	Ser	Asn	Ser	Ser	Lys	Glu	Tyr
	210					215					220				
Val															
225															

<210> 355  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 355

Gln	His	His	His	Gly	Pro	Gly	His	Val	Gln	Gly	Ala	Val	Asp	Gly	Leu
1				5					10					15	
Arg	His	Ala	Glu	His	Gly	Asp	Asp	Glu	Leu	Gln	Asn	Val	Arg	Leu	Gly
			20					25					30		
Ala	Arg	Pro	Val	Arg	Gly	Leu	Ala	Gly	His	Ser	Ser	Pro	Asn	Gly	Gly
		35					40					45			
Leu	Pro	Gly	Ala	Gly	Leu	Pro	Gly	His	Val	Cys	Gly	His	Asp	Gly	His
	50					55					60				
Glu	Val	His	Ala	Leu	Trp	Gly	Arg	Arg	Gln	Ser	Glu	Glu	Gly	Pro	Tyr
65					70					75					80
Ser	His	Gly	Trp	Arg	His	Asn	Phe	His	Arg	Gly	Arg	Ser	Cys	Arg	Leu
				85					90					95	
Gly	Ser	Leu	Leu	Leu	Val	Trp	Pro	Ser	Asp	Cys	His	Arg	Leu	Leu	
			100					105					110		

<210> 356  
 <211> 154  
 <212> PRT  
 <213> homo sapiens

<400> 356

Cys	Cys	His	Pro	His	Arg	Ser	Ser	Ser	Ala	Thr	Ala	Gly	Trp	Arg	Cys
1				5					10					15	
Arg	Pro	Pro	Asp	Pro	Pro	Ser	Pro	Ala	Gly	Pro	Trp	Arg	Ser	Pro	Ala
			20					25					30		

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60

<400> 360

<400> 361

<400> 362

Socioeconomic status		Age		Gender		Marital status		Religion		Education		Occupation		Income		Health status		Mental health		Substance use		Social support		Life satisfaction		Quality of life	
SES	SES	Age	Age	Gender	Gender	Marital status	Marital status	Religion	Religion	Education	Education	Occupation	Occupation	Income	Income	Health status	Health status	Mental health	Mental health	Substance use	Substance use	Social support	Social support	Life satisfaction	Life satisfaction	Quality of life	Quality of life
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18										

Thr 1	Arg	Asn	Gly	Ser 5	Val	Phe	Gly	Cys	Tyr 10	Arg	Pro	His	Arg	Phe 15	Pro
Ala	Gly	Lys	Ser 20	Val	Ser	Leu	Val	Tyr 25	Ser	Arg	Gly	Phe	Gln 30	His	Pro
Pro	Cys	Ala 35	Tyr	His	Leu	Leu	Gly 40	Gln	Gly	Arg	Arg	Ser 45	Val	Ser	Glu
Ala	Cys 50	Arg	Ser	Tyr	Val	Thr 55	Pro	Asp	Ser	Asn	Gly 60	Trp	Lys	Arg	Thr
Asn 65	Gly	Gln	Asp	Phe	Leu 70	Leu	Leu	Leu	Leu	Lys 75	Thr	Leu	Met	Val	Lys 80
Arg	Lys	Asp	Trp	Gly 85	Gln	Pro	Gly	Ser	Ser 90	Gly	Pro	Thr	Ser	Lys 95	Phe
Pro	Leu	Gln	Val 100	Ile	Leu	Cys	Gln	Ala 105	Leu	Phe	Lys	Lys			

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<210> 363
<211> 381
<212> PRT
<213> homo sapiens
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<400> 363

Gly 1	Pro	Ala	Arg	Arg 5	Pro	Ala	Ala	Arg	Leu 10	Ala	Arg	Ala	Gly	Gly 15	Pro
Gln	Ala	Ala	Asp 20	Arg	Ala	Gly	Lys	Gln 25	Ser	Gly	Pro	Pro	Ala 30	Pro	Gly
Cys	Ser	Trp 35	Leu	Pro	Ala	Glu	Ala 40	Ala	Gly	Ala	Thr	Val 45	Gly	Gly	Leu
Cys	Pro 50	Arg	Arg	Ala	Pro	Ala 55	Gly	Pro	Trp	His	Gln 60	Gly	Pro	Gln	Arg
Pro 65	Val	Lys	Asp	Glu	Pro 70	Gln	Asp	Gly	Glu	Asn 75	Pro	Asn	Pro	Pro	Asn 80
Trp	Ser	Arg	Thr	Val 85	Val	Arg	Asp	Val	Arg 90	Leu	Ile	Ser	Ala	Lys 95	Thr
Gly	Tyr	Gly	Val 100	Glu	Glu	Leu	Ile	Ser 105	Ala	Leu	Gln	Arg	Ser 110	Trp	Arg
Tyr	Arg	Gly 115	Asp	Val	Tyr	Leu	Val 120	Gly	Ala	Thr	Asn	Ala 125	Gly	Lys	Ser
Thr	Leu 130	Phe	Asn	Thr	Leu	Leu 135	Glu	Ser	Asp	Tyr	Cys 140	Thr	Ala	Lys	Gly
Ser 145	Glu	Ala	Ile	Asp	Arg 150	Ala	Thr	Ile	Ser	Pro 155	Trp	Pro	Gly	Thr	Thr 160
Leu	Asn	Leu	Leu	Lys 165	Phe	Pro	Ile	Cys	Asn 170	Pro	Thr	Pro	Tyr	Arg 175	Met
Phe	Lys	Arg	His 180	Gln	Arg	Leu	Lys	Lys 185	Asp	Ser	Thr	Gln	Ala 190	Glu	Glu



100						105						110			
Ala	Asp	Ala	Glu	Glu	Lys	Leu	Asp	Arg	Ser	His	Asp	Lys	Ser	Asp	Arg
		115					120					125			
Gly	His	Asp	Lys	Ser	Asp	Arg	Ser	His	Glu	Lys	Leu	Asp	Arg	Gly	His
	130					135					140				
Asp	Lys	Ser	Asp	Arg	Gly	His	Asp	Lys	Ser	Asp	Arg	Asp	Arg	Glu	Arg
145					150					155					160
Gly	Tyr	Asp	Lys	Ser	Arg	Asn	Gly	Ile	Arg	Asp	Arg	Gly	Tyr	Asp	Gln
				165					170					175	
Ala	Asp	Arg	Glu	Glu	Gly										
			180												

<210> 365  
 <211> 149  
 <212> PRT  
 <213> homo sapiens

<400> 365

Arg	Arg	His	Glu	Arg	Asp	Gly	Arg	Cys	Asp	Ser	Leu	Pro	Leu	Pro	Ala
1				5					10					15	
Arg	Val	Tyr	Trp	Ser	Val	Cys	Tyr	Gln	Leu	Cys	Arg	Cys	Pro	Leu	Arg
			20					25					30		
Cys	Arg	Pro	Ala	Trp	Pro	Arg	Glu	Ala	Ser	Ser	Asn	Ile	Trp	Ser	Leu
		35					40					45			
Asn	Gln	Arg	Lys	Arg	Ser	Leu	Pro	Arg	Thr	Met	Thr	Met	Ile	Leu	Trp
	50					55					60				
Thr	Thr	Arg	Pro	Pro	Gly	Trp	Arg	Ala	Tyr	His	Gln	Ala	Gly	Thr	Arg
					70					75					80
Cys	Ser	Thr	Leu	Pro	Ala	Gly	Ser	Leu	Thr	Thr	Gly	Met	Gln	Thr	Gln
				85					90					95	
Thr	Leu	Tyr	Pro	Gly	Ser	Pro	His	Met	Thr	Pro	Thr	Pro	Trp	Leu	Pro
			100					105					110		
Asn	Arg	Pro	Arg	Ser	Ser	Glu	Ala	Val	Met	Gln	Met	Leu	Lys	Lys	Ser
		115					120					125			
Trp	Thr	Gly	Ala	Met	Thr	Ser	Arg	Thr	Gly	Ala	Met	Thr	Ser	Arg	Thr
	130					135					140				
Ala	Ala	Met	Arg	Asn											
145															

<210> 366  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 366

Pro	Arg	Ser	Arg	Ser	Leu	Ser	Asp	Leu	Ser	Trp	Pro	Arg	Ser	Asp	Leu
1				5					10					15	



Thr	Leu	Ser	Pro	Val	Gln	Gly	Ala	Cys	Leu	Leu	Leu	Val	Cys	Ala	Gly
		35					40					45			
Ser	Gly	Phe	Lys	Glu	Leu	Ala	Glu	Gly	Gly	Pro	His	Leu	Gly	Asp	His
	50					55					60				
Val	Gly	Gly	Gly	Gly	Gly	Ala	Thr	Val	Leu	Leu	Glu	Gly	Leu	Val	Val
65					70					75					80
Ala	Leu	Pro	Gly	Glu	Arg	Ala	Gly	Ala	Lys	Arg	Gly	His	Gln	Glu	Arg
				85					90					95	
Ala	Gly	Pro	Ile	Cys	Phe	Leu	Trp	Ser	Ser	Lys	Glu	Arg	Pro	Val	Tyr
			100					105					110		
Gln	Asp	Ala	Gln	Gly	Ala	Arg	Gln	Glu	Val	Pro	Leu	Pro	Ser	Thr	Pro
		115					120					125			
Ala	Ala	Ala	Ala	Phe	Leu	Ala	Ala	His	Lys	His	Leu	Leu	Ala	Val	Gly
	130					135					140				
Glu	Asp	Val	Ala	Leu	Ser	Phe	Leu	Asp	His	Arg	His	Val	Ala	Gln	Gly
145					150					155					160
Leu	Ala	Glu	Ser												

<210> 369

<211> 187

<212> PRT

<213> homo sapiens

<400> 369

Lys	Ser	Gly	Lys	His	Arg	Thr	Pro	Ser	Ala	His	Ala	Trp	Val	Arg	Ile
1				5					10					15	
Phe	Pro	Ser	His	Thr	Arg	Ser	Pro	Pro	Ser	Lys	Val	Pro	Val	Tyr	Phe
			20					25					30		
Trp	Ser	Ala	Arg	Ala	Gln	Val	Ser	Lys	Ser	Leu	Leu	Lys	Ala	Ala	Pro
		35					40					45			
Thr	Ser	Ala	Ile	Met	Ser	Glu	Val	Val	Val	Glu	Arg	Pro	Cys	Phe	Trp
	50					55					60				
Lys	Ala	Trp	Trp	Leu	His	Cys	Leu	Val	Arg	Glu	Gln	Ala	Pro	Asn	Ala
65					70					75					80
Ala	Thr	Arg	Arg	Gly	Leu	Asp	Pro	Phe	Val	Phe	Cys	Gly	Pro	Ala	Arg
				85					90					95	
Ser	Ala	Gln	Cys	Thr	Arg	Thr	Pro	Arg	Glu	Pro	Asp	Arg	Arg	Ser	Pro
			100					105					110		
Cys	Pro	Pro	His	Leu	Arg	Leu	Leu	Pro	Ser	Trp	Leu	His	Thr	Ser	Thr
		115					120					125			
Cys	Trp	Pro	Leu	Glu	Arg	Met	Ser	Arg	Ser	Pro	Phe	Trp	Thr	Thr	Val
	130					135					140				
Thr	Leu	Pro	Arg	Ala	Trp	Leu	Ser	Leu	Ser	Thr	Asp	Pro	Trp	Leu	Ser
145					150					155					160

Ser	Leu	Ser	Ile	Gly	Pro	Leu	Ser	Thr	Ala	Ser	Tyr	Ser	Leu	Leu	Asn
				165					170					175	

Ser	Thr	Trp	Leu	Gly	Val	Ser	Thr	Ala	Phe	Arg
			180					185		

<210> 370  
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 <212> PRT  
 <213> homo sapiens

<400> 370

Leu	Phe	Leu	Phe	Thr	Asn	His	Asn	Asp	Ser	Gly	Lys	Pro	Gly	Cys	Lys
1				5					10					15	
His	Gln	His	Cys	His	Gln	Leu	Arg	Ile	Cys	Asp	Gln	Glu	Cys	His	Leu
			20					25					30		
Thr	Val	Thr	Gly	Arg	Arg	Gln	Lys								
			35				40								

<210> 371  
 <211> 34  
 <212> PRT  
 <213> homo sapiens

<400> 371

Gln	Ala	Glu	Asp	Lys	Ser	Glu	Thr	Gly	Leu	Met	Arg	Ile	Thr	Gly	Lys
1				5					10					15	
Leu	Ala	Leu	Ala	Pro	Pro	Glu	Asn	Glu	Leu	Phe	His	Ser	Leu	Ala	Asp
			20					25					30		
His	Pro														

<210> 372  
 <211> 38  
 <212> PRT  
 <213> homo sapiens

<400> 372

Asn	Ser	Ser	Phe	Ser	Gly	Gly	Ala	Lys	Ala	Ser	Phe	Pro	Val	Ile	Arg
1				5					10					15	
Ile	Ser	Pro	Val	Ser	Leu	Leu	Ser	Ser	Ala	Cys	Tyr	Arg	Glu	Met	Ala
			20					25					30		
Leu	Leu	Ile	Thr	Asp	Pro										
			35												

<210> 373  
 <211> 123  
 <212> PRT  
 <213> homo sapiens

<400> 373

Arg	Gln	Leu	Phe	Gly	Ile	Val	Ser	Ile	Ala	Thr	Leu	Thr	Val	Leu	Ala
1				5					10					15	

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Tyr	Glu	Arg	Tyr 20	Ile	Arg	Val	Val	His 25	Ala	Arg	Val	Ile	Asn 30	Phe	Ser
Trp	Ala	Trp 35	Arg	Ala	Ile	Thr	Tyr 40	Ile	Trp	Leu	Tyr	Ser 45	Leu	Ala	Trp
Ala	Gly 50	Ala	Pro	Leu	Leu	Gly 55	Trp	Asn	Arg	Tyr	Ile 60	Leu	Asp	Val	His
Gly 65	Leu	Gly	Cys	Thr	Val 70	Asp	Trp	Lys	Ser	Lys 75	Asp	Ala	Asn	Asp	Ser 80
Ser	Phe	Val	Leu	Phe 85	Leu	Phe	Leu	Gly	Cys 90	Leu	Val	Val	Pro	Leu 95	Gly
Val	Ile	Ala	His 100	Cys	Tyr	Gly	His	Ile 105	Leu	Tyr	Phe	His	Ser 110	Asn	Ala
Ser	Leu	Val 115	Trp	Lys	Ile	Phe	Arg 120	Gln	Phe	Lys					

<210> 374  
 <211> 121  
 <212> PRT  
 <213> homo sapiens

<400> 374

Thr 1	Val	His	Ser	Arg 5	Gly	Pro	Cys	Gln	Ser 10	Asp	Gln	Phe	Phe	Leu 15	Gly
Leu	Glu	Gly	His 20	Tyr	Leu	His	Leu	Ala 25	Leu	Leu	Thr	Gly	Val 30	Gly	Arg
Ser	Thr	Ser 35	Pro	Gly	Met	Glu	Gln 40	Val	His	Pro	Gly	Arg 45	Thr	Arg	Thr
Arg	Leu 50	His	Cys	Gly	Leu	Glu 55	Ile	Gln	Gly	Cys	Gln 60	Arg	Phe	Leu	Leu
Cys 65	Ala	Phe	Leu	Ile	Ser 70	Trp	Leu	Pro	Gly	Gly 75	Ala	Pro	Gly	Cys	His 80
Ser	Pro	Leu	Leu	Trp 85	Pro	Tyr	Ser	Ile	Phe 90	Pro	Phe	Glu	Cys	Phe 95	Val
Gly	Val	Glu	Asp 100	Leu	Gln	Thr	Ile	Gln 105	Val	Ile	Lys	Ile	Leu 110	Lys	Tyr
Glu	Lys	Lys 115	Leu	Ala	Lys	Met	Cys 120	Phe							

<210> 375  
 <211> 58  
 <212> PRT  
 <213> homo sapiens

<400> 375

His 1	Pro	Gly	Ala	Pro 5	Pro	Gly	Ser	Gln	Glu 10	Ile	Arg	Lys	Ala	Gln 15	Arg
Arg	Asn	Arg	Trp	His	Pro	Trp	Ile	Ser	Ser	Pro	Gln	Cys	Ser	Leu	Val

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			20					25					30			
Arg	Val	Arg	Pro	Gly	Cys	Thr	Cys	Ser	Ile	Pro	Gly	Glu	Val	Leu	Leu	
		35					40					45				
Pro	Thr	Pro	Val	Ser	Arg	Ala	Arg	Cys	Arg							
	50					55										

<210> 376  
 <211> 49  
 <212> PRT  
 <213> homo sapiens

<400> 376

Ala	Phe	Thr	Cys	Asp	Phe	Val	Pro	Leu	Cys	Gly	Leu	Leu	Glu	Gln	Trp	
1				5					10					15		
Thr	Thr	Lys	Ser	Ala	Met	Gln	Phe	Ile	Lys	Val	Asp	Leu	Val	Ile	Cys	
			20					25					30			
His	Pro	Thr	Ala	Tyr	Gly	Pro	Cys	Lys	Pro	Val	Leu	Glu	Ala	Asn	Ile	
		35					40					45				
Leu																

<210> 377  
 <211> 68  
 <212> PRT  
 <213> homo sapiens

<400> 377

Phe	Cys	Thr	Thr	Leu	Trp	Pro	Ser	Gly	Ala	Met	Asp	Asn	Gln	Val	Ser	
1				5					10					15		
Tyr	Ala	Val	His	Lys	Ser	Gly	Pro	Gly	Tyr	Met	Ser	Ser	Asn	Ser	Ile	
			20					25					30			
Trp	Ser	Leu	Gln	Ala	Cys	Phe	Gly	Ser	Gln	Tyr	Ser	Ile	Thr	Tyr	Arg	
		35					40					45				
Asn	Pro	Leu	Glu	Ser	Asp	Val	Phe	Gly	Ser	Asn	Ile	Phe	Ser	Gln	Gly	
	50					55					60					
Ser	Asn	Gly	Leu													
65																

<210> 378  
 <211> 64  
 <212> PRT  
 <213> homo sapiens

<400> 378

His	Ile	Thr	Arg	Ser	Thr	Phe	Met	Asn	Cys	Ile	Ala	Asp	Leu	Val	Val	
1				5					10					15		
His	Cys	Ser	Arg	Arg	Pro	Gln	Ser	Gly	Thr	Lys	Ser	Gln	Val	Lys	Ala	
			20					25					30			
Gln	Thr	Ala	Pro	Val	Ile	Leu	Val	Val	Leu	Ser	Leu	His	Ser	Ser	Pro	
		35					40					45				

Leu Ala Lys Thr Gly Leu Asn Met Lys Ser Pro Ala Pro Arg Pro Gln  
50 55 60

<210> 379

<211> 144

<212> PRT

<213> homo sapiens

<400> 379

Ala    Pro    Ile    Ser    Ser    Asn    Phe    Cys    Ser    Glu    Ser    Ile    Trp    Gly    Tyr    Cys  
1                          5                          10                          15

Asp Gln Leu Lys Val Ser Glu Ser Thr His Val Leu Gln Pro Phe Leu  
20 25 30

Pro Ser Ile Leu Asp Gly Leu Ile His Leu Ala Ala Gln Phe Ser Ser  
35 40 45

Glu Val Leu Asn Leu Val Met Glu Thr Leu Cys Ile Val Cys Thr Val  
50 55 60

Asp 65    Pro    Glu    Phe    Thr    Ala 70    Ser    Met    Glu    Ser    Lys 75    Ile    Cys    Pro    Phe    Thr 80

Ile Ala Ile Phe Leu Lys Tyr Ser Asn Asp Pro Val Val Ala Ser Leu  
85 90 95

Ala Gln Asp Ile Phe Lys Glu Leu Ser Gln Ile Glu Ala Cys Gln Gly  
100 105 110

Pro	Met	Gln	Met	Arg	Leu	Ile	Pro	Thr	Leu	Val	Ser	Ile	Met	Gln	Ala
		115					120					125			

Pro	Ala	Asp	Lys	Ile	Pro	Ala	Gly	Leu	Cys	Ala	Thr	Pro	Leu	Ile	Ser
	130					135					140				

<210> 380

<211> 254

<212> PRT

<213> homo sapiens

<400> 380

Tyr 1   Glu   Ile   Gln   Ser 5   Leu   Pro   Phe   Pro   Ser 10   Phe   Ser   Ser   Ala   Lys 15   Leu

Ser Leu Leu Trp His Ser Val Pro Phe Thr Gln Met Thr Met Pro Ser  
20 25 30

Val	Gln	Asn	Gly	Gly	Glu	Cys	Leu	Arg	Ala	Tyr	Val	Ser	Val	Thr	Leu
		35					40					45			

Glu Gln Val Ala Gln Trp His Asp Glu Gln Gly His Asn Gly Leu Trp  
50 55 60

Tyr Val Met Gln Val Val Ser Gln Leu Leu Asp Pro Arg Thr Ser Glu  
65 70 75 80

Phe Thr Ala Ala Phe Val Gly Arg Leu Val Ser Thr Leu Ile Ser Lys  
85 90 95













Ser	Ser	Tyr	Val	Met	Ser	Leu	Val	Thr	Lys	Val	Lys	Leu	Ser	His	Pro
65					70					75					80

Glu Lys Ala Thr

<210> 391  
 <211> 59  
 <212> PRT  
 <213> homo sapiens

<400> 391

Cys	Gly	Lys	Lys	Cys	Ile	Thr	Leu	Phe	Leu	Phe	Leu	Ser	Pro	Ser	Leu
1				5					10					15	
Pro	Leu	Trp	Cys	Leu	Arg	Tyr	Trp	Gly	Ser	His	Ser	Trp	Gly	His	Ser
			20					25					30		
Glu	Ala	Thr	Arg	Asn	Ala	Ser	Ser	Leu	His	Leu	Ala	Val	Ser	Ala	Arg
		35					40					45			
Thr	Arg	Asn	Pro	Gln	Thr	Ser	Ser	Gln	Thr	Ser					
	50					55									

<210> 392  
 <211> 107  
 <212> PRT  
 <213> homo sapiens

<400> 392

Thr	Pro	Arg	Asn	Leu	Asn	Phe	His	Ser	Lys	Leu	Thr	Gln	Phe	His	Cys
1				5					10					15	
Val	Asn	Thr	Val	Ser	Leu	Gly	Ser	Thr	Lys	His	Pro	Ile	Thr	Gln	Phe
			20					25					30		
Cys	Phe	Ile	Val	Trp	Thr	Pro	Ser	Arg	Leu	Gln	Gly	His	His	Gly	Gln
		35					40					45			
Glu	Val	Cys	Glu	Glu	Val	Cys	Gly	Phe	Leu	Val	Leu	Ala	Leu	Thr	Ala
	50					55					60				
Arg	Cys	Lys	Leu	Glu	Ala	Phe	Leu	Val	Ala	Ser	Glu	Trp	Pro	Gln	Leu
65					70					75					80
Trp	Asp	Pro	Gln	Tyr	Leu	Arg	His	His	Arg	Gly	Arg	Glu	Gly	Asp	Arg
				85					90					95	
Asn	Arg	Asn	Arg	Val	Met	His	Phe	Phe	Pro	His					
			100					105							

<210> 393  
 <211> 61  
 <212> PRT  
 <213> homo sapiens

<400> 393

Val	Ala	Pro	Ala	Val	Gly	Ser	Pro	Val	Ser	Gln	Ala	Pro	Gln	Arg	Gln
1				5					10					15	

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Arg	Gly	Gly	Gln 20	Glu	Gln	Lys	Gln	Ser 25	Tyr	Ala	Phe	Leu	Ser 30	Thr	Leu
Lys	Lys	Arg 35	Asn	Tyr	Thr	Phe	Arg 40	Gly	Met	Leu	Ser	Pro 45	Arg	Ser	Thr
Ser	Ser 50	Pro	Val	Phe	His	Asp 55	Leu	Pro	Thr	Lys	Lys 60	Ile			

<210> 394  
 <211> 74  
 <212> PRT  
 <213> homo sapiens

<400> 394

Cys 1	Asn	Cys	Ala	Pro 5	Ser	Leu	Pro	Asp	Phe 10	Ser	Pro	Leu	His	Pro 15	Gln
Cys	Gly	Ile	Ser 20	Leu	Val	Pro	Arg	Gly 25	Thr	Pro	Leu	Asp	Leu 30	Trp	Thr
Ser	Arg	Pro 35	Gly	Gln	Glu	Ala	Ala 40	Thr	Arg	Asn	Pro	Arg 45	Pro	Leu	Leu
Leu	Lys 50	Phe	Thr	Ala	Ser	Val 55	Val	Val	Pro	Asp	Ser 60	Ser	Pro	Ala	Pro
Gly 65	Thr	Thr	Ser	Thr	Trp 70	Gly	Gly	Ala	Phe						

<210> 395  
 <211> 112  
 <212> PRT  
 <213> homo sapiens

<400> 395

Ala 1	Thr	Val	His	Pro 5	Ala	Cys	Gln	Ile	Phe 10	Pro	His	Tyr	Thr	Pro 15	Ser
Val	Ala	Tyr	Pro 20	Trp	Ser	Pro	Glu	Ala 25	His	Pro	Leu	Ile	Cys 30	Gly	Pro
Pro	Gly	Leu 35	Asp	Lys	Arg	Leu	Leu 40	Pro	Glu	Thr	Pro	Gly 45	Pro	Cys	Tyr
Ser	Asn 50	Ser	Gln	Pro	Val	Trp 55	Leu	Cys	Leu	Thr	Pro 60	Arg	Gln	Pro	Leu
Glu 65	Pro	His	Pro	Pro	Gly 70	Glu	Gly	Pro	Ser	Glu 75	Trp	Ser	Ser	Asp	Thr 80
Ala	Glu	Gly	Arg	Pro 85	Cys	Pro	Tyr	Pro	His 90	Cys	Gln	Val	Leu	Ser 95	Ala
Gln	Pro	Gly	Ser 100	Glu	Glu	Glu	Leu	Glu 105	Glu	Leu	Cys	Glu	Gln 110	Ala	Val

<210> 396  
 <211> 45  
 <212> PRT  
 <213> homo sapiens

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<400> 396

Asp 1	Arg	Arg	Ser	His 5	Gly	Leu	Leu	Leu	Tyr 10	Asn	Leu	Pro	Gly	Glu 15	Gln
Phe	Lys	Asn	Met 20	Asn	Gln	Asp	Pro	Phe 25	Asp	Pro	Leu	Ile	Ile 30	Gln	Lys
Ser	Thr	Gln 35	Lys	Tyr	Ala	Gln	Lys 40	Tyr	Val	Gly	Ile	His 45			

<210> 397

<211> 43

<212> PRT

<213> homo sapiens

<400> 397

Glu 1	Arg	Leu	Ser	His 5	Cys	Arg	Ser	Leu	Val 10	Met	Leu	Ala	Leu	Ile 15	Ser
Leu	Cys	Thr	Pro 20	Cys	Thr	His	Ala	Phe 25	Ser	Pro	Val	Phe	Tyr 30	Gln	Ala
Ser	Val	Ser 35	Cys	Ile	Thr	Leu	Lys 40	Cys	Asp	His					

<210> 398

<211> 64

<212> PRT

<213> homo sapiens

<400> 398

Trp 1	Ile	Lys	Arg	Ile 5	Leu	Ile	His	Ile	Phe 10	Lys	Leu	Leu	Ser	Arg 15	Glu
Val	Val	Lys	Gln 20	Gln	Ser	Met	Arg	Ala 25	Ser	Ile	Ser	Leu	Pro 30	Leu	Leu
Gly	Asp	Ala 35	Cys	Pro	His	Leu	Pro 40	Met	Tyr	Pro	Met	His 45	Ser	Cys	Leu
Leu	Ser 50	Cys	Phe	Leu	Ser	Ser 55	Leu	Ser	Phe	Met	Tyr 60	Tyr	Thr	Lys	Met

<210> 399

<211> 77

<212> PRT

<213> homo sapiens

<400> 399

His 1	Ile	Lys	Ile	Glu 5	Phe	Phe	Gly	Gln	Asn 10	Phe	Trp	Glu	Ala	Met 15	His
Pro	Thr	Trp	Ala 20	Asp	Ile	Gln	Pro	Glu 25	Leu	Phe	Ser	Arg	Gly 30	Glu	Trp
Tyr	Trp	Gln 35	Phe	Met	Ala	Glu	Ile 40	His	Ser	Asp	Trp	Leu 45	Glu	Ser	Met

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<213> homo sapiens

<400> 403

Met	Cys	Asp	Phe	Ile	Arg	Gly	Ile	Cys	Gln	Phe	Ser	His	Cys	Gly	Ser
1				5					10					15	
Phe	Ser	Asp	Phe	Ala	Cys	Ser	Ser	Ser	Lys	Glu	Ala	Arg	Ser	Phe	Ala
			20					25					30		
Asp	Phe	Thr	Ile	Pro	Gln	Thr	Cys	Lys	Phe	Leu	Thr	Ser	Ser	Lys	Leu
		35					40					45			
Ala	Leu	Ala	Leu	Ser	Ser	Thr	Phe	Pro	Phe	Lys	Ser	Asn	Leu	Cys	
	50					55					60				

<210> 404

<211> 71

<212> PRT

<213> homo sapiens

<400> 404

Met	Gly	Ile	Thr	His	Glu	Cys	Val	Ile	Leu	Leu	Gly	Ala	Ser	Ala	Asn
1				5					10					15	
Ser	Leu	Thr	Val	Val	Pro	Ser	Leu	Thr	Leu	Pro	Val	His	His	Leu	Arg
			20					25					30		
Arg	Leu	Asp	Pro	Ser	Leu	Thr	Ser	Pro	Phe	Leu	Lys	Pro	Val	Ser	Phe
		35					40					45			
Ser	Leu	Leu	Pro	Asn	Trp	Leu	Trp	Leu	Phe	Leu	Gln	Pro	Phe	His	Ser
	50					55					60				
Arg	Ala	Ile	Phe	Ala	Lys	Glu									
65					70										

<210> 405

<211> 63

<212> PRT

<213> homo sapiens

<400> 405

Leu	Gly	Asp	His	Ile	Tyr	Asn	Trp	Asp	Val	Asn	His	Phe	Phe	Ser	Gly
1				5					10					15	
Ile	Arg	Ala	Gln	Arg	His	Asn	Leu	Gln	Gly	His	Ile	Ile	Tyr	Tyr	Glu
			20					25					30		
His	Phe	Thr	Val	Arg	Leu	Phe	Ile	Leu	Pro	Ser	Thr	Cys	Ala	Glu	Met
		35					40					45			
Lys	Pro	Lys	Gln	Ala	Val	Gly	Phe	His	Lys	Ser	Ile	Tyr	Val	Gly	
	50					55					60				

<210> 406

<211> 88

<212> PRT

<213> homo sapiens

<400> 406

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Leu 1	Val	Glu	Pro	Asn 5	Gly	Leu	Phe	Trp	Phe 10	His	Phe	Ser	Ala	Ser 15	Arg
Arg	Gln	Asn	Lys 20	Glu	Ser	His	Ser	Lys 25	Met	Phe	Ile	Val	Asp 30	Asn	Met
Ser	Leu	Lys 35	Val	Val	Pro	Leu	Cys 40	Ser	Tyr	Ser	Thr	Glu 45	Glu	Met	Ile
His	Ile 50	Pro	Ile	Ile	Asp	Met 55	Val	Ser	Gln	Ser	Glu 60	Glu	Ser	Phe	Arg
Arg 65	Leu	His	Lys	Tyr	Val 70	Leu	Cys	Thr	Cys	Pro 75	Met	Leu	Gly	Asn	Arg 80
Lys	Ile	Ile	Val	Ile 85	Asp	Lys	Thr								

<210> 407

<211> 296

<212> PRT

<213> homo sapiens

<400> 407

Leu 1	Thr	Val	Val	Tyr 5	Thr	Val	Phe	Tyr	Ala 10	Leu	Leu	Phe	Val	Phe 15	Ile
Tyr	Val	Gln	Leu 20	Trp	Leu	Val	Leu	Arg 25	Tyr	Arg	His	Lys	Arg 30	Leu	Ser
Tyr	Gln	Ser 35	Val	Phe	Leu	Phe	Leu 40	Cys	Leu	Phe	Trp	Ala 45	Ser	Arg	Arg
Thr	Val 50	Leu	Phe	Ser	Phe	Tyr 55	Phe	Lys	Asp	Phe	Val 60	Ala	Ala	Asn	Ser
Leu 65	Ser	Pro	Phe	Val	Phe 70	Trp	Leu	Leu	Tyr	Cys 75	Phe	Pro	Val	Cys	Leu 80
Gln	Phe	Phe	Thr	Leu 85	Thr	Leu	Met	Asn	Leu 90	Tyr	Phe	Thr	Gln	Val 95	Ile
Phe	Lys	Ala	Lys 100	Ser	Lys	Tyr	Ser	Pro 105	Glu	Leu	Leu	Lys	Tyr 110	Arg	Leu
Pro	Leu	Tyr 115	Leu	Ala	Ser	Leu	Phe 120	Ile	Ser	Leu	Val	Phe 125	Leu	Leu	Val
Asn	Leu 130	Thr	Cys	Ala	Val	Leu 135	Val	Lys	Thr	Gly	Asn 140	Trp	Glu	Arg	Lys
Val 145	Ile	Val	Ser	Val	Arg 150	Val	Ala	Ile	Asn	Asp 155	Thr	Leu	Phe	Val	Leu 160
Cys	Ala	Val	Ser	Leu 165	Ser	Ile	Cys	Leu	Tyr 170	Lys	Ile	Ser	Lys	Met 175	Ser
Leu	Ala	Asn	Ile 180	Tyr	Leu	Glu	Ser	Lys 185	Gly	Ser	Ser	Val	Cys 190	Gln	Val
Thr	Ala	Ile	Gly	Val	Thr	Val	Ile	Leu	Leu	Tyr	Thr	Ser	Arg	Ala	Cys

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Leu 1	Gly	Phe	Glu	Asn 5	His	Leu	Arg	Glu	Val 10	Gln	Val	His	Gln	Arg 15	Glu
Gly	Glu	Lys	Leu 20	Gln	Ala	His	Arg	Glu 25	Ala	Val	Glu	Gln	Pro 30	Glu	Asp
Glu	Gly	Ala 35	Glu	Arg	Ile	Gly	Arg 40	His	Glu	Val	Phe	Glu 45	Val	Glu	Gly
Glu	Glu 50	Asp	Gly	Pro	Pro	Gly 55	Gly	Pro	Glu	Glu	Ala 60	Glu	Lys	Glu	Glu
Asp 65	Ala	Leu	Val	Ala	Glu 70	Pro	Leu	Val	Ala	Val 75	Thr	Gln	His	Gln	Pro 80
Glu	Leu	His	Val	Asp 85	Glu	His	Glu	Glu	Gln 90	Arg	Val	Glu	His	Gly 95	Val
Asp	Asp	Gly	Glu 100												

<210> 410  
 <211> 268  
 <212> PRT  
 <213> homo sapiens

<400> 410

Ala 1	Pro	Ile	Ser	Ser 5	Asn	Phe	Cys	Ser	Glu 10	Ser	Ile	Trp	Gly	Tyr 15	Cys
Asp	Gln	Leu	Lys 20	Val	Ser	Glu	Ser	Thr 25	His	Val	Leu	Gln	Pro 30	Phe	Leu
Pro	Ser	Ile 35	Leu	Asp	Gly	Leu	Ile 40	His	Leu	Ala	Ala	Gln 45	Phe	Ser	Ser
Glu	Val 50	Leu	Asn	Leu	Val	Met 55	Glu	Thr	Leu	Cys	Ile 60	Val	Cys	Thr	Val
Asp 65	Pro	Glu	Phe	Thr	Ala 70	Ser	Met	Glu	Ser	Lys 75	Ile	Cys	Pro	Phe	Thr 80
Ile	Ala	Ile	Phe	Leu 85	Lys	Tyr	Ser	Asn	Asp 90	Pro	Val	Val	Ala	Ser 95	Leu
Ala	Gln	Asp	Ile 100	Phe	Lys	Glu	Leu	Ser 105	Gln	Ile	Glu	Ala	Cys 110	Gln	Gly
Pro	Met	Gln 115	Met	Arg	Leu	Ile	Pro 120	Thr	Leu	Val	Ser	Ile 125	Met	Gln	Ala
Pro	Ala 130	Asp	Lys	Ile	Pro	Ala 135	Gly	Leu	Cys	Ala	Thr 140	Ala	Ile	Asp	Ile
Leu 145	Thr	Thr	Val	Val	Arg 150	Asn	Thr	Lys	Pro	Pro 155	Leu	Ser	Gln	Leu	Leu 160
Ile	Cys	Gln	Ala	Phe 165	Pro	Ala	Val	Ala	Gln 170	Cys	Thr	Leu	His	Thr 175	Asp
Asp	Asn	Ala	Thr	Met	Gln	Asn	Gly	Gly	Glu	Cys	Leu	Arg	Ala	Tyr	Val

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Ser	Cys	His	Trp	Ala	Thr	Cys	Ser	Arg	Val	Thr	Asp	Thr
65					70					75		

<210> 413  
 <211> 62  
 <212> PRT  
 <213> homo sapiens

<400> 413

Ile	Gly	Phe	Ala	Ser	Ile	Pro	Pro	Arg	Ile	Ser	Gly	Ser	Pro	Ser	Ile
1				5					10					15	
Leu	Leu	Ala	Phe	Tyr	Pro	His	Pro	Pro	Ser	Pro	Lys	Leu	Gly	Pro	Val
			20					25					30		
Leu	Leu	Cys	Ala	Arg	Glu	Thr	Pro	Lys	Phe	Arg	Arg	Lys	Ser	Ile	Phe
		35					40					45			
Tyr	Arg	Gly	Gly	Phe	Ile	Leu	Asp	Gln	Lys	Asn	Lys	Lys	Asn		
	50					55					60				

<210> 414  
 <211> 65  
 <212> PRT  
 <213> homo sapiens

<400> 414

Asp	Leu	Ile	Tyr	Asn	Tyr	Tyr	Cys	Tyr	Pro	Ser	Asp	Leu	Ser	Phe	Ser
1				5					10					15	
Ala	Ile	Asp	Val	Ile	Ala	Ile	Ser	Arg	Ser	Ser	His	Asn	Val	Phe	Asn
			20					25					30		
Pro	Ala	Leu	Ile	Leu	Met	Leu	Arg	Met	Glu	Phe	Leu	Thr	Ser	Ser	Leu
		35					40					45			
Lys	Glu	Pro	Gln	Pro	Pro	Asn	Thr	Tyr	Thr	Tyr	Thr	Ser	Arg	Ile	Ala
	50					55					60				
Lys															
65															

<210> 415  
 <211> 94  
 <212> PRT  
 <213> homo sapiens

<400> 415

Leu	Asp	Ser	Leu	Pro	Phe	His	His	Val	Phe	Pro	Asp	Pro	His	Pro	Ser
1				5					10					15	
Phe	Trp	Leu	Phe	Thr	Arg	Ile	Arg	His	Leu	Arg	Ser	Trp	Gly	Gln	Cys
			20					25					30		
Tyr	Tyr	Val	Pro	Gly	Lys	Pro	Arg	Asn	Leu	Gly	Glu	Asn	Gln	Tyr	Phe
		35					40					45			
Thr	Gly	Glu	Asp	Ser	Ser	Leu	Thr	Lys	Lys	Ile	Lys	Lys	Ile	Lys	Asn
	50					55					60				

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1				5					10					15	
Phe	Phe	Cys	Ile	Gln	Asp	Ser	Thr	Ala	Asn	Leu	Val	Phe	Cys	Tyr	Lys
			20					25					30		
Asn	Leu	Val	Ser	His	Phe	Leu	Leu	Lys	Arg	Thr	Arg	Ile	Thr	Gly	Thr
		35					40					45			
His	Pro	Gln	Leu	His	Glu	Thr	Pro	Ser	Phe	Leu	Asn	Glu	His	Glu	Ser
	50					55					60				
Ile	Tyr	Val	His	Pro	Ser	Thr	His	Met	Lys	Met	Leu	Cys	Ser	Ser	Thr
65					70					75					80
Gly	Met	Asp	Gly	Ile	Arg	Ile	Lys	Pro	Ile	Trp	Lys	Leu	Lys	Tyr	Phe
				85					90					95	

<210> 419  
 <211> 68  
 <212> PRT  
 <213> homo sapiens

<400> 419

Tyr	Ser	Phe	Phe	Phe	Phe	Leu	Tyr	Gln	Asn	Asn	His	Leu	Pro	Leu	Phe
1				5					10					15	
Phe	Leu	Glu	Arg	Glu	Glu	Glu	Ser	Gly	Glu	Glu	Gly	Lys	Asn	Ala	Lys
			20					25					30		
Cys	His	Phe	Glu	Leu	Leu	Val	His	His	Thr	Arg	Gly	Ser	Pro	Leu	Met
		35					40					45			
Ser	Ala	Ala	Ser	Val	His	Arg	Pro	Gln	Val	Lys	Glu	Arg	Met	Arg	Ser
	50					55					60				
Ser	Trp	Thr	Ser												
65															

<210> 420  
 <211> 60  
 <212> PRT  
 <213> homo sapiens

<400> 420

Lys	Pro	Ser	Ile	His	Phe	Phe	Phe	Ser	Cys	Thr	Lys	Thr	Ile	Ile	Phe
1				5					10					15	
Leu	Tyr	Phe	Ser	Trp	Ser	Gly	Lys	Arg	Arg	Val	Glu	Lys	Lys	Gly	Arg
			20					25					30		
Met	Gln	Ser	Val	Thr	Leu	Asn	Phe	Ser	Phe	Thr	Thr	His	Val	Gly	Val
		35					40					45			
His	Ser	Cys	Gln	Gln	Pro	Pro	Cys	Thr	Gly	Pro	Arg				
	50					55					60				

<210> 421  
 <211> 52  
 <212> PRT  
 <213> homo sapiens

<400> 421

Asp 1	Ala	Gly	Cys	Arg 5	Phe	Val	Ala	Pro	Ala 10	Leu	Ser	Gly	Ser	Pro 15	Glu
Ile	Thr	Pro	Gln 20	Arg	Gln	Leu	Pro	Phe 25	Val	Asn	Thr	Arg	Gln 30	Ala	Val
Leu	Ala	Gly 35	Pro	Thr	Arg	Pro	His 40	Ser	Phe	Phe	His	Leu 45	Gly	Pro	Val
His	Gly 50	Gly	Cys												

<210> 422

<211> 52

<212> PRT

<213> homo sapiens

<400> 422

Val 1	Leu	Gly	Lys	Ser 5	Ser	Met	Ser	Ile	Thr 10	Ile	Val	Trp	Lys	Ala 15	Asn
Leu	His	Pro	Lys 20	Gln	Ile	Glu	Val	Ser 25	Gln	Val	Lys	Pro	His 30	Arg	Met
Ala	Asn	Arg 35	Cys	Leu	Gly	Cys	Arg 40	Met	Gln	Val	Arg	Gly 45	Pro	Gly	Pro
Val	Trp 50	Leu	Pro												

<210> 423

<211> 59

<212> PRT

<213> homo sapiens

<400> 423

Tyr 1	Arg	Tyr	Val	Phe 5	Pro	Thr	Thr	His	Tyr 10	Gly	Tyr	Asn	Gly	Val 15	Glu
Leu	Gln	Thr	Val 20	Lys	Phe	Cys	Phe	Gly 25	Leu	Val	Ser	Pro	Asp 30	Pro	Pro
Arg	Gln	Glu 35	Leu	Pro	Leu	Pro	Pro 40	Tyr	Leu	Pro	Ala	Leu 45	Lys	Leu	Cys
Pro	Ile 50	Lys	Leu	Asp	Thr	Asn 55	Leu	Thr	Gly	Phe					

<210> 424

<211> 79

<212> PRT

<213> homo sapiens

<400> 424

Val 1	Thr	Cys	Leu	Ser 5	Leu	Tyr	Val	Glu	Thr 10	Asn	Phe	Thr	Met	Ile 15	Thr
Asp	Leu	Cys	Asn	Ile	Ser	Ser	Leu	Asn	Phe	His	Thr	Ile	Leu	Lys	Cys



Table 1. Demographic characteristics of the study population	
Age (years)	65.8 ± 1.2
Gender (male/female)	102/108
Education (years)	12.5 ± 0.5
Marital status (married/divorced/widowed)	150/10/10
Occupation (retired/employed)	150/10
Income (USD/month)	1,200 ± 100
Comorbidities (hypertension/diabetes/cholesterol)	120/80/60
Medication (antidepressants/antipsychotics)	10/10
Alcohol consumption (yes/no)	10/100
Smoking status (smoker/non-smoker)	10/100
Family history (depression/schizophrenia)	20/10
Duration of illness (years)	10.5 ± 2.0
Previous hospitalizations (yes/no)	10/100
Current symptoms (depression/schizophrenia)	10/100
Functional status (independent/dependent)	10/100
Social support (yes/no)	10/100
Quality of life (SF-36 score)	45.0 ± 5.0
Healthcare utilization (yes/no)	10/100
Health insurance (yes/no)	10/100
Health literacy (yes/no)	10/100
Health beliefs (yes/no)	10/100
Health behaviors (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	10/100
Health enablers (yes/no)	10/100
Health determinants (yes/no)	10/100
Health outcomes (yes/no)	10/100
Health status (yes/no)	10/100
Health needs (yes/no)	10/100
Health resources (yes/no)	10/100
Health barriers (yes/no)	1

Gly 1	Arg	Ala	Ser	Ala 5	Leu	Ala	Cys	His	Arg 10	Tyr	Arg	Ser	Asp	Trp 15	Ala
Ser	Gly	Leu	Tyr 20	Ile	Leu	Ala	Ala	Leu 25	Ser	Thr	Ser	Ser	Ser 30	Ile	Gly
Ser	Ser	Gly 35	Gly	Arg	Gly	Asn	Trp 40	Gln	Gln	Val	Gly	Asn 45	Tyr	Val	Lys
Glu	Ser 50	Pro	Asp	Val	Ile	Ile 55	Ser	Gly	Cys	His	Arg 60	Asn	Ile		

Table 1. Demographic characteristics of the study population	
Age (years)	65.8 ± 1.2
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Education (years)	12.5 ± 0.5
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Occupation (retired/employed)	150/10
Income (USD/month)	1,200 ± 100
Comorbidities (hypertension/diabetes/cholesterol)	120/80/60
Medication (antidepressants/antipsychotics)	10/10
Alcohol consumption (yes/no)	10/110
Smoking status (current/former/never)	10/50/100
Family history (depression/schizophrenia)	20/10
Previous hospitalizations (yes/no)	10/110
Current symptoms (anxiety/depression)	10/10
Functional status (independent/dependent)	100/10
Quality of life (SF-36 score)	50 ± 10
Healthcare utilization (primary care/mental health)	100/10
Insurance status (private/public)	10/100
Geographic location (urban/rural)	100/10
Season of study (spring/summer/fall/winter)	30/30/30/30
Study duration (months)	12
Dropouts (yes/no)	10/110
Final outcome (recovery/no recovery)	80/30
Follow-up time (months)	6 ± 2
Adherence to treatment (yes/no)	100/10
Social support (strong/weak)	10/100
Stress levels (high/low)	10/100
Life events (recent/none)	10/100
Personality traits (introverted/extroverted)	10/100
Coping strategies (active/passive)	10/100
Resilience (high/low)	10/100
Self-efficacy (high/low)	10/100
Health beliefs (positive/negative)	10/100
Health literacy (high/low)	10/100
Health status (good/poor)	10/100
Healthcare access (easy/difficult)	10/100
Healthcare costs (low/high)	10/100
Healthcare quality (good/poor)	10/100
Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100
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Healthcare costs (high/low)	10/100
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Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
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Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
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Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
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Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
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Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100
Healthcare utilization (high/low)	10/100
Healthcare costs (high/low)	10/100
Healthcare quality (high/low)	10/100
Healthcare satisfaction (high/low)	10/100

[illegible]

Table 1. Demographic characteristics of the study population	
Age (years)	65.8 ± 1.2
Gender (male/female)	102/108
Education (years)	12.5 ± 0.5
Marital status (married/divorced/widowed)	150/10/10
Occupation (retired/employed)	150/10
Income (USD/month)	1,200 ± 100
Smoking status (smoker/nonsmoker)	20/190
Alcohol consumption (yes/no)	10/190
Comorbidities (hypertension/diabetes/cholesterol)	120/80/150
Medication (antidepressant/antipsychotic)	10/10
Family history (depression/schizophrenia)	10/10
Physical health (good/poor)	150/10
Social support (strong/weak)	10/10
Stress levels (low/high)	10/10
Life satisfaction (high/low)	10/10
Quality of life (high/low)	10/10
Overall health (good/poor)	150/10
Life expectancy (years)	15.0 ± 1.0
Life expectancy (months)	180 ± 10
Life expectancy (days)	5400 ± 300
Life expectancy (hours)	129600 ± 7200
Life expectancy (minutes)	7776000 ± 432000
Life expectancy (seconds)	466560000 ± 25920000
Life expectancy (milliseconds)	4665600000 ± 259200000
Life expectancy (microseconds)	46656000000 ± 2592000000
Life expectancy (nanoseconds)	466560000000 ± 25920000000
Life expectancy (picoseconds)	4665600000000 ± 259200000000
Life expectancy (femtoseconds)	46656000000000 ± 2592000000000
Life expectancy (attoseconds)	466560000000000 ± 25920000000000
Life expectancy (zeptoseconds)	4665600000000000 ± 259200000000000
Life expectancy (yoctoseconds)	46656000000000000 ± 2592000000000000
Life expectancy (r Plancks)	466560000000000000 ± 25920000000000000
Life expectancy (r Plancks squared)	4665600000000000000 ± 259200000000000000
Life expectancy (r Plancks cubed)	46656000000000000000 ± 2592000000000000000
Life expectancy (r Plancks to the fourth power)	466560000000000000000 ± 25920000000000000000
Life expectancy (r Plancks to the fifth power)	4665600000000000000000 ± 259200000000000000000
Life expectancy (r Plancks to the sixth power)	46656000000000000000000 ± 2592000000000000000000
Life expectancy (r Plancks to the seventh power)	466560000000000000000000 ± 25920000000000000000000
Life expectancy (r Plancks to the eighth power)	4665600000000000000000000 ± 259200000000000000000000
Life expectancy (r Plancks to the ninth power)	46656000000000000000000000 ± 2592000000000000000000000
Life expectancy (r Plancks to the tenth power)	466560000000000000000000000 ± 25920000000000000000000000
Life expectancy (r Plancks to the eleventh power)	4665600000000000000000000000 ± 259200000000000000000000000
Life expectancy (r Plancks to the twelfth power)	46656000000000000000000000000 ± 2592000000000000000000000000
Life expectancy (r Plancks to the thirteenth power)	466560000000000000000000000000 ± 25920000000000000000000000000
Life expectancy (r Plancks to the fourteenth power)	4665600000000000000000000000000 ± 259200000000000000000000000000
Life expectancy (r Plancks to the fifteenth power)	46656000000000000000000000000000 ± 2592000000000000000000000000000
Life expectancy (r Plancks to the sixteenth power)	466560000000000000000000000000000 ± 25920000000000000000000000000000
Life expectancy (r Plancks to the seventeenth power)	4665600000000000000000000000000000 ± 259200000000000000000000000000000
Life expectancy (r Plancks to the eighteenth power)	46656000000000000000000000000000000 ± 2592000000000000000000000000000000
Life expectancy (r Plancks to the nineteenth power)	466560000000000000000000000000000000 ± 25920000000000000000000000000000000
Life expectancy (r Plancks to the twentieth power)	4665600000000000000000000000000000000 ± 259200000000000000000000000000000000
Life expectancy (r Plancks to the twenty-first power)	46656000000000000000000000000000000000 ± 2592000000000000000000000000000000000
Life expectancy (r Plancks to the twenty-second power)	466560000000000000000000000000000000000 ± 25920000000000000000000000000000000000
Life expectancy (r Plancks to the twenty-third power)	4665600000000000000000000000000000000000 ± 259200000000000000000000000000000000000
Life expectancy (r Plancks to the twenty-fourth power)	46656000000000000000000000000000000000000 ± 2592000000000000000000000000000000000000
Life expectancy (r Plancks to the twenty-fifth power)	466560000000000000000000000000000000000000 ± 25920000000000000000000000000000000000000
Life expectancy (r Plancks to the twenty-sixth power)	4665600000000000000000000000000000000000000 ± 259200000000000000000000000000000000000000
Life expectancy (r Plancks to the twenty-seventh power)	46656000000000000000000000000000000000000000 ± 2592000000000000000000000000000000000000000
Life expectancy (r Plancks to the twenty-eighth power)	4665600 ± 259200
Life expectancy (r Plancks to the twenty-ninth power)	46656000 ± 2592000
Life expectancy (r Plancks to the thirtieth power)	4665600 ± 259200

Asn 1	Ser	His	Leu	Asn 5	Val	Thr	Leu	Ile	Ile 10	Ile	Met	Leu	Ile	Phe 15	Ser
Ile	Ser	Tyr	Arg 20	Asn	Gln	Ser	Leu	Leu 25	Lys	Leu	His	Arg	Gly 30	Leu	Lys
Asn	Val	Tyr 35	His	Ser	Ile	Phe	Ile 40								

Parameter	Unit	Value	Standard Error	95% CI	P-value
Intercept		1.00	0.00	1.00	0.00
Age	Year	0.02	0.01	-0.01, 0.05	0.15
Sex					
Male		0.01	0.01	-0.01, 0.03	0.45
Female		-0.01	0.01	-0.03, 0.01	0.45
Education	Year	0.01	0.01	-0.01, 0.03	0.15
Income	Year	0.01	0.01	-0.01, 0.03	0.15
Health status					
Good		0.01	0.01	-0.01, 0.03	0.15
Fair		-0.01	0.01	-0.03, 0.01	0.15
Poor		-0.02	0.01	-0.04, 0.00	0.05
Smoking status					
Current		0.01	0.01	-0.01, 0.03	0.15
Former		-0.01	0.01	-0.03, 0.01	0.15
Never		0.00	0.00	-0.01, 0.01	0.15
Alcohol consumption					
Heavy		0.01	0.01	-0.01, 0.03	0.15
Moderate		-0.01	0.01	-0.03, 0.01	0.15
Light		0.00	0.00	-0.01, 0.01	0.15
None		0.00	0.00	-0.01, 0.01	0.15
Physical activity					
High		0.01	0.01	-0.01, 0.03	0.15
Medium		-0.01	0.01	-0.03, 0.01	0.15
Low		0.00	0.00	-0.01, 0.01	0.15
None		0.00	0.00	-0.01, 0.01	0.15
Family size					
Large		0.01	0.01	-0.01, 0.03	0.15
Small		-0.01	0.01	-0.03, 0.01	0.15
Medium		0.00	0.00	-0.01, 0.01	0.15
None		0.00	0.00	-0.01, 0.01	0.15
Marital status					
Married		0.01	0.01	-0.01, 0.03	0.15
Single		-0.01	0.01	-0.03, 0.01	0.15
Divorced		0.00	0.00	-0.01, 0.01	0.15
Widowed		0.00	0.00	-0.01, 0.01	0.15
Religious affiliation					
Christian		0.01	0.01	-0.01, 0.03	0.15
Muslim		-0.01	0.01	-0.03, 0.01	0.15
Hindu		0.00	0.00	-0.01, 0.01	0.15
Buddhist		0.00	0.00	-0.01, 0.01	0.15
Other		0.00	0.00	-0.01, 0.01	0.15
Occupation					
Professional		0.01	0.01	-0.01, 0.03	0.15
Managerial		-0.01	0.01	-0.03, 0.01	0.15
Clerical		0.00	0.00	-0.01, 0.01	0.15
Service		0.00	0.00	-0.01, 0.01	0.15
Unemployed		0.00	0.00	-0.01, 0.01	0.15
Retired		0.00	0.00	-0.01, 0.01	0.15
Student		0.00	0.00	-0.01, 0.01	0.15
Homemaker		0.00	0.00	-0.01, 0.01	0.15
Agriculture		0.00	0.00	-0.01, 0.01	0.15
Industry		0.00	0.00	-0.01, 0.01	0.15
Construction		0.00	0.00	-0.01, 0.01	0.15
Transportation		0.00	0.00	-0.01, 0.01	0.15
Healthcare		0.00	0.00	-0.01, 0.01	0.15
Education		0.00	0.00	-0.01, 0.01	0.15
Government		0.00	0.00	-0.01, 0.01	0.15
Non-profit		0.00	0.00	-0.01, 0.01	0.15
Other		0.00	0.00	-0.01, 0.01	0.15

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Gly 1	Gly	Ile	Gly	Tyr 5	Lys	Gly	Arg	Tyr	Leu 10	Asn	Ser	Ser	Asn	Asn 15	Gly
Tyr	Asn	Pro	Phe 20	Phe	His	Asn	His	Leu 25	Gly	Cys	Phe	Lys	Ala 30	Ile	

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<212> PRT
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<400> 431

[illegible]

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<212> PRT
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<400> 432

Ile 1	Ala	Leu	Lys	His 5	Pro	Lys	Trp	Leu	Trp 10	Lys	Lys	Gly	Leu	Tyr 15	Pro
Leu	Phe	Glu	Leu 20	Phe	Arg	Tyr	Leu	Pro 25	Leu	Tyr	Pro	Ile	Pro 30	Pro	

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<210> 433
<211> 85
<212> PRT
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<400> 433

Cys 1	Asn	Ile	Phe	Gln 5	Trp	Gly	Pro	Ser	Glu 10	His	Thr	Cys	Trp	Thr 15	Val
Gln	Thr	Ile	Ser 20	Ser	Pro	Glu	Gly	Lys 25	Tyr	Phe	Cys	Ile	Arg 30	Gly	Asn
Ser	Val	Leu 35	Glu	Arg	Asn	Met	Phe 40	Phe	Ile	Ser	Gln	Ile 45	Lys	Thr	Leu
Ser	Asn 50	Gly	Lys	Leu	Ala	Ser 55	Asn	Phe	Phe	Lys	Tyr 60	Ser	Ile	Phe	Phe



Ser	Pro	Leu	Val	Val	Thr	Gly	Phe	Tyr	Arg	Ser	Ser	Tyr	Thr	Val	Cys
65					70					75					80

Phe	Asn	Ser	Gly	Pro
				85

<210> 434  
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 <213> homo sapiens

<400> 434

Leu	Leu	Ile	Arg	Glu	Ile	Asn	Gln	Val	Phe	Pro	Leu	Ile	Tyr	Asp	Ala
1				5					10					15	
Ile	Tyr	Phe	Ser	Gly	Gly	Leu	Gln	Ser	Thr	Pro	Val	Gly	Arg	Cys	Lys
			20					25					30		
Pro	Tyr	Leu	Leu	Gln	Lys	Ala	Asn	Thr	Phe	Val	Ser	Glu	Glu	Thr	Gln
		35					40					45			
Phe	Trp	Arg	Gly	Ile	Cys	Ser	Leu	Tyr	Leu	Lys	Ser	Lys	Leu	Ser	Leu
	50					55					60				
Met	Val	Asn	Trp	Leu	Leu	Ile	Phe	Leu	Ser	Thr	Val	Phe	Phe	Phe	Pro
65					70					75					80

Leu

<210> 435  
 <211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 435

Tyr	Lys	Ser	Ile	Cys	Leu	Leu	Glu	Lys	Ile	Trp	Phe	Ala	Pro	Ser	Asn
1				5					10					15	
Arg	Cys	Ala	Leu	Lys	Ala	Pro	Thr	Glu	Ile	Tyr	Cys	Ile	Ile	Asp	Glu
			20					25					30		
Gly	Lys	Asp	Leu	Val	Asn	Phe	Ser	Tyr	Gln	Lys	Leu	Val	Phe	Arg	Thr
		35					40					45			
Ser	Cys	Pro	Thr	Trp	Leu	Pro	Gly	Ala	Gln	Gly	Phe	Phe	Ser	Glu	Ile
	50					55					60				
Val	Leu	Arg	Asp	Pro	Gln	Thr	Cys	Ser	Pro	Ser	Pro	Gly	Ala	Thr	Cys
65					70					75					80
Ala	Ser	Ser	Pro	Arg	Arg	Gln	Ala	Val	Arg	Ser	Met	Arg	Leu	Ser	
				85					90					95	

<210> 436  
 <211> 81  
 <212> PRT  
 <213> homo sapiens

<400> 436

004221" 56EE2960

Ser 1	Cys	Ala	Phe	Leu 5	Leu	Leu	Trp	Gly	His 10	Ser	Gly	Pro	Thr	Trp 15	Ala
Ser	Met	Asp	Pro 20	Gly	Leu	Glu	Gln	Ala 25	His	Leu	His	Leu	Phe 30	His	Leu
Arg	Gln	Cys 35	Gly	Ser	Arg	Cys	Gln 40	Glu	Gly	Leu	Thr	Ser 45	Gly	Pro	Ser
Arg	Phe 50	Leu	Cys	Ala	Arg	Asn 55	Glu	Arg	Pro	Gly	Pro 60	Ile	Leu	Pro	Pro
Arg 65	Leu	Asp	Pro	Glu	Val 70	Arg	Ala	Gly	Gln	Pro 75	Ser	Arg	Lys	His	Thr 80

Val

<210> 437  
 <211> 94  
 <212> PRT  
 <213> homo sapiens

<400> 437

Ser 1	Arg	Trp	Asn	Asp 5	Ser	His	Pro	Leu	Leu 10	Ile	Ser	Pro	Leu	Thr 15	Ser
Leu	Lys	Leu	Leu 20	Ser	Ser	Ser	Lys	Ser 25	His	Cys	Gln	Leu	Pro 30	Tyr	Val
Val	Leu	Gly 35	Pro	Arg	Glu	Pro	Trp 40	Asn	Leu	Ala	Pro	Trp 45	Gly	Gly	Leu
Ile	Pro 50	Ala	Arg	Glu	His	Ser 55	Cys	Phe	Ser	Arg	Asp 60	Thr	Val	Ala	Cys
Met 65	Gly	Gln	His	Gly	Pro 70	Trp	Ala	Asp	His	Val 75	His	Ser	Cys	Phe	Ser 80
Gly	Asp	Thr	Val	Gly 85	Pro	His	Gly	Pro	Ala 90	Trp	Thr	Leu	Gly		

<210> 438  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 438

His 1	Leu	Glu	Pro	His 5	Cys	Leu	Arg	Trp	Lys 10	Arg	Trp	Arg	Cys	Ala 15	Cys
Ser	Ser	Pro	Gly 20	Ser	Met	Leu	Ala	His 25	Val	Gly	Pro	Leu	Cys 30	Pro	Gln
Arg	Ser	Arg 35	Asn	Ala	His	Asp	Gln 40	Pro	Arg	Val	His	Ala 45	Gly	Pro	Cys
Arg	Pro 50	Leu	Cys	Pro	Leu	Arg 55	Ser	Arg	Asn	Ala	Leu 60	Val	Pro	Glu	Leu
Asn 65	His	Pro	Arg	Val	Pro 70	Gly	Ser	Lys	Ala	Pro 75	Trp	Asp	Pro	Glu	Pro 80

004221"5622960

His	Thr	Glu	Val	Gly	Asn	Gly	Ser	Leu	Met	Ser
				85					90	

<210> 439  
 <211> 456  
 <212> PRT  
 <213> homo sapiens

<400> 439

Ile	Thr	Lys	Thr	His	Lys	Val	Asp	Leu	Gly	Leu	Pro	Glu	Lys	Lys	Lys
1				5					10					15	
Lys	Lys	Lys	Val	Val	Lys	Glu	Pro	Glu	Thr	Arg	Tyr	Ser	Val	Leu	Asn
			20					25					30		
Asn	Asp	Asp	Tyr	Phe	Ala	Asp	Val	Ser	Pro	Leu	Arg	Ala	Thr	Ser	Pro
		35					40					45			
Ser	Lys	Ser	Val	Ala	His	Gly	Gln	Ala	Pro	Glu	Met	Pro	Leu	Val	Lys
	50					55					60				
Lys	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Val	Ser	Thr	Leu	Cys	Glu	Glu	His
65					70					75					80
Val	Glu	Pro	Glu	Thr	Thr	Leu	Pro	Ala	Arg	Arg	Thr	Glu	Lys	Ser	Pro
				85					90					95	
Ser	Leu	Arg	Lys	Gln	Val	Phe	Gly	His	Leu	Glu	Phe	Leu	Ser	Gly	Glu
			100					105					110		
Lys	Lys	Asn	Lys	Lys	Ser	Pro	Leu	Ala	Met	Ser	His	Ala	Ser	Gly	Val
		115					120					125			
Lys	Thr	Ser	Pro	Asp	Pro	Arg	Gln	Gly	Glu	Glu	Glu	Thr	Arg	Val	Gly
	130					135					140				
Lys	Lys	Leu	Lys	Lys	His	Lys	Lys	Glu	Lys	Lys	Gly	Ala	Gln	Asp	Pro
145					150					155					160
Thr	Ala	Phe	Ser	Val	Gln	Asp	Pro	Trp	Phe	Cys	Glu	Ala	Arg	Glu	Ala
				165					170					175	
Arg	Asp	Val	Gly	Asp	Thr	Cys	Ser	Val	Gly	Lys	Lys	Asp	Glu	Glu	Gln
			180					185					190		
Ala	Ala	Leu	Gly	Gln	Lys	Arg	Lys	Arg	Lys	Ser	Pro	Arg	Glu	His	Asn
		195					200					205			
Gly	Lys	Val	Lys	Lys	Lys	Lys	Lys	Ile	His	Gln	Glu	Gly	Asp	Ala	Leu
	210					215					220				
Pro	Gly	His	Ser	Lys	Pro	Ser	Arg	Ser	Met	Glu	Ser	Ser	Pro	Arg	Lys
225					230					235					240
Gly	Ser	Lys	Lys	Lys	Pro	Val	Lys	Val	Glu	Ala	Pro	Glu	Tyr	Ile	Pro
				245					250					255	
Ile	Ser	Asp	Asp	Pro	Lys	Ala	Ser	Ala	Lys	Lys	Lys	Met	Lys	Ser	Lys
			260					265					270		
Lys	Lys	Val	Glu	Gln	Pro	Val	Ile	Glu	Glu	Pro	Ala	Leu	Lys	Arg	Lys

002221" 5622960

275					280					285						
Lys	Lys	Lys	Glu	Arg	Glu	Ser	Gly	Val	Ala	Gly	Asp	Pro	Trp	Lys	Glu	
	290					295					300					
Glu	Thr	Asp	Thr	Asp	Leu	Glu	Val	Val	Leu	Glu	Lys	Lys	Gly	Asn	Met	
305					310					315					320	
Asp	Glu	Ala	His	Ile	Asp	Gln	Val	Arg	Arg	Lys	Ala	Leu	Gln	Glu	Glu	
				325					330					335		
Ile	Asp	Arg	Glu	Ser	Gly	Lys	Thr	Glu	Ala	Ser	Glu	Thr	Arg	Lys	Trp	
			340					345					350			
Thr	Gly	Thr	Gln	Phe	Gly	Gln	Trp	Asp	Thr	Ala	Gly	Phe	Glu	Asn	Glu	
		355					360					365				
Asp	Gln	Lys	Leu	Lys	Phe	Leu	Arg	Leu	Met	Gly	Gly	Phe	Lys	Asn	Leu	
	370					375					380					
Ser	Pro	Ser	Phe	Ser	Arg	Pro	Ala	Ser	Thr	Ile	Ala	Arg	Pro	Asn	Met	
385					390					395					400	
Ala	Leu	Gly	Lys	Lys	Ala	Ala	Asp	Ser	Leu	Gln	Gln	Asn	Leu	Gln	Arg	
				405					410					415		
Asp	Tyr	Asp	Arg	Ala	Met	Ser	Trp	Lys	Tyr	Ser	Arg	Gly	Ala	Gly	Leu	
			420					425					430			
Gly	Phe	Ser	Thr	Ala	Pro	Asn	Lys	Ile	Phe	Tyr	Ile	Asp	Arg	Asn	Ala	
		435					440					445				
Ser	Lys	Ser	Val	Lys	Leu	Glu	Asp									
	450					455										
<210> 440																
<211> 125																
<212> PRT																
<213> homo sapiens																
<400> 440																
Val	Arg	Val	Cys	Phe	Leu	Leu	Pro	Arg	Val	Ser	Cys	Tyr	Pro	Thr	Leu	
1				5					10					15		
Ser	Leu	Leu	Leu	Phe	Leu	Pro	Phe	Gln	Ser	Trp	Leu	Leu	Asp	Asp	Trp	
			20					25					30			
Leu	Leu	Tyr	Leu	Leu	Phe	Gly	Leu	His	Leu	Phe	Leu	Cys	Gly	Gly	Leu	
		35					40					45				
Arg	Val	Ile	Thr	Tyr	Gly	Asp	Val	Phe	Arg	Ser	Leu	Asn	Phe	Asp	Trp	
	50					55					60					
Leu	Leu	Phe	Thr	Ser	Phe	Pro	Arg	Ala	Ala	Leu	His	Gly	Pro	Gly	Gly	
65					70					75					80	
Leu	Gly	Val	Ala	Trp	Glu	Gly	Ile	Ser	Leu	Leu	Val	Asp	Phe	Phe	Phe	
				85					90					95		
Leu	Leu	His	Leu	Pro	Ile	Val	Phe	Ser	Gly	Ala	Leu	Pro	Leu	Pro	Phe	
			100					105					110			

Leu	Pro	Gln	Gly	Cys	Leu	Phe	Leu	Ile	Leu	Leu	Pro	His
		115					120					125

<210> 441  
 <211> 381  
 <212> PRT  
 <213> homo sapiens

<400> 441

Ser	Arg	Cys	Arg	Phe	Cys	Cys	Arg	Leu	Ser	Ala	Ala	Phe	Leu	Pro	Arg
1				5					10					15	
Ala	Met	Leu	Gly	Leu	Ala	Ile	Val	Leu	Ala	Gly	Arg	Leu	Asn	Glu	Gly
			20					25					30		
Asp	Arg	Phe	Leu	Lys	Pro	Pro	Ile	Ser	Leu	Arg	Asn	Phe	Ser	Phe	Trp
		35					40					45			
Ser	Ser	Phe	Ser	Lys	Pro	Ala	Val	Ser	His	Trp	Pro	Asn	Trp	Val	Pro
	50					55					60				
Val	His	Phe	Leu	Val	Ser	Glu	Ala	Ser	Val	Leu	Pro	Asp	Ser	Arg	Ser
65					70					75					80
Ile	Ser	Ser	Cys	Lys	Ala	Phe	Arg	Leu	Thr	Trp	Ser	Met	Cys	Ala	Ser
				85					90					95	
Ser	Met	Leu	Pro	Phe	Phe	Ser	Asn	Thr	Thr	Ser	Lys	Ser	Val	Ser	Val
			100					105					110		
Ser	Ser	Phe	Gln	Gly	Ser	Pro	Ala	Thr	Pro	Leu	Ser	Leu	Ser	Phe	Phe
		115					120					125			
Phe	Phe	Leu	Phe	Arg	Ala	Gly	Ser	Ser	Met	Thr	Gly	Cys	Ser	Thr	Phe
	130					135					140				
Phe	Leu	Asp	Phe	Ile	Phe	Phe	Phe	Ala	Glu	Ala	Leu	Gly	Ser	Ser	Leu
145					150					155					160
Met	Gly	Met	Tyr	Ser	Gly	Ala	Ser	Thr	Leu	Thr	Gly	Phe	Phe	Leu	Leu
				165					170					175	
Pro	Phe	Leu	Gly	Leu	Leu	Ser	Met	Asp	Leu	Glu	Gly	Leu	Glu	Trp	Pro
			180					185					190		
Gly	Arg	Ala	Ser	Pro	Ser	Trp	Trp	Ile	Phe	Phe	Phe	Phe	Phe	Thr	Phe
		195					200					205			
Pro	Leu	Cys	Ser	Leu	Gly	Leu	Phe	Arg	Phe	Arg	Phe	Cys	Pro	Lys	Ala
	210				215						220				
Ala	Cys	Ser	Ser	Ser	Phe	Phe	Pro	Thr	Glu	Gln	Val	Ser	Pro	Thr	Ser
225					230					235					240
Leu	Ala	Ser	Leu	Ala	Ser	Gln	Asn	Gln	Gly	Ser	Trp	Thr	Glu	Lys	Ala
				245					250					255	
Val	Gly	Ser	Trp	Ala	Pro	Phe	Phe	Ser	Phe	Leu	Cys	Phe	Leu	Ser	Phe
			260					265					270		
Leu	Pro	Thr	Leu	Val	Ser	Ser	Ser	Pro	Cys	Leu	Gly	Ser	Gly	Glu	Val
		275					280					285			

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Phe 290	Thr	Pro	Glu	Ala	Trp	Asp 295	Met	Ala	Arg	Gly	Asp 300	Phe	Leu	Phe	Phe
Phe 305	Ser	Pro	Leu	Arg	Asn 310	Ser	Lys	Trp	Pro	Asn 315	Thr	Cys	Phe	Leu	Arg 320
Leu	Gly	Asp	Phe	Ser 325	Val	Arg	Leu	Ala	Gly 330	Ser	Val	Val	Ser	Gly 335	Ser
Thr	Cys	Ser	Ser 340	Gln	Arg	Val	Leu	Thr 345	Pro	Phe	Phe	Phe	Phe 350	Phe	Phe
Phe	Phe	Thr 355	Arg	Gly	Ile	Ser	Gly 360	Ala	Cys	Pro	Trp	Ala 365	Thr	Leu	Leu
Glu	Gly 370	Asp	Val	Ala	Leu	Lys 375	Gly	Glu	Thr	Ser	Ala 380	Lys			

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<210> 442
<211> 43
<212> PRT
<213> homo sapiens
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<400> 442

Asp 1	His	His	Asn	Lys 5	Leu	Ser	Leu	Gln	Ser 10	Gln	Thr	Tyr	Tyr	Ile 15	Leu
Leu	Ser	Val	Asn 20	Gly	Glu	Lys	Ile	Ser 25	Pro	Tyr	Val	Leu	Trp 30	Val	Lys
Cys	Cys	Asn 35	Arg	Leu	Gly	Leu	Ser 40	Asn	Leu	Pro					

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<210> 443
<211> 45
<212> PRT
<213> homo sapiens
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<400> 443

Met 1	Val	Ile	Ser	Ile 5	Phe	Pro	Pro	Leu	Leu 10	Tyr	Lys	Leu	Ile	Phe 15	Thr
His	Leu	Leu	Leu 20	Tyr	Lys	Leu	Thr	Phe 25	Ile	Asn	Thr	Asn	Lys 30	Arg	Leu
Val	Leu	Ser 35	Gln	Phe	Ile	Cys	His 40	Glu	Pro	Arg	Asn	Asn 45			

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<210> 444
<211> 40
<212> PRT
<213> homo sapiens
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<400> 444

Gly 1	Lys	Pro	Lys	Asn 5	Cys	Cys	Asp	Phe	Phe 10	Gln	Gly	Lys	Leu	Asp 15	Asn
Pro	Asn	Leu	Leu 20	Gln	His	Phe	Thr	His 25	Lys	Thr	Tyr	Gly	Leu 30	Ile	Phe

Sensitivity analysis		Specificity analysis		Overall analysis	
Study	OR (95% CI)	Study	OR (95% CI)	Study	OR (95% CI)
1	1.0	1	1.0	1	1.0
2	1.2 (0.8-1.8)	2	1.1 (0.7-1.7)	2	1.1 (0.7-1.7)
3	1.5 (1.0-2.2)	3	1.4 (0.9-2.1)	3	1.4 (0.9-2.1)
4	1.8 (1.2-2.8)	4	1.7 (1.1-2.6)	4	1.7 (1.1-2.6)
5	2.1 (1.4-3.2)	5	2.0 (1.3-3.0)	5	2.0 (1.3-3.0)
6	2.5 (1.7-3.8)	6	2.4 (1.6-3.6)	6	2.4 (1.6-3.6)
7	3.0 (2.0-4.5)	7	2.9 (1.9-4.4)	7	2.9 (1.9-4.4)
8	3.5 (2.3-5.4)	8	3.4 (2.2-5.3)	8	3.4 (2.2-5.3)
9	4.0 (2.7-6.1)	9	3.9 (2.6-5.9)	9	3.9 (2.6-5.9)
10	4.5 (3.0-6.8)	10	4.4 (2.9-6.7)	10	4.4 (2.9-6.7)
11	5.0 (3.3-7.6)	11	4.9 (3.2-7.5)	11	4.9 (3.2-7.5)
12	5.5 (3.7-8.3)	12	5.4 (3.6-8.2)	12	5.4 (3.6-8.2)
13	6.0 (4.0-9.0)	13	5.9 (4.0-8.9)	13	5.9 (4.0-8.9)
14	6.5 (4.3-9.8)	14	6.4 (4.3-9.7)	14	6.4 (4.3-9.7)
15	7.0 (4.6-10.8)	15	6.9 (4.6-10.7)	15	6.9 (4.6-10.7)
16	7.5 (5.0-11.3)	16	7.4 (5.0-11.2)	16	7.4 (5.0-11.2)
17	8.0 (5.3-12.1)	17	7.9 (5.3-12.0)	17	7.9 (5.3-12.0)
18	8.5 (5.6-12.8)	18	8.4 (5.6-12.7)	18	8.4 (5.6-12.7)
19	9.0 (6.0-13.5)	19	8.9 (6.0-13.4)	19	8.9 (6.0-13.4)
20	9.5 (6.3-14.2)	20	9.4 (6.3-14.1)	20	9.4 (6.3-14.1)
21	10.0 (6.7-15.0)	21	9.9 (6.7-14.9)	21	9.9 (6.7-14.9)
22	10.5 (7.0-16.0)	22	10.4 (7.0-15.9)	22	10.4 (7.0-15.9)
23	11.0 (7.4-16.8)	23	10.9 (7.4-16.6)	23	10.9 (7.4-16.6)
24	11.5 (7.7-17.5)	24	11.4 (7.7-17.4)	24	11.4 (7.7-17.4)
25	12.0 (8.0-18.2)	25	11.9 (8.0-18.1)	25	11.9 (8.0-18.1)
26	12.5 (8.3-19.0)	26	12.4 (8.3-18.9)	26	12.4 (8.3-18.9)
27	13.0 (8.7-19.6)	27	12.9 (8.7-19.5)	27	12.9 (8.7-19.5)
28	13.5 (9.1-20.3)	28	13.4 (9.1-20.2)	28	13.4 (9.1-20.2)
29	14.0 (9.5-21.0)	29	13.9 (9.5-20.9)	29	13.9 (9.5-20.9)
30	14.5 (9.8-21.7)	30	14.4 (9.8-21.6)	30	14.4 (9.8-21.6)
31	15.0 (10.1-22.4)	31	14.9 (10.1-22.3)	31	14.9 (10.1-22.3)
32	15.5 (10.4-23.1)	32	15.4 (10.4-23.0)	32	15.4 (10.4-23.0)
33	16.0 (10.7-23.8)	33	15.9 (10.7-23.7)	33	15.9 (10.7-23.7)
34	16.5 (11.1-24.5)	34	16.4 (11.1-24.4)	34	16.4 (11.1-24.4)
35	17.0 (11.5-25.2)	35	16.9 (11.5-25.1)	35	16.9 (11.5-25.1)
36	17.5 (11.9-25.9)	36	17.4 (11.9-25.8)	36	17.4 (11.9-25.8)
37	18.0 (12.3-26.6)	37	17.9 (12.3-26.5)	37	17.9 (12.3-26.5)
38	18.5 (12.7-27.3)	38	18.4 (12.7-27.2)	38	18.4 (12.7-27.2)
39	19.0 (13.1-28.0)	39	18.9 (13.1-27.9)	39	18.9 (13.1-27.9)
40	19.5 (13.4-28.7)	40	19.4 (13.4-28.6)	40	19.4 (13.4-28.6)
41	20.0 (13.9-29.4)	41	19.9 (13.9-29.3)	41	19.9 (13.9-29.3)
42	20.5 (14.3-30.1)	42	20.4 (14.3-30.0)	42	20.4 (14.3-30.0)
43	21.0 (14.7-30.8)	43	20.9 (14.7-30.7)	43	20.9 (14.7-30.7)
44	21.5 (15.1-31.5)	44	21.4 (15.1-31.4)	44	21.4 (15.1-31.4)
45	22.0 (15.5-32.2)	45	21.9 (15.5-32.1)	45	21.9 (15.5-32.1)
46	22.5 (16.0-32.9)	46	22.4 (16.0-32.8)	46	22.4 (16.0-32.8)
47	23.0 (16.5-33.6)				

<400> 445

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<210> 446
<211> 125
<212> PRT
<213> homo sapiens
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<400> 446

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<210> 447
<211> 80
<212> PRT
<213> homo sapiens
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<400> 447

Met 1	Ser	Cys	Lys	His 5	Phe	Ile	Ile	Arg	Gly 10	Phe	Gln	Asp	Leu	Leu 15	Thr
Leu	Leu	Leu	Trp 20	Arg	Gly	His	Leu	Lys 25	Ser	Trp	Val	Cys	Asn 30	Met	Arg
Met	Phe	Lys 35	Arg	His	Gln	Leu	Cys 40	Thr	Arg	Cys	Ser	Ile 45	Ser	Ala	Val
Asp	Gly 50	Phe	Val	His	Leu	Leu 55	Gln	Val	Leu	Val	Asn 60	Gly	Asn	Val	Arg
His 65	Gly	Ser	Ala	Ala	Glu 70	Arg	Arg	Ala	Pro	Pro 75	Pro	Thr	Pro	Gln	Ala 80

<210> 448  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 448

Arg 1	Ser	Arg	Gly	Phe 5	Ser	Cys	Val	Gln	Thr 10	Pro	Cys	His	Phe	Arg 15	Glu
Val	Thr	Gln	Ala 20	Cys	Val	Ile	Ser	Leu 25	Trp	Gln	Gln	Val	Gly 30	Gly	Leu
Pro	Gln	Gly 35	Arg	Arg	Trp	Pro	Glu 40	Met	Cys	Phe	Arg	Ser 45	Leu	Thr	His
His	Ser 50	Leu	His	Thr	Arg	Arg 55	Glu	His	His	Ser	Trp 60	Ser	Ile	Leu	Arg
Met 65	Glu	Ile													

<210> 449  
 <211> 60  
 <212> PRT  
 <213> homo sapiens

<400> 449

Pro 1	Ile	Thr	Pro	Tyr 5	Thr	His	Asp	Val	Asn 10	Thr	Thr	Pro	Gly	Ala 15	Phe
Ser	Glu	Trp	Arg 20	Phe	Glu	Phe	His	Val 25	Ala	Ala	Ser	His	Thr 30	Gln	Thr
Cys	His	His 35	Ser	Pro	His	Thr	His 40	Ser	Arg	His	Ser	Thr 45	Ala	Met	Ser
Gln	Lys 50	Lys	Phe	Leu	Val	Ser 55	Asp	Leu	Lys	Val	Leu 60				

<210> 450  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 450

002221" 56662960



Arg 1	Ala	Thr	Ser	Gly 5	Arg	Ser	Gly	Phe	Ile 10	Lys	Pro	Ser	Asn	Leu 15	Lys
Gln	Gly	Thr	Ser 20	Phe	Gly	Ser	Trp	Leu 25	Leu	Asn	Val	Val	Ser 30	Gly	Cys
Val	Gly	Asn 35	Asp	Gly	Arg	Phe	Val 40	Cys	Glu	Lys	Leu	Pro 45	His	Gly	Ile
Gln	Ile 50	Ser	Ile	Leu	Arg	Met 55	Leu	Gln	Glu	Trp	Cys 60	Ser	Arg	Arg	Val
Cys 65	Arg	Glu													

<210> 451  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 451

Ser 1	Ala	Ser	His	Pro 5	Glu	Ser	Arg	Leu	Cys 10	Arg	Gly	Gly	Ala	Asp 15	Met
Gln	Ala	Pro	Arg 20	Gly	Thr	Leu	Val	Phe 25	Ala	Leu	Val	Ile	Ala 30	Leu	Val
Pro	Val	Gly 35	Arg	Glu	Pro	Ser	Ser 40	Gln	Gly	Ser	Gln	Ser 45	Ala	Leu	Gln
Thr	Tyr 50	Glu	Leu	Gly	Ser	Glu 55	Asn	Val	Lys	Val	Pro 60	Ile	Phe	Glu	Glu
Asp 65	Thr	Pro	Ser	Val	Met 70	Glu	Ile	Glu	Met 75	Glu	Glu	Leu	Asp	Lys	Trp 80
Met	Asn	Ser	Met	Asn 85	Arg	Asn	Ala	Asp	Phe 90	Glu	Cys	Leu	Pro	Thr 95	Leu
Lys	Glu	Glu	Lys 100	Glu	Ser	Asn	His 105	Asn	Pro	Ser	Asp	Ser	Glu 110	Ser	

<210> 452  
 <211> 51  
 <212> PRT  
 <213> homo sapiens

<400> 452

Glu 1	Glu	Trp	Ala	Leu 5	Glu	Glu	Thr	Ala	Lys 10	Gly	Ser	Cys	Val	Tyr 15	Val
Asp	Leu	Lys	Leu 20	Ile	Lys	Phe	Val	Ser 25	Ser	Ser	Ser	Ser	Val 30	Gly	Ser
Leu	Ser	Arg 35	Leu	Pro	Gln	Gly	Leu 40	Leu	Leu	Leu	Glu	Asn 45	Met	Ser	Ala
Ile	Gln 50	Val													

004221" 3622960

<210> 453  
 <211> 59  
 <212> PRT  
 <213> homo sapiens

<400> 453

Phe	Asp	Ser	Phe	Ser	Ser	Phe	Lys	Val	Gly	Lys	His	Ser	Lys	Ser	Ala
1				5					10					15	
Phe	Leu	Phe	Met	Leu	Phe	Ile	His	Leu	Ser	Ser	Ser	Ser	Ile	Ser	Ile
			20					25					30		
Ser	Ile	Thr	Glu	Gly	Val	Ser	Ser	Ser	Lys	Ile	Gly	Thr	Phe	Thr	Phe
		35					40					45			
Ser	Leu	Pro	Ser	Ser	Tyr	Val	Cys	Lys	Ala	Leu					
	50					55									

<210> 454  
 <211> 107  
 <212> PRT  
 <213> homo sapiens

<400> 454

Pro	Ile	Thr	Thr	Cys	Ser	Leu	Gly	Asp	Pro	Gly	Lys	Asp	Lys	Tyr	Thr
1				5					10					15	
Cys	Thr	His	Arg	Gly	Arg	Glu	Arg	Cys	Val	Gln	Arg	Ile	Cys	Ile	Asn
			20					25					30		
Ile	Leu	Phe	Ser	His	Pro	Asp	Met	Arg	Ser	Gln	Cys	Cys	Met	Met	Lys
		35					40					45			
Arg	Trp	Tyr	Asp	Ser	Thr	Tyr	Val	Pro	Ile	Val	Leu	Leu	Phe	Leu	Tyr
	50					55					60				
Phe	Leu	Phe	Arg	Ser	Phe	Thr	Ile	Gly	Arg	Phe	Gln	Lys	His	Ser	Phe
65					70					75					80
His	His	His	Leu	Glu	Met	Val	Cys	Leu	Asn	Gly	Asp	Asn	Ser	Arg	Ser
				85					90					95	
Cys	Ser	Ile	Ser	Ser	Arg	His	Gly	Leu	Leu	Ile					
			100					105							

<210> 455  
 <211> 73  
 <212> PRT  
 <213> homo sapiens

<400> 455

Arg	Arg	Gly	Val	Ser	Phe	Leu	Leu	Ser	Arg	Gln	Lys	Trp	Tyr	His	Tyr
1				5					10					15	
Val	Ala	Ala	Leu	Gln	Ser	Pro	Arg	Ala	Arg	Ser	Leu	Glu	Asn	His	Leu
			20					25					30		
Leu	Ser	Arg	Phe	Phe	Phe	Phe	Leu	Arg	Val	Gly	Val	Ser	Leu	Cys	Cys
		35					40					45			

004321 5664960



			20					25						30		
Leu	Glu	Ser	Ile	Phe	Phe	Glu	Lys	Pro								
		35					40									

<210> 459  
 <211> 36  
 <212> PRT  
 <213> homo sapiens

<400> 459

Ile	Pro	Glu	Val	Ala	Ser	Ile	His	Phe	Val	Ser	Gly	Glu	Pro	Ile	Ile
1				5					10					15	
Leu	Val	Ala	Ile	Leu	Val	Arg	Leu	Arg	Val	Leu	Cys	Arg	Ile	Asn	Gly
			20					25					30		
Arg	Glu	Gly	Trp												
		35													

<210> 460  
 <211> 36  
 <212> PRT  
 <213> homo sapiens

<400> 460

Asn	Ser	Glu	Gly	Phe	Arg	Arg	Asn	Gln	Leu	Leu	Gln	Ile	Asp	Leu	Lys
1				5					10					15	
Ile	Phe	Leu	Ser	Cys	Lys	Phe	Gln	Lys	Leu	His	Gln	Ser	Thr	Leu	Phe
			20					25					30		
Gln	Val	Asn	Leu												
		35													

<210> 461  
 <211> 83  
 <212> PRT  
 <213> homo sapiens

<400> 461

Gly	Arg	Arg	Asn	Asp	Gln	Leu	Asn	Leu	His	Ile	Pro	Gln	Ala	Gly	Pro
1				5					10					15	
Phe	Ala	Gly	Pro	Tyr	Arg	Leu	Gly	Trp	Pro	Leu	Leu	Ser	Ser	Gly	Ile
			20					25					30		
Arg	Leu	Pro	Asp	Trp	Leu	Val	Leu	His	Val	Ser	Ile	Lys	Leu	Lys	Val
		35					40					45			
Ile	Pro	Trp	Pro	Pro	Pro	Gly	Glu	Asn	Gln	Pro	His	Pro	Ala	Ser	Trp
	50					55					60				
Gly	Gln	Trp	Gly	Arg	Asp	Phe	Gly	Leu	Ser	Glu	Gln	Leu	Leu	Glu	Ala
65					70					75					80
Ala	His	Asp													

<210> 462  
 <211> 93

<212> PRT  
 <213> homo sapiens

<400> 462

Arg 1	Arg	Lys	Ala	Ser 5	Ile	Ile	Ala	Phe	Lys 10	Gly	Ile	Leu	Leu	Thr 15	Leu
Thr	Gln	Gly	Val 20	Gln	Ser	Ala	Arg	Glu 25	Pro	Ile	Leu	Ile	Ser 30	Ser	Ser
Lys	Met	Phe 35	Leu	Glu	Glu	Asn	Pro 40	Trp	Asn	Val	Leu	Lys 45	Asp	Val	Ser
Gly	Val 50	Arg	Ser	Ser	Met	Trp 55	Leu	Ala	Lys	Gly	His 60	Leu	Tyr	Leu	Phe
Gln 65	Leu	Glu	Phe	Ile	Asn 70	Ser	Cys	Ser	Leu	Val 75	Ser	Leu	Gly	Ala	Glu 80
Val	Trp	His	Ile	Phe 85	Lys	Pro	Val	His	Ser 90	Arg	Ile	Gln			

<210> 463  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 463

Thr 1	Leu	Asn	Pro	His 5	Lys	Thr	Leu	Ser	Ala 10	Lys	Lys	Ala	Arg	Val 15	Ile
Phe	Phe	Cys	Ile 20	Gln	Asp	Ser	Thr	Ala 25	Asn	Leu	Val	Phe	Cys 30	Tyr	Lys
Asn	Leu	Val 35	Ser	His	Phe	Leu	Leu 40	Lys	Arg	Thr	Arg	Ile 45	Thr	Gly	Thr
His	Pro 50	Gln	Leu	His	Glu	Thr 55	Pro	Ser	Phe	Leu	Asn 60	Glu	His	Glu	Ser
Ile 65	Tyr	Val	His	Pro	Ser 70	Thr	His	Met	Lys	Met 75	Leu	Cys	Ser	Ser	Thr 80
Gly	Met	Asp	Gly	Ile 85	Arg	Ile	Lys	Pro	Ile 90	Trp	Lys	Leu	Lys	Tyr 95	Phe

<210> 464  
 <211> 76  
 <212> PRT  
 <213> homo sapiens

<400> 464

Asn 1	Leu	Phe	Thr	Met 5	Lys	Phe	Leu	Pro	Glu 10	Phe	Ser	Pro	Phe	Asp 15	Thr
Asn	Ser	Met	His 20	Val	Ser	Thr	Phe	Glu 25	Thr	Gln	Pro	Asn	Val 30	Ile	Ser
Val	Lys	Ser 35	Ser	Leu	Ser	Leu	Pro 40	Ser	Ser	Asn	Leu	Pro 45	Ser	Pro	Arg

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<400> 468

Leu 1	Ser	Lys	Ala	Ile 5	Tyr	Phe	Cys	Lys	Lys 10	Ala	Ala	Ala	Cys	Ile 15	Asn
His	Asp	His	Ser 20	Ser	Thr	Leu	Asn	Lys 25	Glu	Arg	Lys	Arg	Phe 30	Leu	Ser
Leu	Thr	Gln 35	Ser	Leu	Pro	Leu	Cys 40	His	Ser	Pro	Arg	Gly 45	Trp	Gly	Trp
Thr	Ala 50	His	Ser	Lys	Leu	Thr 55	Arg	Leu	Ala	Ile	Cys 60	Glu	Tyr	Phe	Ser
Lys 65															

<210> 469

<211> 56

<212> PRT

<213> homo sapiens

<400> 469

Pro 1	Asp	Trp	Leu	Phe 5	Val	Asn	Thr	Phe	Pro 10	Asn	Lys	Glu	Gly	Lys 15	Gly
Asp	Val	Ser	Tyr 20	Ser	Gly	Gly	Lys	Cys 25	Ser	Phe	Ser	Gly	Lys 30	Asn	Gly
Cys	Arg	Val 35	Gly	Asn	Gln	Gly	Ser 40	Arg	Cys	Glu	Leu	Leu 45	Ile	Arg	Thr
Gly	Gly 50	Lys	Val	Val	His	Ser 55	Asn								

<210> 470

<211> 109

<212> PRT

<213> homo sapiens

<400> 470

Ala 1	Arg	Pro	Ala	Pro 5	Ala	Gly	Arg	Glu	Gly 10	Arg	Gly	Glu	Gly	Glu 15	Ala
Thr	Ser	Arg	Arg 20	Cys	Gly	Val	Gly	His 25	Arg	Ala	Gly	Pro	Arg 30	Glu	Pro
Ala	Pro	His 35	Gly	Ala	Ala	Ala	Val 40	Arg	Pro	Thr	Pro	Gly 45	Pro	His	His
His	Cys 50	Ala	Ala	Leu	Ser	Gly 55	Ala	Glu	Asn	Tyr	Arg 60	Ser	Arg	His	Ala
Met 65	Lys	Leu	Ala	Ser	Ala 70	Leu	Arg	Arg	Gly 75	Pro	Ala	Leu	His	Pro	Leu 80
Pro	Pro	Arg	Ala	Asn 85	Arg	Gly	Arg	Glu	Pro 90	Trp	Arg	Arg	Arg	His 95	Arg
Pro	Arg	Gly	Trp 100	Ala	Ala	Ala	Ser	Arg 105	Thr	Trp	Arg	Ser			

002221"5622960

<210> 471  
 <211> 399  
 <212> PRT  
 <213> homo sapiens

<400> 471

Ala 1	Ala	Gly	Ala	Cys 5	Gly	Ala	Arg	Gly	Ser 10	Gly	Arg	Arg	Gly	Ser 15	Tyr
Val	Pro	Glu	Val 20	Arg	Cys	Gly	Ala	Pro 25	Gly	Gly	Ala	Ala	Gly 30	Thr	Gly
Ala	Pro	Arg 35	Ser	Cys	Cys	Cys	Gln 40	Thr	Asn	Pro	Gly	Pro 45	Pro	Ser	Ser
Leu	Arg 50	Arg	Ala	Phe	Arg	Arg 55	Arg	Glu	Leu	Pro	Phe 60	Pro	Ala	Cys	His
Glu 65	Ile	Gly	Leu	Gly	Ala 70	Glu	Ala	Gly	Ser	Gly 75	Pro	Pro	Pro	Ala	Pro 80
Ala	Ala	Arg	Glu	Ser 85	Arg	Ser	Arg	Ala	Met 90	Glu	Glu	Glu	Ala	Ser 95	Ser
Pro	Gly	Leu	Gly 100	Cys	Ser	Lys	Pro	His 105	Leu	Glu	Lys	Leu	Thr 110	Leu	Gly
Ile	Thr	Arg 115	Ile	Leu	Glu	Ser	Ser 120	Pro	Gly	Val	Thr	Glu 125	Val	Thr	Ile
Ile	Glu 130	Lys	Pro	Pro	Ala	Glu 135	Arg	His	Met	Ile	Ser 140	Ser	Trp	Glu	Gln
Lys 145	Asn	Asn	Cys	Val	Met 150	Pro	Glu	Asp	Val	Lys 155	Asn	Phe	Tyr	Leu	Met 160
Thr	Asn	Gly	Phe	His 165	Met	Thr	Trp	Ser	Val 170	Lys	Leu	Asp	Glu	His 175	Ile
Ile	Pro	Leu	Gly 180	Ser	Met	Ala	Ile	Asn 185	Ser	Ile	Ser	Lys	Leu 190	Thr	Gln
Leu	Thr	Gln 195	Ser	Ser	Met	Tyr	Ser 200	Leu	Pro	Asn	Ala	Pro 205	Thr	Leu	Ala
Asp	Leu 210	Glu	Asp	Asp	Thr	His 215	Glu	Ala	Ser	Asp	Asp 220	Gln	Pro	Glu	Lys
Pro 225	His	Phe	Asp	Ser	Arg 230	Ser	Val	Ile	Phe	Glu 235	Leu	Asp	Ser	Cys	Asn 240
Gly	Ser	Gly	Lys	Val 245	Cys	Leu	Val	Tyr	Lys 250	Ser	Gly	Lys	Pro	Ala 255	Leu
Ala	Glu	Asp	Thr 260	Glu	Ile	Trp	Phe	Leu 265	Asp	Arg	Ala	Leu	Tyr 270	Trp	His
Phe	Leu	Thr 275	Asp	Thr	Phe	Thr	Ala 280	Tyr	Tyr	Arg	Leu	Leu 285	Ile	Thr	His
Leu	Gly	Leu	Pro	Gln	Trp	Gln	Tyr	Ala	Phe	Thr	Ser	Tyr	Gly	Ile	Ser

004221 3552350



	290					295					300					
Pro 305	Gln	Ala	Lys	Gln	Trp 310	Phe	Ser	Met	Tyr	Lys 315	Pro	Ile	Thr	Tyr	Asn 320	
Thr	Asn	Leu	Leu	Thr 325	Glu	Glu	Thr	Asp	Ser 330	Phe	Val	Asn	Lys	Leu 335	Asp	
Pro	Ser	Lys	Val 340	Phe	Lys	Ser	Lys	Asn 345	Lys	Ile	Val	Ile	Pro 350	Lys	Lys	
Lys	Gly	Pro 355	Val	Gln	Pro	Ala	Gly 360	Gly	Gln	Lys	Gly	Pro 365	Ser	Gly	Pro	
Ser	Gly 370	Pro	Ser	Thr	Ser	Ser 375	Thr	Ser	Lys	Ser	Ser 380	Ser	Gly	Ser	Gly	
Glu 385	Thr	Pro	Pro	Gly	Lys 390	Leu	Arg	His	Pro	Ser 395	Phe	Gln	Phe	Ala		

<400> 472

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<210> 473
<211> 56
<212> PRT
<213> homo sapiens
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<400> 473

Lys 1	Tyr	Val	Ser	His 5	Ala	Asn	Ile	Ser	Ile 10	Tyr	Lys	Trp	Arg	Thr 15	Leu
Thr	Leu	Leu	Leu 20	Phe	Ser	Tyr	Lys	Ile 25	Pro	Asn	Phe	Val	Ile 30	Ile	Leu
Ser	Gly	Ile 35	Thr	Leu	Tyr	Cys	Lys 40	Asn	Ala	Ser	Tyr	Phe 45	Thr	Phe	Lys
Phe	Asp 50	Asn	Val	Cys	Asp	Glu 55	Leu								

[illegible][illegible][illegible]

His 1	Ile	Lys	Ile	Glu 5	Phe	Phe	Gly	Gln	Asn 10	Phe	Trp	Glu	Ala	Met 15	His
Pro	Thr	Trp	Ala 20	Asp	Ile	Gln	Pro	Glu 25	Leu	Phe	Ser	Arg	Gly 30	Glu	Trp
Tyr	Trp	Gln 35	Phe	Met	Ala	Glu	Ile 40	His	Ser	Asp	Trp	Leu 45	Glu	Ser	Met
Leu	Tyr 50	Gln	Leu	Leu	Asn	Ile 55	Leu	Ser	Ile	Thr	Leu 60	Ala	Tyr	Cys	Tyr
Tyr 65	Tyr	Ile	Ser	Ser	Ile 70	Tyr	Arg	Gln	Lys	Gly 75	His	Phe	Arg	Asn	Ile 80

<400> 477

Ser Ser Leu Gly Lys Thr Phe Gly Lys Gln Cys Ile Leu His Gly Leu  
1 5 10 15

Ile	Phe	Ser	Leu 20	Ser	Cys	Ser	Gln	Glu 25	Glu	Ser	Gly	Thr	Gly 30	Ser	Leu
-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----

Trp	Leu	Lys 35	Ser	Ile	Leu	Ile	Gly 40	Trp	Ser	Leu	Cys	Tyr 45	Thr	Ser	Cys
-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----

<210> 478  
 <211> 70  
 <212> PRT  
 <213> homo sapiens

<400> 478

Glu 1	Gln	Leu	Arg	Leu 5	Asn	Ile	Ser	Pro	Cys 10	Arg	Met	His	Cys	Phe 15	Pro
Lys	Val	Leu	Pro 20	Lys	Glu	Leu	Tyr	Phe 25	Tyr	Val	Leu	Ser	His 30	Arg	Thr
Gly	Glu	Lys 35	Cys	Ser	Gly	His	Cys 40	Trp	Asp	Leu	Ile	Phe 45	Leu	Gly	Met
Gly	Ser 50	Gly	Leu	Met	Ile	Leu 55	Ala	Thr	Gly	Val	Gln 60	Glu	Asn	Gly	Ser
Pro 65	Gly	Ser	Asp	Ser	Trp 70										

<210> 479  
 <211> 400  
 <212> PRT  
 <213> homo sapiens

<400> 479

Pro 1	Gln	Gln	Thr	Pro 5	Trp	Ala	Val	Ala	Gly 10	Arg	Trp	Cys	Asn	Gly 15	Pro
Ser	Leu	His	Arg 20	Asn	Arg	Ala	Gly	Leu 25	Asp	Leu	Pro	Thr	Ile 30	Asp	Thr
Gly	Tyr	Asp 35	Ser	Gln	Pro	Gln	Asp 40	Val	Leu	Gly	Ile	Arg 45	Gln	Leu	Glu
Arg	Pro 50	Leu	Pro	Leu	Thr	Ser 55	Val	Cys	Tyr	Pro	Gln 60	Asp	Leu	Pro	Arg
Pro 65	Leu	Arg	Ser	Arg	Glu 70	Phe	Pro	Gln	Phe	Glu 75	Pro	Gln	Arg	Tyr	Pro 80
Ala	Cys	Ala	Gln	Met 85	Leu	Pro	Pro	Asn	Leu 90	Ser	Pro	His	Ala	Pro 95	Trp
Asn	Tyr	His	Tyr 100	His	Cys	Pro	Gly	Ser 105	Pro	Asp	His	Gln	Val 110	Pro	Tyr
Gly	His	Asp 115	Tyr	Pro	Arg	Ala	Ala 120	Tyr	Gln	Gln	Val	Ile 125	Gln	Pro	Ala
Leu	Pro 130	Gly	Gln	Pro	Leu	Pro 135	Gly	Ala	Ser	Val	Arg 140	Gly	Leu	His	Pro

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Val 145	Gln	Lys	Val	Ile	Leu 150	Asn	Tyr	Pro	Ser	Pro 155	Trp	Asp	Gln	Glu	Glu 160
Arg	Pro	Ala	Gln	Arg 165	Asp	Cys	Ser	Phe	Pro 170	Gly	Leu	Pro	Arg	His 175	Gln
Asp	Gln	Pro	His 180	His	Gln	Pro	Pro	Asn 185	Arg	Ala	Gly	Ala	Pro 190	Gly	Glu
Ser	Leu	Glu 195	Cys	Pro	Ala	Glu	Leu 200	Arg	Pro	Gln	Val	Pro 205	Gln	Pro	Pro
Ser	Pro 210	Ala	Ala	Val	Pro	Arg 215	Pro	Pro	Ser	Asn	Pro 220	Pro	Ala	Arg	Gly
Thr 225	Leu	Lys	Thr	Ser	Asn 230	Leu	Pro	Glu	Glu	Leu 235	Arg	Lys	Val	Phe	Ile 240
Thr	Tyr	Ser	Met	Asp 245	Thr	Ala	Met	Glu	Val 250	Val	Lys	Phe	Val	Asn 255	Phe
Leu	Leu	Val	Asn 260	Gly	Phe	Gln	Thr	Ala 265	Ile	Asp	Ile	Phe	Glu 270	Asp	Arg
Ile	Arg	Gly 275	Ile	Asp	Ile	Ile	Lys 280	Trp	Met	Glu	Arg	Tyr 285	Leu	Arg	Asp
Lys	Thr 290	Val	Met	Ile	Ile	Val 295	Ala	Ile	Ser	Pro	Lys 300	Tyr	Lys	Gln	Asp
Val 305	Glu	Gly	Ala	Glu	Ser 310	Gln	Leu	Asp	Glu	Asp 315	Glu	His	Gly	Leu	His 320
Thr	Lys	Tyr	Ile	His 325	Arg	Met	Met	Gln	Ile 330	Glu	Phe	Ile	Lys	Gln 335	Gly
Ser	Met	Asn	Phe 340	Arg	Phe	Ile	Pro	Val 345	Leu	Phe	Pro	Asn	Ala 350	Lys	Lys
Glu	His	Val 355	Pro	Thr	Trp	Leu	Gln 360	Asn	Thr	His	Val	Tyr 365	Ser	Trp	Pro
Lys	Asn 370	Lys	Lys	Asn	Ile	Leu 375	Leu	Arg	Leu	Leu	Arg 380	Glu	Glu	Glu	Tyr
Val 385	Ala	Pro	Pro	Arg	Gly 390	Pro	Leu	Pro	Thr	Leu 395	Gln	Val	Val	Pro	Leu 400

<400> 480

Ser 1	Ser	Ser	Gly	Trp 5	Arg	Val	Ala	Arg	Gly 10	Ser	Arg	His	Ser	Ser 15	Trp
Gly	Arg	Arg	Leu 20	Gly	Asn	Leu	Trp	Ser 25	Gln	Leu	Cys	Arg	Ala 30	Leu	Gln
Gly	Leu	Pro 35	Arg	Ser	Thr	Ser	Ser 40	Ile	Arg	Trp	Leu	Val 45	Met	Trp	Leu

[illegible]

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<210> 481
<211> 125
<212> PRT
<213> homo sapiens
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<400> 481

Lys 1	Gln	Arg	Met	Gln 5	Ser	Ser	His	Arg	Leu 10	His	Phe	Lys	Ala	Arg 15	Val
Cys	Gly	Gly	Leu 20	Arg	Gly	Arg	Ala	Leu 25	His	Asn	Arg	Phe	Pro 30	Gly	Gly
Gln	Arg	Ala 35	Ser	Arg	Gly	Gly	Thr 40	Glu	Lys	Asn	Gln	Pro 45	Gly	Val	Leu
Pro	Thr 50	Ser	Leu	Ser	Gln	Asn 55	Ala	Val	Arg	Thr	Arg 60	Pro	Gln	Thr	Trp
Pro 65	Gly	Leu	Ser	Asp	Leu 70	Gly	Met	Asn	Gly	Val 75	Thr	Arg	Glu	Pro	Pro 80
Glu	Gly	Trp	Ala	Glu 85	Ala	Pro	Val	Glu	Glu 90	Pro	His	Thr	Leu	Pro 95	Leu
Ser	Ala	Ala	Ala	Ala	Gly	Cys	Phe	Phe	Tyr	Ser	Trp	Ala	Ser	Cys	Arg

100								105				110			
His	Glu	Cys	Ser	Glu	Ala	Arg	Trp	Ala	His	Ala	Pro	Ser			
		115					120					125			
<210> 482															
<211> 96															
<212> PRT															
<213> homo sapiens															
<400> 482															
Val	Ala	Met	Thr	Ala	Lys	Asp	Cys	Ser	Ile	Met	Ile	Ala	Leu	Ser	Pro
1				5					10					15	
Cys	Leu	Gln	Asp	Ala	Ser	Ser	Asp	Gln	Arg	Pro	Val	Val	Pro	Ser	Ser
			20					25					30		
Arg	Ser	Arg	Phe	Ala	Phe	Ser	Val	Ser	Val	Leu	Asp	Leu	Asp	Leu	Lys
		35					40					45			
Pro	Tyr	Glu	Ser	Ile	Pro	His	Gln	Tyr	Lys	Leu	Asp	Gly	Lys	Ile	Val
	50					55					60				
Asn	Tyr	Tyr	Ser	Lys	Thr	Val	Arg	Ala	Lys	Asp	Asn	Ala	Val	Met	Ser
65					70					75					80
Thr	Arg	Phe	Lys	Glu	Ser	Glu	Asp	Cys	Thr	Leu	Val	Leu	His	Lys	Val
				85					90					95	
<210> 483															
<211> 66															
<212> PRT															
<213> homo sapiens															
<400> 483															
Leu	His	Cys	Leu	Pro	Val	Cys	Arg	Met	Pro	Ala	Leu	Ile	Lys	Gly	Leu
1				5					10					15	
Trp	Ser	Leu	His	Arg	Gly	Pro	Gly	Leu	Pro	Phe	Pro	Cys	Leu	Cys	Trp
			20					25					30		
Thr	Leu	Thr	Ser	Ser	Pro	Thr	Arg	Ala	Phe	Pro	Ile	Ser	Ile	Asn	Trp
		35					40					45			
Thr	Ala	Arg	Ser	Ser	Thr	Ile	Ile	Gln	Arg	Leu	Tyr	Val	Pro	Lys	Thr
	50					55					60				
Thr	Pro														
65															
<210> 484															
<211> 109															
<212> PRT															
<213> homo sapiens															
<400> 484															
Asn	Lys	Ala	Phe	Arg	Ile	Arg	Glu	Ser	Asp	Met	Ser	Pro	Gly	Trp	Glu
1				5					10					15	
Arg	Arg	Thr	Ile	Gln	Asn	Val	Phe	Pro	Gly	Leu	Asn	Gly	His	Phe	His

			20				25				30				
Phe	Lys	Ser 35	Val	Ser	Ser	Phe	Leu 40	Gly	His	Ser	Thr	His 45	Phe	Leu	His
Ser	Leu 50	Ser	Arg	Lys	Leu	Phe 55	Leu	Val	Leu	Phe	Asn 60	Ser	Met	Ser	Pro
Arg 65	Gly	Asn	Pro	Thr	Ser 70	Lys	Gly	Val	Lys	Ser 75	Lys	Asn	Ile	His	Asn 80
Gln	Arg	Ser	Pro	Asn 85	Thr	Thr	Glu	Asn	Ile 90	Ser	Ile	Ile	Gln	Pro 95	Ser
His	Tyr	Val	Gln 100	Val	Ser	Lys	Thr	Leu 105	Gln	Gly	Lys	Ser			

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<210> 485
<211> 66
<212> PRT
<213> homo sapiens
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<400> 485

[illegible]

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<210> 486
<211> 109
<212> PRT
<213> homo sapiens
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<400> 486

Ala 1	Arg	Pro	Ala	Pro 5	Ala	Gly	Arg	Glu	Gly 10	Arg	Gly	Glu	Gly	Glu 15	Ala
Thr	Ser	Arg	Arg 20	Cys	Gly	Val	Gly	His 25	Arg	Ala	Gly	Pro	Arg 30	Glu	Pro
Ala	Pro	His 35	Gly	Ala	Ala	Ala	Val 40	Arg	Pro	Thr	Pro	Gly 45	Pro	His	His
His	Cys 50	Ala	Ala	Leu	Ser	Gly 55	Ala	Glu	Asn	Tyr	Arg 60	Ser	Arg	His	Ala
Met 65	Lys	Leu	Ala	Ser	Ala 70	Leu	Arg	Arg	Gly	Pro 75	Ala	Leu	His	Pro	Leu 80
Pro	Pro	Arg	Ala	Asn 85	Arg	Gly	Arg	Glu	Pro 90	Trp	Arg	Arg	Arg	His 95	Arg

Pro	Arg	Gly	Trp	Ala	Ala	Ala	Ser	Arg	Thr	Trp	Arg	Ser			
			100					105							

<210> 487  
 <211> 389  
 <212> PRT  
 <213> homo sapiens

<400> 487

Ala	Ala	Gly	Ala	Cys	Gly	Ala	Arg	Gly	Ser	Gly	Arg	Arg	Gly	Ser	Tyr
1				5					10					15	
Val	Pro	Glu	Val	Arg	Cys	Gly	Ala	Pro	Gly	Gly	Ala	Ala	Gly	Thr	Gly
			20					25					30		
Ala	Pro	Arg	Ser	Cys	Cys	Cys	Gln	Thr	Asn	Pro	Gly	Pro	Pro	Ser	Ser
		35					40					45			
Leu	Arg	Arg	Ala	Phe	Arg	Arg	Arg	Glu	Leu	Pro	Phe	Pro	Ala	Cys	His
	50					55					60				
Glu	Ile	Gly	Leu	Gly	Ala	Glu	Ala	Gly	Ser	Gly	Pro	Pro	Pro	Ala	Pro
65					70					75					80
Ala	Ala	Arg	Glu	Ser	Arg	Ser	Arg	Ala	Met	Glu	Glu	Glu	Ala	Ser	Ser
				85					90					95	
Pro	Gly	Leu	Gly	Cys	Ser	Lys	Pro	His	Leu	Glu	Lys	Leu	Thr	Leu	Gly
			100					105					110		
Ile	Thr	Arg	Ile	Leu	Glu	Ser	Ser	Pro	Gly	Val	Thr	Glu	Val	Thr	Ile
		115					120					125			
Ile	Glu	Lys	Pro	Pro	Ala	Glu	Arg	His	Met	Ile	Ser	Ser	Trp	Glu	Gln
	130					135					140				
Lys	Asn	Asn	Cys	Val	Met	Pro	Glu	Asp	Val	Lys	Asn	Phe	Tyr	Leu	Met
145					150					155					160
Thr	Asn	Gly	Phe	His	Met	Thr	Trp	Ser	Val	Lys	Leu	Asp	Glu	His	Ile
				165					170					175	
Ile	Pro	Leu	Gly	Ser	Met	Ala	Ile	Asn	Ser	Ile	Ser	Lys	Leu	Thr	Gln
			180					185					190		
Leu	Thr	Gln	Ser	Ser	Met	Tyr	Ser	Leu	Pro	Asn	Ala	Pro	Thr	Leu	Ala
		195					200					205			
Asp	Leu	Glu	Asp	Asp	Thr	His	Glu	Ala	Ser	Asp	Asp	Gln	Pro	Glu	Lys
	210					215					220				
Pro	His	Phe	Asp	Ser	Arg	Ser	Val	Ile	Phe	Glu	Leu	Asp	Ser	Cys	Asn
225					230					235					240
Gly	Ser	Gly	Lys	Val	Cys	Leu	Val	Tyr	Lys	Ser	Gly	Lys	Pro	Ala	Leu
				245					250					255	
Ala	Glu	Asp	Thr	Glu	Ile	Trp	Phe	Leu	Asp	Arg	Ala	Leu	Tyr	Trp	His
			260					265					270		
Phe	Leu	Thr	Asp	Thr	Phe	Thr	Ala	Tyr	Tyr	Arg	Leu	Leu	Ile	Thr	His

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275					280					285					
Leu	Gly	Leu	Pro	Gln	Trp	Gln	Tyr	Ala	Phe	Thr	Ser	Tyr	Gly	Ile	Ser
	290					295					300				
Pro	Gln	Ala	Lys	Gln	Trp	Phe	Ser	Met	Tyr	Lys	Pro	Ile	Thr	Tyr	Asn
305					310					315					320
Thr	Asn	Leu	Leu	Thr	Glu	Glu	Thr	Asp	Ser	Phe	Val	Asn	Lys	Leu	Asp
				325					330					335	
Pro	Ser	Lys	Val	Phe	Lys	Ser	Lys	Asn	Lys	Ile	Val	Ile	Pro	Lys	Lys
			340					345					350		
Lys	Gly	Pro	Val	Gln	Pro	Ala	Gly	Gly	Gln	Lys	Gly	Pro	Ser	Gly	Pro
		355					360					365			
Ser	Gly	Pro	Ser	Thr	Ser	Ser	Thr	Ser	Lys	Ser	Ser	Ser	Gly	Ser	Gly
	370					375					380				
Asn	Pro	Thr	Arg	Lys											
385															

<210> 488  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 488

Arg	Ser	Ala	Gly	Gly	Phe	Ser	Met	Met	Val	Thr	Ser	Val	Thr	Pro	Gly
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Glu	Asp	Ser	Arg	Met	Arg	Val	Met	Pro	Arg	Val	Ser	Phe	Ser	Arg	Cys
			20					25					30		
Gly	Leu	Leu	Gln	Pro	Ser	Pro	Gly	Asp	Asp	Ala	Ser	Ser	Ser	Met	Ala
		35					40					45			
Arg	Asp	Arg	Asp	Ser	Arg	Ala	Ala	Gly	Ala	Gly	Gly	Gly	Pro	Asp	Pro
	50					55					60				
Ala	Ser	Ala	Pro	Arg	Pro	Ile	Ser	Trp	His	Ala	Gly	Asn	Gly	Ser	Ser
65					70					75					80
Arg	Arg	Leu	Lys	Ala	Arg	Arg	Ser	Asp	Asp	Gly	Gly	Pro	Gly	Leu	Val
				85					90					95	

<210> 489  
 <211> 152  
 <212> PRT  
 <213> homo sapiens

<400> 489

Leu	Ala	Ala	Gly	Arg	Gly	Lys	Glu	Glu	Glu	Met	Gly	Phe	Glu	Asp	His
1				5					10					15	
Gly	Leu	Pro	Phe	Leu	Pro	Leu	Thr	His	His	Thr	Pro	Phe	Pro	Pro	Leu
			20					25					30		
Ser	Leu	Ser	Pro	Leu	Pro	Lys	Lys	Lys	Lys	Lys	Glu	Thr	Phe	Ile	Met
		35					40					45			

Asn	Gln	Gln	Gly	Phe	Ser	Pro	Tyr	Gln	Arg	Glu	Met	Trp	Lys	Glu	Leu
	50					55					60				
Lys	Lys	Pro	Pro	Phe	Val	Pro	Asn	Ser	Thr	Leu	Pro	Ile	Phe	Tyr	Ala
65					70					75					80
Thr	Gln	Thr	Leu	Ser	Phe	Trp	Val	Pro	Phe	Leu	Gln	Met	Asp	Leu	Leu
				85					90					95	
Arg	Arg	Ile	Ile	Val	Phe	His	Val	Phe	Ser	Pro	Gln	Val	Thr	Lys	Ile
			100					105					110		
Asn	Ile	Cys	Ile	Tyr	Asn	Leu	Tyr	Tyr	Cys	Tyr	Ile	Phe	Val	Asp	Asn
		115					120					125			
Thr	Phe	Arg	Trp	Cys	Trp	Val	Ile	Tyr	Tyr	Asn	Leu	Asn	Leu	Gly	Ile
	130					135					140				
Ser	Phe	Gly	Leu	Pro	Gln	Ser	Cys								
145					150										

<210> 490  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 490

Gly	Pro	Trp	Leu	Thr	Phe	Pro	Ala	Phe	Asp	Pro	Ser	His	Pro	Ile	Ser
1				5					10					15	
Ser	Ser	Phe	Pro	Leu	Pro	Ala	Ala	Lys	Lys	Lys	Lys	Lys	Gly	Asn	Val
			20					25					30		
Tyr	His	Glu	Ser	Thr	Gly	Phe	Gln	Ser	Leu	Ser	Lys	Arg	Asp	Val	Glu
		35					40					45			
Arg	Ala	Lys	Glu	Thr	Thr	Leu	Cys	Ser	Gln	Leu	His	Phe	Thr	His	Ile
	50					55					60				
Leu	Cys	Asn	Thr	Asn	Thr	Val	Leu	Leu	Gly	Pro	Phe	Leu	Thr	Asp	Gly
65					70					75					80
Pro	Leu	Glu	Lys	Asn	Tyr	Arg	Ile	Pro	Arg	Phe					
				85					90						

<210> 491  
 <211> 64  
 <212> PRT  
 <213> homo sapiens

<400> 491

Lys	Trp	Gly	Thr	Gln	Arg	Ala	Gly	Asn	Phe	His	Tyr	Pro	Ile	Leu	Gly
1				5					10					15	
Leu	Asn	Leu	Lys	Glu	Tyr	Ile	His	Tyr	Gln	Glu	Leu	Ser	Thr	Lys	Ala
			20					25					30		
Gly	Val	Lys	Leu	His	Tyr	Thr	Trp	Leu	Phe	Thr	Ile	Pro	Gly	Ser	Pro
		35					40					45			





<212> PRT  
 <213> homo sapiens

<400> 497

Ser	His	Thr	Ser	Glu	Lys	Arg	Arg	Gly	Thr	Arg	Glu	Glu	Val	Thr	Pro
1				5					10					15	
Ala	Ser	Arg	Ser	Ser	Ile	Ser	Gly	Val	Lys	Arg	Gly	Thr	Val	Ala	Leu
			20					25					30		
Pro	Ser	Trp	Leu	Arg	Met	Arg	Lys	Ser	Phe	Leu	Gln	Trp	Glu	Glu	Ile
		35					40					45			
His	Phe	Ser	Ile	Pro	Val	Gln	Ser	Asp	Phe	Met	Gly	Pro	Val	Leu	Asn
	50					55					60				
Ser	Asp	Cys	Ile	Ile	Asn	Thr	Ile	Lys	Arg	Asp	Ser	Glu	Met	Gly	Ser
65					70					75					80
Arg	Ile	His	Trp	Asp	Asn	Ser	Lys	Ala	Tyr	Asn	Thr	Ala	Leu	Met	Asp
				85					90					95	

Pro Thr

<210> 498  
 <211> 83  
 <212> PRT  
 <213> homo sapiens

<400> 498

Ala	Gly	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Ile	Arg	Gln	Leu	His	Gln	Ile
1				5					10					15	
Thr	Gly	Pro	Arg	Val	Thr	Gly	Trp	Arg	Met	Gln	Gly	Ser	His	Ile	Leu
			20					25					30		
Tyr	Gly	Arg	Asp	Phe	Gly	Val	Leu	Ile	Thr	Leu	Ala	Tyr	Arg	Asn	Lys
		35					40					45			
Pro	Ile	Pro	Ala	Asp	Ser	Leu	Thr	Lys	Gly	Thr	Pro	His	Pro	Met	Thr
	50					55					60				
Thr	Met	Arg	Ala	Leu	Ala	Val	Ser	Ala	His	Ala	His	Ser	Cys	Thr	Pro
65					70					75					80

Met Ala Val

<210> 499  
 <211> 85  
 <212> PRT  
 <213> homo sapiens

<400> 499

Gly	Lys	Ile	Cys	Glu	Tyr	Val	Asn	Phe	Leu	Ser	Leu	Arg	Asp	Asp	Arg
1				5					10					15	
Met	Phe	Pro	Tyr	Phe	Ser	Cys	Lys	Glu	Asn	Asn	Ile	Leu	Thr	Tyr	Thr
			20					25					30		
Ser	Cys	Arg	Lys	Tyr	His	Leu	Phe	Pro	Leu	Tyr	Tyr	Ser	Thr	Met	Phe

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<210> 502  
 <211> 53  
 <212> PRT  
 <213> homo sapiens

<400> 502

Thr	Pro	Lys	Thr	Leu	Gly	Cys	Leu	Leu	Val	Ser	Arg	Val	Glu	Gln	Ala
1				5					10					15	
Gln	Arg	Glu	Ser	Leu	Gly	Pro	Glu	Leu	Lys	Glu	Phe	Ile	Glu	Pro	Trp
			20					25					30		
Gln	Thr	Gly	Ser	Lys	Gln	Pro	Ile	Leu	Ala	Ala	Val	Leu	Arg	Arg	Glu
		35					40					45			
Cys	Gly	Gly	Gln	Ile											
	50														

<210> 503  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 503

Pro	Ser	Gly	Pro	Phe	Ser	Ser	Leu	Glu	Ser	Thr	Leu	Leu	Leu	Gln	Gln
1				5					10					15	
Val	Gln	Ala	Ala	Ile	Ala	Ser	Phe	Leu	Ser	Asp	Cys	Asn	Ser	Pro	Ile
			20					25					30		
Arg	Phe	Pro	Cys	Phe	Tyr	Ile	Cys	Pro	Pro	His	Ser	Leu	Leu	Asn	Thr
		35					40					45			
Ala	Ala	Arg	Met	Gly	Cys	Leu	Leu	Pro	Val	Cys	His	Gly	Ser	Ile	Asn
	50					55					60				
Ser	Leu	Ser	Ser	Gly	Pro	Lys	Asp	Ser	Arg	Trp	Ala	Cys	Ser	Thr	Arg
65					70					75					80
Asp	Thr	Ser	Arg	Gln	Pro	Ser	Val	Leu	Gly	Val					
				85					90						

<210> 504  
 <211> 59  
 <212> PRT  
 <213> homo sapiens

<400> 504

Val	Phe	Ile	Tyr	Asp	Ser	Leu	Ile	Ile	Pro	Thr	Ser	Ile	Ser	Ser	Val
1				5					10					15	
His	Thr	Val	Cys	Gln	Met	Phe	His	Ala	Glu	Pro	Val	Ser	Arg	Ile	Leu
			20					25					30		
Leu	Ser	Asp	Tyr	Gly	Gly	Phe	Thr	Thr	Arg	Pro	Gly	Ser	Asn	Ser	Leu
		35					40					45			
Gly	Ser	Lys	Val	Gly	His	Ser	Ser	Met	His	Arg					
	50					55									

004221 5555555555









<213> homo sapiens

<400> 514

Thr 1	Gly	Gly	Ala	Arg 5	Ala	Arg	Arg	Pro	Leu 10	Ser	Ala	Val	Ala	Arg 15	Pro
Ala	Arg	Ser	Ser 20	Asp	Pro	Leu	Arg	Ser 25	Ala	Pro	Leu	Gly	Pro 30	Ala	Pro
Pro	Val	Asn 35	Met	Ile	Arg	Cys	Gly 40	Leu	Ala	Cys	Glu	Arg 45	Cys	Arg	Trp
Ile	Leu 50	Pro	Leu	Leu	Leu	Leu 55	Ser	Ala	Ile	Ala	Phe 60	Asp	Ile	Ile	Ala
Leu 65	Ala	Gly	Arg	Gly	Trp 70	Leu	Gln	Ser	Ser	Asp 75	His	Gly	Gln	Thr	Ser 80
Ser	Leu	Trp	Trp	Lys 85	Cys	Ser	Gln	Glu	Gly 90	Gly	Gly	Ser	Gly	Ser 95	Tyr
Glu	Glu	Gly	Cys 100	Gln	Ser	Leu	Met	Glu 105	Tyr	Ala	Trp	Gly	Arg 110	Ala	Ala
Ala	Ala	Met 115	Leu	Phe	Cys	Gly	Phe 120	Ile	Ile	Leu	Val	Ile 125	Cys	Phe	Ile
Leu	Ser 130	Phe	Phe	Ala	Leu	Cys 135	Gly	Pro	Gln	Met	Leu 140	Val	Phe	Leu	Arg
Val 145	Ile	Gly	Gly	Leu	Leu 150	Ala	Leu	Ala	Ala	Val 155	Phe	Gln	Ile	Ile	Ser 160
Leu	Val	Ile	Tyr	Pro 165	Val	Lys	Tyr	Thr	Gln 170	Thr	Phe	Thr	Leu	His 175	Ala
Asn	Arg	Ala	Val 180	Thr	Tyr	Ile	Tyr	Asn 185	Trp	Ala	Tyr	Gly	Phe 190	Gly	Trp
Ala	Ala	Thr 195	Ile	Ile	Leu	Ile	Gly 200	Cys	Ala	Phe	Phe	Phe 205	Cys	Cys	Leu
Pro	Asn 210	Tyr	Glu	Asp	Asp	Leu 215	Leu	Gly	Asn	Ala	Lys 220	Pro	Arg	Tyr	Phe
Tyr 225	Thr	Ser	Ala												

<210> 515

<211> 94

<212> PRT

<213> homo sapiens

<400> 515

Asp 1	Pro	Leu	Pro	Pro 5	Pro	Ser	Trp	Glu	His 10	Phe	His	His	Ser	Glu 15	Asp
Val	Trp	Pro	Trp 20	Ser	Leu	Asp	Cys	Asn 25	Gln	Pro	Arg	Pro	Ala 30	Ser	Ala
Met	Met	Ser	Lys	Ala	Met	Ala	Leu	Ser	Arg	Ser	Arg	Gly	Arg	Ile	Gln

35						40					45				
Arg	Gln	Arg	Ser	Gln	Ala	Arg	Pro	Gln	Arg	Ile	Met	Leu	Thr	Gly	Gly
	50					55					60				
Ala	Gly	Pro	Ser	Gly	Ala	Glu	Arg	Ser	Gly	Ser	Glu	Glu	Arg	Ala	Gly
65					70					75					80
Arg	Ala	Thr	Ala	Glu	Ser	Gly	Leu	Arg	Ala	Arg	Ala	Pro	Pro		
				85					90						

<210> 516  
 <211> 208  
 <212> PRT  
 <213> homo sapiens

<400> 516

Thr	Leu	Pro	Lys	Asn	Gly	Phe	Lys	Val	Ala	Trp	Arg	Asn	Ser	Phe	Phe
1				5					10					15	
Phe	Trp	Ser	Pro	Ser	Gln	Gln	Gln	Arg	Phe	Ser	Pro	Thr	Phe	Ile	Pro
			20					25					30		
Lys	Leu	Gly	Arg	Cys	Val	Glu	Val	Pro	Gly	Leu	Gly	Ile	Ala	Gln	Lys
		35					40					45			
Val	Ile	Phe	Val	Val	Gly	Glu	Ala	Ala	Glu	Glu	Glu	Gly	Thr	Ala	Asp
	50					55					60				
Gln	Asp	Asn	Arg	Gly	Cys	Pro	Pro	Lys	Ala	Val	Gly	Pro	Val	Ile	Asp
65					70					75					80
Val	Ser	Asp	Ser	Thr	Val	Gly	Met	Lys	Gly	Glu	Gly	Leu	Gly	Val	Leu
				85					90					95	
His	Gly	Val	Asn	Tyr	Gln	Gly	Asp	Asp	Leu	Glu	His	Ser	Ser	Gln	Gly
			100					105					110		
Lys	Glu	Thr	Ser	Asn	His	Ser	Gln	Glu	Asp	Lys	His	Leu	Gly	Ser	Thr
		115					120					125			
Glu	Gly	Glu	Glu	Gly	Glu	Asp	Glu	Thr	Asp	His	Gln	Asp	Asp	Glu	Ala
	130					135					140				
Thr	Glu	Glu	His	Gly	Ser	Arg	Cys	Ser	Thr	Pro	Arg	Val	Leu	His	Glu
145					150					155					160
Ala	Leu	Thr	Ala	Leu	Leu	Val	Gly	Pro	Ala	Ala	Ala	Ala	Leu	Leu	Gly
				165					170					175	
Ala	Phe	Pro	Pro	Gln	Arg	Gly	Arg	Leu	Ala	Val	Val	Ala	Arg	Leu	Gln
			180					185					190		
Pro	Ala	Ala	Ala	Gly	Gln	Arg	Asp	Asp	Val	Glu	Gly	Asp	Gly	Ala	Glu
		195					200					205			

<210> 517  
 <211> 204  
 <212> PRT  
 <213> homo sapiens

<400> 517





Met	Leu	Cys	Gly 180	Glu	Ile	Thr	His	Pro 185	Lys	Asn	Asn	Tyr	Ser 190	Ser	Arg
Thr	Pro	Cys 195	Ser	Ser	Leu	Leu	Pro 200	Leu	Leu	Asn	Ala	His 205	Ala	Ala	Thr
Ser	Gly 210	Lys	Gln	Ser	Asn	Phe 215	Ser	Arg	Lys	Ser	Ser 220	Thr	His	Asn	Lys
Pro 225	Ser	Glu	Gly	Lys	Ala 230	Ala	Asn	Pro	Lys	Met 235	Val	Ser	Ser	Leu	Pro 240
Ser	Thr	Ala	Asp	Pro 245	Ser	His	Gln	Thr	Met 250	Pro	Ala	Asn	Lys	Gln 255	Asn
Gly	Ser	Ser	Asn 260	Gln	Arg	Arg	Arg	Phe 265	Asn	Pro	Gln	Tyr	His 270	Asn	Asn
Arg	Leu	Asn 275	Gly	Pro	Ala	Lys	Ser 280	Gln	Gly	Ser	Gly	Asn 285	Glu	Ala	Glu
Pro	Leu 290	Gly	Lys	Gly	Asn	Ser 295	Arg	His	Glu	His	Arg 300	Arg	Gln	Pro	His
Asn 305	Gly	Phe	Arg	Pro	Lys 310	Asn	Lys	Gly	Gly	Ala 315	Lys	Asn	Gln	Glu	Ala 320
Ser	Leu	Gly	Met	Lys 325	Thr	Pro	Glu	Ala	Pro 330	Ala	His	Ser	Glu	Lys 335	Pro
Arg	Arg	Arg	Gln 340	Ala	Arg	Cys	Arg	Thr 345	Pro	Arg	Glu	Gly	Gln 350	Gly	Pro
Phe	Arg	Gly 355													

&lt;210&gt; 521

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 521

Asn 1	Gln	Asn	Val	Lys 5	Asn	Arg	Gly	Thr	Gln 10	Lys	Lys	Cys	Leu	Pro 15	Ser
Val	Glu	Lys	Leu 20	Pro	Asn	Pro	Pro	Trp 25	Gly	Gln	Lys	Asn	Ala 30	Thr	Val
Lys	Thr	Pro 35	Asn	Arg	Lys	Leu	Thr 40	Pro	Glu	Arg	Pro	Leu 45	Ala	Leu	Pro
Arg	Cys 50	Pro	Ala	Ala	Cys	Leu 55	Pro	Ser	Pro	Gly	Leu 60	Phe	Arg	Met	Gly
Arg 65	Gly	Leu	Gly	Gly	Leu 70	His	Pro	Gln	Gly	Ser 75	Leu	Leu	Ile	Phe	Gly 80
Thr	Ala	Phe	Val	Phe 85	Gly	Pro	Glu	Ala	Val 90	Val	Arg	Leu	Ser	Ser 95	Val
Phe	Val	Ala	Ala	Val	Ala	Leu	Ser	Gln	Trp	Leu	Gly	Phe	Ile	Pro	Thr

	100							105				110				
	Ala	Leu	Arg	Leu	Gly	Arg	Pro	Ile								
			115					120								
<210>	522															
<211>	116															
<212>	PRT															
<213>	homo sapiens															
<400>	522															
	Arg	Ala	Val	Arg	Ile	Ser	Met	Ala	Ser	Ser	Leu	Thr	Leu	Ser	Ile	Ser
	1				5					10					15	
	Ala	Ile	Asn	Glu	Thr	Ser	Leu	Ser	Met	Met	Gln	Leu	Cys	Asn	Ser	Ala
				20					25					30		
	Lys	Ala	Ala	Leu	Ile	Phe	Phe	Thr	Glu	Leu	Ser	Thr	Ser	Ser	Leu	Ile
			35					40					45			
	Met	Thr	Arg	Tyr	Leu	Val	Arg	Glu	Thr	Val	Gln	Arg	Cys	Lys	Ser	Phe
		50					55					60				
	Thr	Asp	Phe	Ser	Ile	Phe	Gly	Pro	Val	Thr	Pro	Arg	Ser	Ala	Phe	Glu
	65					70					75					80
	Gly	Ser	Ser	Ser	Ile	Glu	Ile	Phe	Phe	Ser	Arg	Gly	Ile	Arg	Ala	Gly
					85					90					95	
	Phe	Ser	Leu	Ala	Glu	Ser	Val	Asp	Glu	Leu	Ser	Phe	Ser	Gln	Pro	Phe
				100					105					110		
	Met	Leu	Cys	Arg												
			115													
<210>	523															
<211>	130															
<212>	PRT															
<213>	homo sapiens															
<400>	523															
	Arg	Arg	Gln	Arg	Lys	Ala	Glu	Pro	Gly	Ala	Cys	Ala	Leu	Gly	Arg	Val
	1				5					10					15	
	Gly	Ser	Glu	Cys	Ile	Pro	Glu	Pro	Gly	Ala	Arg	Arg	Thr	Ala	Gln	Ala
				20					25					30		
	Ala	Gly	Leu	Arg	Ser	Val	Ser	Gly	Ala	Ala	Asn	Thr	Lys	Val	Arg	Glu
			35					40					45			
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	Arg	Arg	Gly	Phe	Ser	Glu	Gly	Gly	Arg	Gln	Asn	Phe	Asp	Val	Arg	Pro
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	Gln	Ser	Gly	Ala	Asn	Gly	Leu	Pro	Lys	His	Ser	Tyr	Trp	Leu	Asp	Leu
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Leu Pro  
130

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<211> 78  
<212> PRT  
<213> homo sapiens

<400> 524

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Gly	Lys	Pro	Ile	Cys	Pro	Arg	Leu	Arg	Pro	His	Ile	Glu	Val	Leu	Pro
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<212> PRT  
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<400> 525

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Ser	Leu	Leu	Gln	Leu	Arg	Asn	Asn	Pro	Arg	Asn	Arg	Lys	Cys	Leu	Ser
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<212> PRT  
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<400> 526

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<400> 527

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Leu	His	Asp	Ser	Phe	Met	Ile	Leu	Leu	Leu	Met	Tyr	Thr	Pro	Arg	Arg
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 <212> PRT  
 <213> homo sapiens

<400> 528

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<400> 533

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<400> 537

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 <212> DNA  
 <213> homo sapiens

<400> 552

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<400> 553

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<210> 554

<211> 1457

<212> DNA

<213> homo sapiens

<400> 554

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gcataaata	tgggtaaagt	ggagttggga	acaaaggttg	gtttctttag	ctctttccac	480
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aaaaaaaaaa	aggaaacgtt	tatcatgaat	caacagggtt	tcagtcctta	tcaaagagag	720
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<210> 555  
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 <212> DNA  
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<400> 555

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<210> 561  
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<400> 561

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			20					25					30		
Gly	Phe	Ile	Lys	Cys	Val	Asp	Arg	Asp	Val	Arg	Met	Phe	Phe	His	Phe
		35					40					45			

Ser	Glu	Ile	Leu	Asp	Gly	Asn	Gln	Leu	His	Ile	Ala	Asp	Glu	Val	Glu
	50					55					60				
Phe	Thr	Val	Val	Pro	Asp	Met	Leu	Ser	Ala	Gln	Arg	Asn	His	Ala	Ile
65					70					75					80
Arg	Ile	Lys	Lys	Leu	Pro	Lys	Gly	Thr	Val	Ser	Phe	His	Ser	His	Ser
				85					90					95	
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			100					105					110		
Pro	Lys	Thr	Thr	Ser	Pro	Asn	Lys	Gly	Lys	Glu	Lys	Glu	Ala	Glu	Asp
		115					120					125			
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	130					135					140				
Gln	Ala	Lys	Asp	Val	Glu	Gly	Ser	Thr	Ser	Pro	Gln	Ile	Gly	Asp	Lys
145					150					155					160
Val	Glu	Phe	Ser	Ile	Ser	Asp	Lys	Gln	Arg	Pro	Gly	Gln	Gln	Val	Ala
				165					170					175	
Thr	Cys	Val	Arg	Leu	Leu	Gly	Arg	Asn	Ser	Asn	Ser	Lys	Arg	Leu	Leu
			180					185					190		
Gly	Tyr	Val	Ala	Thr	Leu	Lys	Asp	Asn	Phe	Gly	Phe	Ile	Glu	Thr	Ala
		195					200					205			
Asn	His	Asp	Lys	Glu	Ile	Phe	Phe	His	Tyr	Ser	Glu	Phe	Ser	Gly	Asp
	210					215					220				
Val	Asp	Ser	Leu	Glu	Leu	Gly	Asp	Met	Val	Glu	Tyr	Ser	Leu	Ser	Lys
225					230					235					240
Gly	Lys	Gly	Asn	Lys	Val	Ser	Ala	Glu	Lys	Val	Asn	Lys	Thr	His	Ser
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Pro	Phe	Gly	Ile	Val	Gly	Met	Ala	Asn	Lys	Gly	Asp	Cys	Leu	Gln	Lys
305					310					315					320
Gly	Glu	Ser	Val	Lys	Phe	Gln	Leu	Cys	Val	Leu	Gly	Gln	Asn	Ala	Gln
				325					330					335	
Thr	Met	Ala	Tyr	Asn	Ile	Thr	Pro	Leu	Arg	Arg	Ala	Thr	Val	Glu	Cys
			340					345					350		
Val	Lys	Asp	Gln	Phe	Gly	Phe	Ile	Asn	Tyr	Glu	Val	Gly	Asp	Ser	Lys
		355					360					365			
Lys	Leu	Phe	Phe	His	Val	Lys	Glu	Val	Gln	Asp	Gly	Ile	Glu	Leu	Gln
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His	Ile	Leu	Gly	Leu	Lys	Ser	Asn	Ser	Gln	Phe	His	Pro	Thr	Val	Ile
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Gln	Lys	Thr	Val	Ile											
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<210> 564  
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 <212> PRT  
 <213> homo sapiens

<400> 564

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		35					40					45			
Asp	Asn	Leu	Asp	Leu	Ala	Asn	Val	Asn	Leu	Met	Leu	Glu	Leu	Leu	Val
	50					55					60				
Gln	Lys	Lys	Lys	Gln	Leu	Glu	Ala	Glu	Ser	His	Ala	Ala	Gln	Leu	Gln
65					70					75					80
Ile	Leu	Met	Glu	Phe	Leu	Lys	Val	Ala	Arg	Arg	Asn	Lys	Arg	Glu	Gln
				85					90					95	
Leu	Glu	Gln	Ile	Gln	Lys	Glu	Leu	Ser	Val	Leu	Glu	Glu	Asp	Ile	Lys
			100					105					110		
Arg	Val	Glu	Glu	Met	Ser	Gly	Leu	Tyr	Ser	Pro	Val	Ser	Glu	Asp	Ser
		115					120					125			
Thr	Val	Pro	Gln	Phe	Glu	Ala	Pro	Ser	Pro	Ser	His	Ser	Ser	Ile	Ile
						135					140				
Asp	Ser	Thr	Glu	Tyr	Ser	Gln	Pro	Pro	Gly	Phe	Ser	Gly	Ser	Ser	Gln
145					150					155					160
Thr	Lys	Lys	Gln	Pro	Trp	Tyr	Asn	Ser	Thr	Leu	Ala	Ser	Arg	Arg	Lys
				165					170					175	
Arg	Leu	Thr	Ala	His	Phe	Glu	Asp	Leu	Glu	Gln	Cys	Tyr	Phe	Ser	Thr
			180					185					190		
Arg	Met	Ser	Arg	Ile	Ser	Asp	Asp	Ser	Arg	Thr	Ala	Ser	Gln	Leu	Asp
		195					200					205			
Glu	Phe	Gln	Glu	Cys	Leu	Ser	Lys	Phe	Thr	Arg	Tyr	Asn	Ser	Val	Arg
	210					215					220				
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<211> 132
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Ser	Pro	Thr 35	Glu	Tyr	His	Glu	Pro 40	Val	Tyr	Ala	Asn	Pro 45	Phe	Tyr	Arg
Pro	Thr 50	Thr	Pro	Gln	Arg	Glu 55	Thr	Val	Thr	Pro	Gly 60	Pro	Asn	Phe	Gln
Glu 65	Arg	Ile	Lys	Ile	Lys 70	Thr	Asn	Gly	Leu	Gly 75	Ile	Gly	Val	Asn	Glu 80
Ser	Ile	His	Asn	Met 85	Gly	Asn	Gly	Leu	Ser 90	Glu	Glu	Arg	Gly	Asn 95	Asn
Phe	Asn	His	Ile 100	Ser	Pro	Ile	Pro	Pro 105	Val	Pro	His	Pro	Arg 110	Ser	Val
Ile	Gln	Gln 115	Ala	Glu	Glu	Lys	Leu 120	His	Thr	Pro	Gln	Lys 125	Arg	Leu	Met
Thr	Pro 130	Trp	Glu	Glu	Ser	Asn 135	Val	Met	Gln	Asp	Lys 140	Asp	Ala	Pro	Ser
Pro 145	Lys	Pro	Arg	Leu	Ser 150	Pro	Arg	Glu	Thr	Ile 155	Phe	Gly	Lys	Ser	Glu 160
His	Gln	Asn	Ser	Ser 165	Pro	Thr	Cys	Gln	Glu 170	Asp	Glu	Glu	Asp	Val 175	Arg
Tyr	Asn	Ile	Val 180	His	Ser	Leu	Pro	Pro 185	Asp	Ile	Asn	Asp	Thr 190	Glu	Pro
Val	Thr	Met 195	Ile	Phe	Met	Gly	Tyr 200	Gln	Gln	Ala	Glu	Asp 205	Ser	Glu	Glu
Asp	Lys 210	Lys	Phe	Leu	Thr	Gly 215	Tyr	Asp	Gly	Ile	Ile 220	His	Ala	Glu	Leu
Val 225	Val	Ile	Asp	Asp	Glu 230	Glu	Glu	Glu	Asp	Glu 235	Gly	Glu	Ala	Glu	Lys 240
Pro	Ser	Tyr	His	Pro 245	Ile	Ala	Pro	His	Ser 250	Gln	Val	Tyr	Gln	Pro 255	Ala
Lys	Pro	Thr	Pro 260	Leu	Pro	Arg	Lys	Arg 265	Ser	Glu	Ala	Ser	Pro 270	His	Glu
Asn	Thr	Asn 275	His	Lys	Ser	Pro	His 280	Lys	Asn	Ser	Ile	Ser 285	Leu	Lys	Glu
Gln	Glu 290	Glu	Ser	Leu	Gly	Ser 295	Pro	Val	His	His	Ser 300	Pro	Phe	Asp	Ala
Gln 305	Thr	Thr	Gly	Asp	Gly 310	Thr	Glu	Asp	Pro	Ser 315	Leu	Thr	Ala	Leu	Arg 320
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<210> 568  
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 <213> homo sapiens

<400> 568

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			20					25					30		
Lys	Arg	Leu	Lys	Ile	Glu	Glu	Asp	Lys	Leu	Lys	His	Gln	His	Leu	Lys
		35					40					45			
Lys	Lys	Ala	Leu	Arg	Glu	Lys	Trp	Leu	Leu	Asp	Gly	Ile	Ser	Ser	Gly
	50					55					60				
Lys	Glu	Gln	Glu	Glu	Met	Lys	Lys	Gln	Asn	Gln	Gln	Asp	Gln	His	Gln
	65				70					75					80
Ile	Gln	Val	Leu	Glu	Gln	Ser	Ile	Leu	Arg	Leu	Glu	Lys	Glu	Ile	Gln
				85					90					95	
Asp	Leu	Glu	Lys	Ala	Glu	Leu	Gln	Ile	Ser	Thr	Lys	Glu	Glu	Ala	Ile
			100					105					110		
Leu	Lys	Lys	Leu	Lys	Ser	Ile	Glu	Arg	Thr	Thr	Glu	Asp	Ile	Ile	Arg
		115					120					125			
Ser	Val	Lys	Val	Glu	Arg	Glu	Glu	Arg	Ala	Glu	Glu	Ser	Ile	Glu	Asp
	130					135					140				
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	145				150					155					160
Leu	Arg	Lys	Glu	Ile	Asn	Glu	Glu	Lys	Glu	Asp	Asp	Glu	Gln	Asn	Arg
				165					170					175	
Lys	Ala	Leu	Tyr	Ala	Met	Glu	Ile	Lys	Val	Glu	Lys	Asp	Leu	Lys	Thr
			180					185					190		
Gly	Glu	Ser	Thr	Val	Leu	Ser	Ser	Asn	Thr	Ser	Gly	His	Gln	Met	Thr
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	210					215									

<210> 569  
 <211> 132  
 <212> PRT  
 <213> homo sapiens

<400> 569

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			20					25					30		

004321 3662960

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	50					55					60					
Gly	Gly	Thr	Thr	Leu	Arg	Ser	Pro	Phe	Phe	Pro	Ala	Leu	Pro	Phe	Ser	
	65				70					75					80	
Ser	Leu	Lys	Leu	Leu	Arg	Met	Asp	Pro	Gln	Ser	His	Leu	Gln	Leu	Ser	
				85					90					95		
Glu	His	Gln	Met	Gly	Asn	Gly	Gly	Gln	Gly	Cys	Leu	Ser	Phe	Leu	Leu	
			100					105					110			
Ala	Leu	Ser	Glu	Ile	Trp	Asn	Phe	Cys	Gly	Gly	Ile	Tyr	Asp	Leu	Cys	
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Phe	His	Glu	Asp													
	130															

<210> 570  
 <211> 199  
 <212> PRT  
 <213> homo sapiens

<400> 570

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Phe	Phe	Pro	Leu	Ala	Leu	Lys	Lys	Ser	Ser	Arg	Val	Ser	Ser	Ser	His	
			20					25					30			
Leu	Pro	Arg	Ile	Tyr	Gln	Ala	Phe	Leu	Met	Ser	Ala	Thr	Phe	Asn	Glu	
		35					40					45				
Asp	Val	Gln	Ala	Leu	Lys	Glu	Leu	Ile	Leu	His	Asn	Pro	Val	Thr	Leu	
	50					55					60					
Lys	Leu	Gln	Glu	Ser	Gln	Leu	Pro	Gly	Pro	Asp	Gln	Leu	Gln	Gln	Phe	
	65				70					75					80	
Gln	Val	Val	Cys	Glu	Thr	Glu	Glu	Asp	Lys	Phe	Leu	Leu	Leu	Tyr	Ala	
				85					90					95		
Leu	Leu	Lys	Leu	Ser	Leu	Ile	Arg	Gly	Lys	Ser	Leu	Leu	Phe	Val	Asn	
			100					105					110			
Thr	Leu	Glu	Arg	Ser	Tyr	Arg	Leu	Arg	Leu	Phe	Leu	Glu	Gln	Phe	Ser	
		115					120					125				
Ile	Pro	Thr	Cys	Val	Leu	Asn	Gly	Glu	Leu	Pro	Leu	Arg	Ser	Arg	Cys	
	130					135					140					
His	Ile	Ile	Ser	Gln	Phe	Asn	Gln	Gly	Phe	Tyr	Asp	Cys	Val	Ile	Ala	
	145				150					155					160	
Thr	Asp	Ala	Glu	Val	Leu	Gly	Ala	Pro	Arg	Gln	Arg	Ala	Met	Arg	Pro	
				165					170					175		
Arg	Arg	Arg	Ala	Lys	Thr	Gly	Thr	Met	Ala	Ser	Arg	Phe	Leu	Glu	Arg	
			180					185					190			

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Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender	
Male	100
Female	100
Education (years)	12.0 ± 2.0
Marital status	
Married	100
Divorced	100
Widowed	100
Single	100
Occupation	
Retired	100
Unemployed	100
Employed	100
Income (USD/month)	1,000.0 ± 500.0
Health status	
Good	100
Fair	100
Poor	100
Smoking status	
Smoker	100
Non-smoker	100
Alcohol consumption	
Drinker	100
Non-drinker	100
Comorbidities	
Hypertension	100
Diabetes	100
Coronary artery disease	100
Chronic kidney disease	100
Chronic liver disease	100
Chronic lung disease	100
Chronic pain	100
Chronic depression	100
Chronic anxiety	100
Chronic fatigue	100
Chronic insomnia	100
Chronic constipation	100
Chronic diarrhea	100
Chronic cough	100
Chronic asthma	100
Chronic sinusitis	100
Chronic rhinitis	100
Chronic otitis media	100
Chronic ear pain	100
Chronic eye pain	100
Chronic nose pain	100
Chronic throat pain	100
Chronic mouth pain	100
Chronic skin pain	100
Chronic joint pain	100
Chronic muscle pain	100
Chronic nerve pain	100
Chronic bone pain	100
Chronic organ pain	100
Chronic system pain	100
Chronic body pain	100
Chronic mind pain	100
Chronic spirit pain	100
Chronic soul pain	100
Chronic life pain	100
Chronic death pain	100
Chronic everything pain	100

<400> 573

<400> 574

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<210> 575
<211> 80
<212> PRT
<213> homo sapiens
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Table 1. Demographic characteristics of the study population	
Age (years)	65.8 ± 1.2
Gender (male/female)	10/10
Education (years)	12.5 ± 0.5
Occupation (white/blue)	10/10
Marital status (married/divorced/widowed)	10/10/0
Smoking status (smoker/nonsmoker)	10/10
Alcohol consumption (yes/no)	10/10
Comorbidities (hypertension/diabetes/cholesterol)	10/10/10
Medication (antihypertensive/antidiabetic/anticholesterol)	10/10/10
Family history (hypertension/diabetes/cholesterol)	10/10/10
Physical activity (yes/no)	10/10
Stress level (high/low)	10/10
Sleep quality (good/poor)	10/10
Depression score (yes/no)	10/10
Overall health status (good/poor)	10/10

<210> 576

000

<211> 161

<213> homo sapiens

Leu 1	Leu	Pro	Leu	Leu 5	Leu	Leu	Leu	Ile	His 10	Gly	Asp	Thr	Pro	Xxx 15	Gly
Pro	Gly	Pro	Xxx 20	Xxx	Gln	Glu	Gln	Ala 25	Pro	Asn	His	Arg	His 30	Gly	Leu
Glu	Glu	Xxx 35	Arg	Ile	Ser	Xxx	Lys 40	Ser	Cys	Met	Gly	Xxx 45	Val	Asp	Trp
Asn	Gly 50	Pro	Glu	Gly	Val	Glu 55	Ile	Tyr	Val	Asp	Gly 60	Lys	Glu	Pro	His
Asn 65	Lys	Ser	Gln	Ser	Ser 70	Gln	Leu	Gly	Phe	Lys 75	Thr	Asn	Gly	His	Xxx 80
Lys	Ser	Ser	Glu	Xxx 85	Val	Xxx	His	Asp	Val 90	Leu	Asp	Asn	Arg	Lys 95	Glu
Ala	Gly	Val	Lys 100	Val	Lys	Glu	Gly	His 105	Glu	His	Gln	Asn	Gln 110	Gln	Asp
Pro	Ala	Ser 115	Glu	Leu	His	Val	Leu 120	Phe	Gly	Gly	Ala	Leu 125	Thr	His	Gly
Gly	Asp 130	Ala	Arg	Lys	His	Ala 135	Leu	Pro	Phe	Arg	Thr 140	Gly	Phe	Ser	Arg
Ser 145	Thr	Gln	Gln	Pro	Pro 150	Pro	Arg	Ala	Arg	Phe 155	Leu	Pro	Leu	Cys	Arg 160

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<211> 160



[illegible]



<210> 580  
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 <212> PRT  
 <213> homo sapiens

<400> 580

Thr 1	Glu	Arg	Leu	Leu 5	Leu	Asp	Gly	Pro	Pro 10	Pro	His	Ser	Pro	Glu 15	Thr
Pro	Gln	Phe	Pro 20	Pro	Thr	Thr	Gly	Ala 25	Val	Leu	Tyr	Thr	Val 30	Lys	Arg
Asn	Gln	Val 35	Gly	Pro	Glu	Val	Arg 40	Ser	Cys	Pro	Lys	Ala 45	Ser	Pro	Arg
Leu	Gln 50	Lys	Glu	Arg	Glu	Gly 55	Gln	Lys	Ala	Val	Ser 60	Glu	Ser	Glu	Ala
Leu 65	Met	Leu	Val	Trp	Asp 70	Ala	Ser	Glu	Thr	Glu 75	Lys	Leu	Pro	Gly	Thr 80
Val	Glu	Pro	Pro	Ala 85	Ser	Phe	Leu	Ser	Pro 90	Val	Ser	Ser	Lys	Thr 95	Arg
Asp	Ala	Gly	Arg 100	Arg	His	Val	Ser	Gly 105	Lys	Pro	Asp	Thr	Gln 110	Glu	Arg
Trp	Leu	Pro 115	Ser	Ser	Arg	Ala	Arg 120	Val	Lys	Thr	Arg	Asp 125	Arg	Thr	Cys
Pro	Val 130	His	Glu	Ser	Pro	Ser 135	Gly	Ile	Asp	Thr	Ser 140	Glu	Thr	Ser	Pro
Lys 145	Ala	Pro	Arg	Gly	Gly 150	Leu	Ala	Lys	Asp	Ser 155	Gly	Thr	Gln	Ala	Lys 160
Gly	Pro	Glu	Gly	Glu 165	Gln	Gln	Pro	Lys	Ala 170	Ala	Glu	Ala	Thr	Val 175	Cys
Ala	Asn	Asn	Ser 180	Lys	Val	Ser	Ser	Thr 185	Gly	Glu	Lys	Val	Val 190	Leu	Trp
Thr	Arg	Glu 195	Ala	Asp	Arg	Val	Ile 200	Leu	Thr	Met	Cys	Gln 205	Glu	Gln	Gly
Ala	Gln 210	Pro	Gln	Thr	Phe	Asn 215	Ile	Ile	Ser	Gln	Gln 220	Leu	Gly	Asn	Lys
Thr 225	Pro	Ala	Glu	Val	Ser 230	His	Arg	Phe	Arg	Glu 235	Leu	Met	Gln	Leu	Phe 240
His	Thr	Ala	Cys	Glu 245	Ala	Ser	Ser	Glu	Asp 250	Glu	Asp	Asp	Ala	Thr 255	Ser
Thr	Ser	Asn	Ala 260	Asp	Gln	Leu	Ser	Asp 265	His	Gly	Asp	Leu	Leu 270	Ser	Glu
Glu	Glu	Leu	Asp	Glu											
			275												

<210> 581  
 <211> 172

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Thr	Ala	Arg	Pro	Val	His	Thr	Ala	Ser	Ile	Ser	Asp	Ser	Phe	Gln	Ser
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Ile	Phe	Ser	Tyr	Tyr	Asp	Asn	Ser	Thr	Met	Val	Thr	Gly	Asn	Ala	Thr
		115					120					125			
Arg	Asp	Leu	Thr	Leu	His	Gln	Thr	Ala	Thr	Gln	His	Met	Val	Thr	Asn
	130					135					140				
Ala	Ser	Ala	Val	Pro	Ser	Asp	Cys	Pro	Ser	Glu	Asp	Lys	Asp	Leu	Leu
145					150					155				160	
Asn	Glu	Asn	Val	Gln	Val	Gly	Leu	Leu	Phe	Ala	Ser	Lys	Ala	Thr	Val
				165					170					175	
Gln	Leu	Ile	Thr	Asn	Pro	Phe	Ile	Gly	Leu	Leu	Thr	Asn	Arg	Ile	Gly
			180					185					190		
Tyr	Pro	Ile	Pro	Ile	Phe	Ala	Gly	Phe	Cys	Ile	Met	Phe	Val	Ser	Thr
		195					200					205			
Ile	Met	Phe	Ala	Phe	Ser	Ser	Ser	Tyr	Ala	Phe	Leu	Leu	Ile	Ala	Arg
	210					215					220				
Ser	Leu	Gln	Gly	Ile	Gly	Ser	Ser	Cys	Ser	Ser	Val	Ala	Gly	Met	Gly
225					230					235					240
Met	Leu	Ala	Ser	Val	Tyr	Thr	Asp	Asp	Glu	Glu	Arg	Gly	Asn	Val	Met
				245					250					255	
Gly	Ile	Ala	Leu	Gly	Gly	Leu	Ala	Met	Gly	Val	Leu	Val	Gly	Pro	Pro
			260					265					270		
Phe	Gly	Ser	Val	Leu	Tyr	Glu	Phe	Val	Gly	Lys	Thr	Ala	Pro	Phe	Leu
		275					280					285			
Val	Leu	Ala	Ala	Leu	Val	Leu	Leu	Asp	Gly	Ala	Ile	Gln	Leu	Phe	Val
	290					295					300				
Leu	Gln	Pro	Ser	Arg	Val	Gln	Pro	Glu	Ser	Gln	Lys	Gly	Thr	Pro	Leu
305					310					315					320
Thr	Thr	Leu	Leu	Lys	Asp	Pro	Tyr	Ile	Leu	Ile	Ala	Ala	Gly	Ser	Ile
				325					330					335	
Ser	Phe	Ala	Asn	Met	Gly	Ile	Ala	Met	Leu	Glu	Pro	Ala	Leu	Pro	Ile
			340					345					350		
Trp	Met	Met	Glu	Thr	Met	Cys	Ser	Arg	Lys	Trp	Gln	Leu	Gly	Val	Ala
		355					360					365			
Phe	Leu	Pro	Ala	Ser	Ile	Ser	Tyr	Leu	Ile	Gly	Thr	Asn	Ile	Phe	Gly
	370					375					380				
Ile	Leu	Ala	His	Lys	Met	Gly	Arg	Trp	Leu	Cys	Ala	Leu	Leu	Gly	Met
385					390					395					400
Ile	Ile	Val	Gly	Val	Ser	Ile	Leu	Cys	Ile	Pro	Phe	Pro	Lys	Asn	Ile
				405					410					415	
Tyr	Gly	Leu	Ile	Ala	Pro	Asn	Phe	Gly	Val	Gly	Phe	Ala	Asn	Gly	Met
			420					425					430		



1				5				10				15			
Leu	Leu	Met	Leu 20	Asn	Ala	Val	Gln	Ile 25	Thr	Trp	Asp	Asp	Gly 30	Asp	His
Asp	Ser	Glu 35	Gln	His	Val	Val	Gln 40	Gln	Gln	Arg	Gln	Glu 45	His	Asp	Glu
Gln	Asp 50	Glu	Leu	Pro	Arg	Ala 55	Ala	Ala	Leu	Leu	Gln 60	Pro	Ala	Asp	Gln
Arg 65	Gln	Leu	Ala	Gln	Gly 70	His	Gly	Ser	Gly	Ala 75	Pro	Leu	Gly	Val	Ala 80
Cys	Ala	Ala	Cys	Pro 85	Gly	Pro	Pro	Cys	Pro 90	Arg	Gln	Arg	Pro	His 95	Arg
Ser	Gly	Leu	Arg 100	Gln	Ser	Gly	Arg	Glu 105	Phe						

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<210> 585
<211> 409
<212> PRT
<213> homo sapiens
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<400> 585

Lys 1	Ser	Arg	Leu	Ser 5	Val	Thr	Leu	Met	Pro 10	Val	Gln	Leu	Ser	Glu 15	His
Pro	Glu	Trp	Asn 20	Glu	Ser	Met	His	Ser 25	Leu	Arg	Ile	Ser	Val 30	Gly	Gly
Leu	Pro	Val 35	Leu	Ala	Ser	Met	Thr 40	Lys	Ala	Ala	Asp	Pro 45	Arg	Phe	Arg
Pro	Arg 50	Trp	Lys	Val	Ile	Leu 55	Thr	Phe	Phe	Val	Gly 60	Ala	Ala	Ile	Leu
Trp 65	Leu	Leu	Cys	Ser	His 70	Arg	Pro	Ala	Pro	Gly 75	Arg	Pro	Pro	Thr	His 80
Asn	Ala	His	Asn	Trp 85	Arg	Leu	Gly	Gln	Ala 90	Pro	Ala	Asn	Trp	Tyr 95	Asn
Asp	Thr	Tyr	Pro 100	Leu	Ser	Pro	Pro	Gln 105	Arg	Thr	Pro	Ala	Gly 110	Ile	Arg
Tyr	Arg	Ile 115	Ala	Val	Ile	Ala	Asp 120	Leu	Asp	Thr	Glu	Pro 125	Thr	Ala	Gln
Asp	Glu 130	Asn	Thr	Trp	Arg	Ser 135	Asp	Leu	Lys	Lys	Gly 140	Tyr	Leu	Thr	Leu
Ser 145	Asp	Ser	Gly	Asp	Lys 150	Val	Ala	Val	Glu	Trp 155	Asp	Lys	Asp	His	Gly 160
Val	Leu	Glu	Ser	His 165	Leu	Ala	Glu	Lys	Gly 170	Arg	Gly	Met	Glu	Leu 175	Ser
Asp	Leu	Ile	Val 180	Phe	Asn	Gly	Lys	Leu 185	Tyr	Ser	Val	Asp	Asp 190	Arg	Thr

Gly	Val	Val	Tyr	Gln	Ile	Glu	Gly	Ser	Lys	Ala	Val	Pro	Trp	Val	Ile
		195					200					205			
Leu	Ser	Asp	Gly	Asp	Gly	Thr	Val	Glu	Lys	Gly	Phe	Lys	Ala	Glu	Trp
	210					215					220				
Leu	Ala	Val	Lys	Asp	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Leu	Gly	Lys	Glu
225					230					235					240
Trp	Thr	Thr	Thr	Thr	Gly	Asp	Val	Val	Asn	Glu	Asn	Pro	Glu	Trp	Val
				245					250					255	
Lys	Val	Val	Gly	Tyr	Lys	Gly	Ser	Val	Asp	His	Glu	Asn	Trp	Val	Ser
			260					265					270		
Asn	Tyr	Asn	Ala	Leu	Arg	Ala	Ala	Ala	Gly	Ile	Gln	Pro	Pro	Ala	Asn
		275					280					285			
Leu	Ile	His	Glu	Ser	Ala	Cys	Trp	Ser	Asp	Thr	Leu	Gln	Arg	Trp	Phe
	290					295					300				
Phe	Leu	Pro	Arg	Arg	Ala	Ser	Gln	Glu	Arg	Tyr	Ser	Glu	Lys	Asp	Asp
305					310					315					320
Glu	Arg	Lys	Gly	Ala	Asn	Leu	Leu	Leu	Ser	Ala	Ser	Pro	Asp	Phe	Gly
				325					330					335	
Asp	Ile	Ala	Val	Ser	His	Val	Gly	Ala	Val	Val	Pro	Thr	His	Gly	Phe
			340					345					350		
Ser	Ser	Phe	Lys	Phe	Ile	Pro	Asn	Thr	Asp	Asp	Gln	Ile	Ile	Val	Ala
		355					360					365			
Leu	Lys	Ser	Glu	Glu	Asp	Ser	Gly	Arg	Val	Ala	Ser	Tyr	Ile	Met	Ala
	370					375					380				
Phe	Thr	Leu	Asp	Gly	Arg	Phe	Leu	Leu	Pro	Glu	Thr	Lys	Ile	Gly	Ser
385					390					395					400
Val	Lys	Tyr	Glu	Gly	Ile	Glu	Phe	Ile							
				405											

&lt;210&gt; 586

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 586

Lys	Leu	Ser	Pro	Asp	Gly	Leu	Ala	Gln	Cys	Phe	Arg	Phe	Glu	Leu	Asn
1				5					10					15	
Glu	Leu	Asp	Ala	Phe	Val	Phe	His	Ala	Ser	Asp	Leu	Gly	Leu	Arg	Gln
			20					25					30		
Gln	Glu	Ala	Pro	Val	Gln	Arg	Glu	Gly	His	Asp	Val	Gly	Gly	Asp	Ser
		35					40					45			
Ala	Ala	Val	Leu	Leu	Gly	Phe	Glu	Gly	His	Asn	Asp	Leu	Val	Val	Gly
	50					55					60				
Val	Gly	Asp	Glu	Leu	Glu	Gly	Arg	Glu	Ala	Val	Ser	Gly	Asp	His	Arg
65					70					75					80



			115						120						125			
Pro	Leu	Lys	Leu	Lys	His	Ser	Cys	Glu	Glu	Gly	Ser	Glu	Glu	Gly	Pro			
	130					135					140							
Leu	Ser	His	Gly	Cys	Leu	Phe	Pro	Pro	Leu	Cys	His	Arg						
145					150					155								

<210> 588  
 <211> 144  
 <212> PRT  
 <213> homo sapiens

<400> 588

Asn	Thr	Met	Ala	Val	Ala	Ala	Val	Lys	Trp	Val	Met	Ser	Lys	Arg	Thr			
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Ile	Leu	Lys	His	Leu	Phe	Pro	Val	Gln	Asn	Gly	Ala	Leu	Tyr	Cys	Val			
			20					25					30					
Cys	His	Lys	Ser	Thr	Tyr	Ser	Pro	Leu	Pro	Asp	Asp	Tyr	Asn	Cys	Asn			
		35					40					45						
Val	Glu	Leu	Ala	Leu	Thr	Ser	Asp	Gly	Arg	Thr	Ile	Val	Cys	Tyr	His			
	50					55					60							
Pro	Ser	Val	Asp	Ile	Pro	Tyr	Glu	His	Thr	Lys	Pro	Ile	Pro	Arg	Pro			
65				70						75					80			
Asp	Pro	Val	His	Asn	Asn	Glu	Glu	Thr	His	Asp	Gln	Val	Leu	Lys	Thr			
				85					90					95				
Arg	Leu	Glu	Glu	Lys	Val	Glu	His	Leu	Glu	Glu	Gly	Pro	Met	Ile	Glu			
			100					105					110					
Gln	Leu	Ser	Lys	Met	Phe	Phe	Thr	Thr	Lys	His	Arg	Trp	Tyr	Pro	His			
		115					120					125						
Gly	Arg	Tyr	His	Arg	Cys	Arg	Lys	Asn	Leu	Asn	Pro	Pro	Lys	Asp	Arg			
	130					135					140							

<210> 589  
 <211> 128  
 <212> PRT  
 <213> homo sapiens

<400> 589

Ile	His	Gln	Thr	Ala	Phe	Ser	Gln	Met	Ala	Asn	Glu	Ala	His	Phe	Ser			
1				5					10					15				
Leu	Ile	Pro	Pro	Gly	Thr	Ser	Ala	Ser	Ser	Val	Phe	Trp	Arg	Ile	Gln			
			20					25					30					
Ile	Leu	Thr	Thr	Ser	Val	Ile	Pro	Ser	Met	Arg	Ile	Pro	Thr	Val	Leu			
		35					40					45						
Ser	Ser	Lys	Glu	His	Phe	Ala	Lys	Leu	Phe	Tyr	His	Arg	Ser	Phe	Leu			
	50					55					60							
Lys	Val	Phe	Asn	Phe	Phe	Phe	Gln	Ser	Gly	Phe	Gln	His	Leu	Ile	Met			
65					70					75					80			



Cys	Phe	Phe	Ile	Ile 85	Met	His	Arg	Ile	Trp 90	Pro	Arg	Asp	Arg	Phe 95	Cys
Val	Phe	Ile	Trp 100	Asn	Val	His	Arg	Arg 105	Val	Val	Ala	Tyr	Tyr 110	Cys	Pro
Ala	Ile	Arg 115	Ser	Gln	Ser	Lys	Leu 120	Tyr	Val	Ala	Ile	Ile 125	Val	Ile	Trp

<210> 590  
 <211> 61  
 <212> PRT  
 <213> homo sapiens

<400> 590

Lys 1	Leu	Val	Cys	Leu 5	Glu	Ala	Asp	Ser	Lys 10	Ser	Ser	Phe	Ser	Ser 15	Glu
His	Leu	Phe	Ser 20	Tyr	His	Leu	Ile	Ser 25	Ile	Leu	Lys	His	His 30	Gly	Cys
Ser	Cys	Ser 35	Lys	Met	Gly	Asp	Val 40	Lys	Glu	Asn	Tyr	Leu 45	Glu	Thr	Phe
Ile	Ser 50	Ser	Pro	Lys	Trp	Ser 55	Phe	Ile	Leu	Cys	Leu 60	Ser			

<210> 591  
 <211> 173  
 <212> PRT  
 <213> homo sapiens

<400> 591

Ala 1	Gln	Glu	Ser	Pro 5	Trp	Gln	Leu	Cys	Arg 10	Gly	Ala	Arg	Thr	Ser 15	Lys
Arg	Lys	Leu	Pro 20	Lys	Leu	Gly	Met	Glu 25	Gln	His	Cys	Asn	Glu 30	Met	Cys
Pro	Pro	Ser 35	Ser	Leu	Phe	Leu	Pro 40	Gly	Ala	Tyr	Lys	Ala 45	Gln	Met	Tyr
Ser	Asp 50	Val	Trp	Thr	Asn	Thr 55	Lys	Lys	Lys	Lys	Lys 60	Lys	Lys	Lys	Lys
Lys 65	Ala	Phe	Leu	Ser	His 70	Arg	His	Lys	Thr	Gln 75	Ile	Ile	Tyr	Cys	Tyr 80
Glu	Ala	Leu	Phe	Thr 85	Asn	Gly	Gln	Phe	Leu 90	His	Phe	Ile	Ala	Ala 95	Cys
Glu	Arg	Leu	Pro 100	Asp	Gly	Arg	Pro	Ile 105	Ser	Leu	Val	Leu	Gln 110	Thr	Ser
Ser	Gln	Ala 115	Ala	Phe	Tyr	Gln	Lys 120	Gly	Glu	Asn	Ser	Cys 125	Leu	Ser	Phe
Leu	Lys 130	Asn	Ala	Phe	Leu	Tyr 135	Leu	Ser	Ile	Arg	His 140	Tyr	Thr	Ser	Glu

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Leu 145	Tyr	Lys	Arg	Pro	Gly 150	Gly	Thr	Met	Ser	Leu 155	Val	Asp	Thr	Phe	His 160
Cys	Ser	Val	Ala	Pro 165	Phe	Leu	Ala	Trp	Glu 170	Ala	Ser	Ala			

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 <212> PRT  
 <213> homo sapiens

<400> 592

Thr 1	Cys	Glu	Pro	Phe 5	Arg	Asn	Pro	Gln	Val 10	Gly	Lys	Asp	Pro	Thr 15	Pro
Ser	Leu	Arg	Ile 20	Ile	Cys	Leu	Ala	Ile 25	Thr	Gly	Ser	Trp	Lys 30	Cys	Phe
Leu	Gly	Cys 35	Val	Lys	Ile	Asn	Gln 40	Gly	Gly	Met	Lys	His 45	Ile	Phe	Leu
Ala	Thr 50	Lys	Leu	Glu	Phe	Leu 55	Arg	Glu	Gln	Met	Gln 60	Arg	Asp	Leu	Leu
Leu 65	Leu	Ala	Arg	Leu	Gln 70	Gly	Pro	Leu	Trp	Ser 75	His	Thr	Glu	Ala	Val 80
Thr	Gly	His	Lys	Pro 85	Arg	Arg	Ala	Arg	Gly 90	Ser	Cys	Ala	Glu	Ala 95	Pro
Gly	Pro	Leu	Ser 100	Gly	Ser	Phe	Pro	Ser 105							

<210> 593  
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 <212> PRT  
 <213> homo sapiens

<400> 593

Thr 1	Cys	Glu	Pro	Phe 5	Arg	Asn	Pro	Gln	Val 10	Gly	Lys	Asp	Pro	Thr 15	Pro
Ser	Leu	Arg	Ile 20	Ile	Cys	Leu	Ala	Ile 25	Thr	Gly	Ser	Trp	Lys 30	Cys	Phe
Leu	Gly	Cys 35	Val	Lys	Ile	Asn	Gln 40	Gly	Gly	Met	Lys	His 45	Ile	Phe	Leu
Ala	Thr 50	Lys	Leu	Glu	Phe	Leu 55	Arg	Glu	Gln	Met	Gln 60	Arg	Asp	Leu	Leu
Leu 65	Leu	Ala	Arg	Leu	Gln 70	Gly	Pro	Leu	Trp	Ser 75	His	Thr	Glu	Ala	Val 80
Thr	Gly	His	Lys	Pro 85	Arg	Arg	Ala	Arg	Gly 90	Ser	Cys	Ala	Glu	Ala 95	Pro
Gly	Pro	Leu	Ser 100	Gly	Ser	Phe	Pro	Ser 105							

<210> 594

004321 3664960

<211> 172  
 <212> PRT  
 <213> homo sapiens

<400> 594

Thr 1	Pro	Ala	Leu	Arg 5	Ala	Arg	Ser	Leu	Arg 10	Asp	Arg	Cys	Ala	Arg 15	Ala
Pro	Cys	Pro	His 20	Gly	Gly	Gln	Gln	Arg 25	Arg	Arg	Arg	Arg	Leu 30	Asn	Ala
Glu	Gly	Ala 35	Glu	Gly	Ala	Arg	Gly 40	Gly	Gly	Ser	Ser	Tyr 45	Ser	Glu	Met
Ala	Glu 50	Thr	Val	Ala	Asp	Thr 55	Arg	Arg	Leu	Ile	Thr 60	Lys	Pro	Gln	Asn
Leu 65	Asn	Asp	Ala	Tyr	Gly 70	Pro	Pro	Ser	Asn	Phe 75	Leu	Glu	Ile	Asp	Val 80
Ser	Asn	Pro	Gln	Thr 85	Val	Gly	Val	Gly	Arg 90	Gly	Arg	Phe	Thr	Thr 95	Tyr
Glu	Ile	Arg	Val 100	Lys	Thr	Asn	Leu	Pro 105	Ile	Phe	Lys	Leu	Lys 110	Glu	Ser
Thr	Val	Arg 115	Arg	Arg	Tyr	Ser	Asp 120	Phe	Glu	Trp	Leu	Arg 125	Ser	Glu	Leu
Glu	Arg 130	Glu	Ser	Lys	Val	Val 135	Val	Pro	Pro	Leu	Pro 140	Gly	Lys	Ala	Phe
Leu 145	Arg	Gln	Phe	Leu	Leu 150	Glu	Glu	Met	Met	Glu 155	Tyr	Leu	Met	Thr	Ile 160
Leu	Leu	Arg	Lys	Glu 165	Asn	Lys	Gly	Trp	Ser 170	Ser	Leu				

<210> 595  
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 <212> PRT  
 <213> homo sapiens

<400> 595

Ser 1	Ala	Ala	Gly	Cys 5	Gln	Pro	Arg	Ser	Pro 10	Pro	Phe	Arg	Cys	Ser 15	Cys
Cys	Arg	Arg	Arg 20	Gly	Leu	Pro	Pro	Pro 25	Pro	Pro	Arg	Ser	Ala 30	Ala	Ala
Ala	Gly	Ala 35	Ala	Ala	Arg	Arg	Gly 40	Asp	Thr	Gly	Leu	Ala 45	Arg	Ser	Gly
Arg	Glu 50	Glu	Asn	Glu	His 55	Val	Glu	Arg	Ala	Phe	Thr 60	Pro	His	Ala	Lys
Leu 65	Leu	Pro	Ala	Pro	Leu 70	Lys	Leu	Pro	Pro	Pro 75	Ser	Pro	Gly	Glu	Lys 80
Arg	Leu	Thr	Ser	Trp 85	Asn	Ala	Thr	Pro	Gly 90	Ser	Arg	Glu	Ala	Arg 95	Pro

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Arg   Leu   Gly   Arg   Gly   Thr   Ala   Asp   Trp   Gly   Val   Arg   Arg   Ser   Gly   Val .  
              100                    105                    110

Met Gly Leu Gly Val Ala Asn Arg Phe Arg Pro Asp Tyr Ser Ala  
115 120 125

<210> 596

<211> 123

<212> PRT

<213> homo sapiens

<400> 596

Phe Thr Ser Gln Pro Phe Lys Val Thr Val Ser Ser Ser Asn Ser Arg  
1 5 10 15

Phe Phe Gln Leu Glu Asn Arg Lys Ile Cys Leu Asp Pro Asp Phe Val  
20 25 30

Ser Gly Glu Ala Ala Pro Ala Asp Pro His Arg Leu Arg Val Ala His  
35 40 45

Ile Asp Leu Glu Glu Val Ala Gly Gly Ser Val Gly Val Ile Gln Val  
50 55 60

Leu 65 Arg Leu Gly Asp 70 Gln Pro Pro Gly Val 75 Ser His Gly Leu Arg His 80

Phe Ala Val Ala Ala Ala Ala Ala Gly Ser Leu Arg Pro Leu Arg  
85 90 95

Val	Gln	Pro	Pro	Pro	Pro	Ala	Leu	Leu	Pro	Ala	Val	Gly	Thr	Arg	Gly
			100					105					110		

Ser Arg Ala Ala Val Ala Lys Arg Thr Ser Thr  
115 120

<210> 597

<211> 262

<212> PRT

<213> homo sapiens

<400> 597

Ser Cys Gly Asp Val Glu Gln Lys Ile Gln Phe Lys Arg Glu Thr Ala  
1 5 10 15

Ser	Leu	Lys	Leu	Leu	Pro	His	Gln	Pro	Arg	Ile	Val	Glu	Met	Lys	Lys
			20					25					30		

Gly Ser Asn Gly Tyr Gly Phe Tyr Leu Arg Ala Gly Ser Glu Gln Lys  
35 40 45

Gly Gln Ile Ile Lys Asp Ile Asp Ser Gly Ser Pro Ala Glu Glu Ala  
50 55 60

Gly 65 Leu Lys Asn Asn Asp 70 Leu Val Val Ala 75 Val Asn Gly Glu Ser Val 80

Glu Thr Leu Asp His Asp Ser Val Val Glu Met Ile Arg Lys Gly Gly  
85 90 95



1				5					10					15		
Pro	Pro	Ala	Pro 20	Asn	Cys	Gly	Asp	Glu 25	Glu	Arg	Lys	Gln	Trp 30	Leu	Trp	
Phe	Leu	Ser 35	Glu	Gly	Arg	Leu	Arg 40	Thr	Glu	Arg	Ser	Asn 45	His	Gln	Gly	
His	Arg 50	Phe	Trp	Lys	Ser	Ser 55	Arg	Gly	Gly	Trp	Leu 60	Glu	Glu	Gln		

<210> 600

<211> 336

<212> PRT

<213> homo sapiens

<400> 600

Lys 1	Leu	Asn	Phe	Asn 5	Thr	Met	Arg	Cys	Cys 10	His	Ile	Cys	Lys	Leu 15	Pro	
Gly	Arg	Val	Met 20	Gly	Ile	Arg	Val	Leu 25	Arg	Leu	Ser	Leu	Val 30	Val	Ile	
Leu	Val	Leu 35	Leu	Leu	Val	Ala	Gly 40	Ala	Leu	Thr	Ala	Leu 45	Leu	Pro	Ser	
Val	Lys 50	Glu	Asp	Lys	Met	Leu 55	Met	Leu	Arg	Arg	Glu 60	Ile	Lys	Ser	Gln	
Gly 65	Lys	Ser	Thr	Met	Asp 70	Ser	Phe	Thr	Leu	Ile 75	Met	Gln	Thr	Tyr	Asn 80	
Arg	Thr	Asp	Leu	Leu 85	Leu	Lys	Leu	Leu	Asn 90	His	Tyr	Gln	Ala	Val 95	Pro	
Asn	Leu	His	Lys 100	Val	Ile	Val	Val	Trp 105	Asn	Asn	Ile	Gly	Glu 110	Lys	Ala	
Pro	Asp	Glu 115	Leu	Trp	Asn	Ser	Leu 120	Gly	Pro	His	Pro	Ile 125	Pro	Val	Ile	
Phe	Lys 130	Gln	Gln	Thr	Ala	Asn 135	Arg	Met	Arg	Asn	Arg 140	Leu	Gln	Val	Phe	
Pro 145	Glu	Leu	Glu	Thr	Asn 150	Ala	Val	Leu	Met	Val 155	Asp	Asp	Asp	Thr	Leu 160	
Ile	Ser	Thr	Pro	Asp 165	Leu	Val	Phe	Ala	Phe 170	Ser	Val	Trp	Gln	Gln 175	Phe	
Pro	Asp	Gln	Ile 180	Val	Gly	Phe	Val	Pro 185	Arg	Lys	His	Val	Ser 190	Thr	Ser	
Ser	Gly	Ile 195	Tyr	Ser	Tyr	Gly	Ser 200	Phe	Glu	Met	Gln	Ala 205	Pro	Gly	Ser	
Gly	Asn 210	Gly	Asp	Gln	Tyr	Ser 215	Met	Val	Leu	Ile	Gly 220	Ala	Ser	Phe	Phe	
Asn 225	Ser	Lys	Tyr	Leu	Glu 230	Leu	Phe	Gln	Arg	Gln 235	Pro	Ala	Ala	Val	His 240	

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Ala	Leu	Ile	Asp	Asp 245	Thr	Gln	Asn	Cys	Asp 250	Asp	Ile	Ala	Met	Asn 255	Phe
Ile	Ile	Ala	Lys 260	His	Ile	Gly	Lys	Thr 265	Ser	Gly	Ile	Phe	Val 270	Lys	Pro
Val	Asn	Met 275	Asp	Asn	Leu	Glu	Lys 280	Glu	Thr	Asn	Ser	Gly 285	Tyr	Ser	Gly
Met	Trp 290	His	Arg	Ala	Glu	His 295	Ala	Leu	Gln	Arg	Ser 300	Tyr	Cys	Ile	Asn
Lys 305	Leu	Val	Asn	Ile	Tyr 310	Asp	Ser	Met	Pro	Leu 315	Arg	Tyr	Ser	Asn	Ile 320
Met	Ile	Ser	Gln	Phe 325	Gly	Phe	Pro	Tyr	Ala 330	Asn	Tyr	Lys	Arg	Lys 335	Ile

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<210> 601
<211> 101
<212> PRT
<213> homo sapiens
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<400> 601

[illegible]

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<210> 602
<211> 90
<212> PRT
<213> homo sapiens
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<400> 602

Phe 1	Lys	Ser	Phe	Asn 5	Lys	Arg	Ser	Val	Leu 10	Leu	Tyr	Val	Cys	Ile 15	Met
Arg	Val	Lys	Glu 20	Ser	Met	Val	Asp	Leu 25	Pro	Trp	Asp	Phe	Ile 30	Ser	Leu
Arg	Asn	Met 35	Ser	Ile	Leu	Ser	Ser 40	Leu	Thr	Leu	Gly	Ser 45	Lys	Ala	Val
Lys	Ala	Pro	Ala	Thr	Ser	Asn	Asn	Thr	Arg	Met	Thr	Thr	Lys	Asp	Asn





[illegible]

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<210> 605
<211> 108
<212> PRT
<213> homo sapiens
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<400> 605

Leu 1	Asp	Phe	Lys	Xxx 5	Gln	Phe	Cys	Glu	Ser 10	Ile	Xxx	Pro	Gln	Ala 15	Lys
Cys	Val	Xxx	Xxx 20	Met	Ile	Lys	Xxx	Xxx 25	Pro	Xxx	Xxx	Ile	Pro 30	Val	Phe
Leu	Lys	Xxx 35	Val	Pro	Xxx	Ile	Ser 40	Xxx	His	Cys	Ile	Tyr 45	Pro	Xxx	Asp
Ile	Asn 50	Xxx	Thr	Leu	Phe	Ser 55	Phe	Tyr	Ser	Ser	Asn 60	Lys	Val	Gly	Thr
Asp 65	Leu	Ser	Thr	Thr	Asn 70	Leu	Pro	Ser	Xxx	Cys 75	Leu	Ala	Ser	Xxx	Pro 80
Cys	Ser	Ala	Pro	Gly 85	Xxx	Xxx	Pro	Leu	Xxx 90	Xxx	Pro	Val	Xxx	Phe 95	Xxx
Val	Lys	Xxx	Pro 100	Asn	Leu	Leu	Leu	Ala 105	Phe	Ser	Trp				

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<210> 606
<211> 203
<212> PRT
<213> homo sapiens
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<400> 606

Gly 1	Pro	Ser	Ala	Leu 5	Val	His	Ser	Val	Arg 10	Pro	Asp	Leu	Cys	Ser 15	Asn
Pro	Leu	Ser	Cys 20	Gly	Ser	Leu	Ala	Cys 25	Met	Ala	Tyr	Thr	Gly 30	Glu	Leu
Gly	Leu	Trp	Ala	Val	Gln	Thr	Gln	Gly	Ser	His	Phe	Ala	Phe	Pro	Leu



Gly 130	Pro	Leu	Gly	Thr	Lys 135	Asp	Met	Pro	His	Trp 140	Gly	Cys	Asn	Gly
Glu 145	Lys	Ser	Gly	Lys	Leu 150	Gly	Ala	Gln	Leu					

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<210> 608
<211> 123
<212> PRT
<213> homo sapiens
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<400> 608

Cys 1	Gly	Val	Leu	Ser 5	Leu	Arg	Trp	Val	Gln 10	Gln	Pro	Trp	Phe	Leu 15	Trp
Gly	Leu	Arg	Ile 20	Arg	Ile	Val	Gly	Arg 25	Glu	Lys	Leu	Leu	Leu 30	Glu	Asp
Phe	Leu	Ser 35	Gln	Ser	Pro	Arg	Glu 40	Val	Glu	Arg	Arg	Asn 45	Phe	Cys	Trp
Thr	Ser 50	Ser	Gly	Gln	Arg	Lys 55	Asp	Gly	Met	Lys	Val 60	Glu	Lys	Ala	Glu
Leu 65	Gln	Leu	Ser	Gly	Asp 70	Asn	Lys	Glu	Phe	Phe 75	Ser	Gly	Lys	Ser	Phe 80
Val	Leu	Glu	Gln	Gly 85	Trp	Lys	Met	Gly	Thr 90	Thr	Lys	Glu	Lys	Gln 95	Ser
Val	Thr	Leu	Gly 100	Phe	Gly	Gln	Pro	Arg 105	Gly	Pro	Ala	Pro	Gln 110	Tyr	Lys
Pro	Tyr	Arg 115	Pro	Gly	Thr	His	Arg 120	Arg	Val	Asp					

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<210> 609
<211> 88
<212> PRT
<213> homo sapiens
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<400> 609

Leu 1	Val	Glu	Pro	Asn 5	Gly	Leu	Phe	Trp	Phe 10	His	Phe	Ser	Ala	Ser 15	Arg
Arg	Gln	Asn	Lys 20	Glu	Ser	His	Ser	Lys 25	Met	Phe	Ile	Val	Asp 30	Asn	Met
Ser	Leu	Lys 35	Val	Val	Pro	Leu	Cys 40	Ser	Tyr	Ser	Thr	Glu 45	Glu	Met	Ile
His	Ile 50	Pro	Ile	Ile	Asp	Met 55	Val	Ser	Gln	Ser	Glu 60	Glu	Ser	Phe	Arg
Arg 65	Leu	His	Lys	Tyr	Val 70	Leu	Cys	Thr	Cys	Pro 75	Met	Leu	Gly	Asn	Arg 80
Lys	Ile	Ile	Val	Ile 85	Asp	Lys	Thr								

<210> 610





<211> 213  
 <212> PRT  
 <213> homo sapiens

<400> 613

Ala 1	Arg	Cys	Ala	Glu 5	Thr	Pro	Ala	Gly	Ala 10	Ala	Ala	Ala	Val	Ser 15	Pro
Asp	Glu	Ala	Arg 20	Ala	Ser	Pro	Ala	Ala 25	Arg	Gln	Arg	Pro	Arg 30	Pro	Asp
Gly	Asp	Pro 35	Ala	Val	Gly	Pro	Ser 40	Pro	Gln	Arg	Leu	Ala 45	Ala	Ala	His
Ala	Asp 50	Pro	Gly	Arg	Ala	Pro 55	Leu	Arg	Glu	Ala	Trp 60	Pro	His	Arg	Arg
Leu 65	His	Arg	Val	Leu	Arg 70	Ala	Ala	Leu	Arg	Val 75	His	Leu	Arg	Ala	Ala 80
Leu	Ala	Gly	Ala	Ala 85	Leu	Pro	Pro	Gln	Ala 90	Ala	Gln	Leu	Pro	Glu 95	Arg
Leu	Pro	Leu	Ser 100	Leu	Pro	Leu	Leu	Gly 105	Leu	Pro	Ala	Asp 110	Pro	Pro	Leu
Leu	Leu	Leu 115	Leu	Gln	Arg	Leu	Arg 120	Gly	Gly	Gln	Phe	Ala 125	Gln	Pro	Leu
Arg	Leu 130	Leu	Ala	Ala	Leu	Leu 135	Leu	Pro	Cys	Val	Pro 140	Ala	Val	Phe	His
Pro 145	His	Ala	Asp	Glu	Leu 150	Val	Leu	His	Ala	Gly 155	Asp	Phe	Gln	Ser	Gln 160
Val	Lys	Ile	Phe	Ser 165	Arg	Ile	Thr	Gln	Ile 170	Pro	Val	Ala	Pro	Leu 175	Pro
Gly	Leu	Pro	Leu 180	His	Gln	Pro	Cys	Phe 185	Pro	Val	Gly	Glu	Phe 190	Asn	Leu
Cys	Cys	Ala 195	Gly	Lys	Asp	Gly	Lys 200	Leu	Gly	Glu	Glu	Gly 205	Tyr	Arg	Leu
Cys	Ala 210	Ser	Gly	His											

<210> 614  
 <211> 161  
 <212> PRT  
 <213> homo sapiens

<400> 614

Leu 1	Gly	Phe	Glu	Asn 5	His	Leu	Arg	Glu	Val 10	Gln	Val	His	Gln	Arg 15	Glu
Gly	Glu	Lys	Leu 20	Gln	Ala	His	Arg	Glu 25	Ala	Val	Glu	Gln	Pro 30	Glu	Asp
Glu	Gly	Ala 35	Glu	Arg	Ile	Gly	Arg 40	His	Glu	Val	Phe	Glu 45	Val	Glu	Gly

002221 5622350







Ser	Ser	Leu	Gln	Gly	Ser	Pro	Ala	Thr	Pro	Leu	Ser	Phe	Leu	Phe	Phe	
		115					120					125				
Leu	Val	Phe	Leu	Phe	Arg	Ala	Gly	Ser	Ser	Met	Thr	Gly	Cys	Ser	Thr	
	130					135					140					
Phe	Phe	Leu	Asp	Phe	Ile	Phe	Phe	Phe	Ala	Glu	Asp	Leu	Gly	Ser	Ser	
145					150					155					160	
Leu	Met	Gly	Met	Tyr	Ser	Gly	Ala	Ser	Thr	Leu	Thr	Gly	Phe	Phe	Leu	
				165					170					175		
Leu	Pro	Phe	Leu	Gly	Leu	Leu	Ser	Met	Asp	Leu	Glu	Gly	Leu	Glu	Trp	
			180					185					190			
Pro	Gly	Arg	Ala	Ser	Pro	Ser	Trp	Trp	Ile	Phe	Phe	Phe	Phe	Phe	Thr	
		195					200					205				
Phe	Pro	Leu	Cys	Ser	Leu	Gly	Leu	Phe	Arg	Leu	Pro	Phe	Leu	Xxx	Pro	
	210					215					220					
Arg	Leu	Pro	Val	Pro	His	Pro	Ser	Ser	Pro	Leu	Xxx	Gln	Val	Ser	Pro	
225					230					235					240	
Thr	Ser	Leu	Ala	Ser	Leu	Ala	Ser	Gln	Asn	Gln	Gly	Ser	Trp	Thr	Glu	
				245					250					255		
Lys	Ala	Xxx	Gly	Val	Leu	Gly	Pro	Pro	Phe	Phe	Pro	Ser	Cys	Xxx	Phe	
			260					265					270			
Leu	Ser	Phe	Leu	Pro	Thr	Leu	Val	Ser	Ser	Ser	Pro	Cys	Leu	Xxx	Val	
		275					280					285				
Leu	Gly	Arg	Phe	Ser	Pro	Gln	Arg	His	Gly	Thr	Trp	Leu	Glu	Val	Thr	
	290					295					300					
Ser	Xxx	Phe	Phe	Phe	Ser	Pro	Leu	Arg	Asn	Ser	Lys	Trp	Pro	Asn	Thr	
305					310					315					320	
Cys	Phe	Leu	Arg	Leu	Gly	Asp	Phe	Ser	Val	Arg	Leu	Ala	Gly	Ser	Val	
				325					330					335		
Val	Ser	Gly	Ser	Thr	Cys	Ser	Ser	Gln	Arg	Val	Leu	Thr	Pro	Phe	Phe	
			340					345					350			
Phe	Phe	Phe	Phe	Phe	Phe	Thr	Arg	Gly	Ile	Ser	Gly	Ala	Cys	Pro	Trp	
		355					360					365				
Ala	Thr	Leu	Leu	Xxx	Gly	Gly	Cys	Ser	Ser							
	370					375										

<210> 619

<211> 269

<212> PRT

<213> homo sapiens

<400> 619

Gly	Thr	Gly	Ser	Leu	Gly	Xxx	Arg	Asn	Gly	Xxx	Arg	Lys	Ser	Pro	Arg	
1				5					10					15		
Glu	His	Asn	Gly	Lys	Val	Lys	Lys	Lys	Lys	Lys	Ile	His	Gln	Glu	Gly	



Leu	Arg	Val	Ile	Thr	Tyr	Gly	Asp	Val	Phe	Arg	Ser	Leu	Asn	Phe	Asp	
	50					55					60					
Trp	Leu	Leu	Phe	Thr	Ser	Phe	Pro	Arg	Ala	Ala	Leu	His	Gly	Pro	Gly	
65					70				75						80	
Gly	Leu	Gly	Val	Ala	Trp	Glu	Gly	Ile	Ser	Leu	Leu	Val	Asp	Phe	Phe	
				85					90					95		
Phe	Leu	Leu	His	Leu	Pro	Ile	Val	Phe	Ser	Gly	Ala	Leu	Pro	Xxx	Ser	
			100					105					110			
Val	Ser	Xxx	Pro	Lys	Ala	Ala	Cys	Ser	Ser	Ser	Phe	Phe	Pro	Thr	Xxx	
		115					120					125				
Ala	Ser	Val	Pro	Asn	Ile	Pro	Gly	Leu	Pro	Gly	Leu	Thr	Glu	Pro	Arg	
	130					135					140					
Val	Leu	Asp	Arg	Glu	Gly	Xxx	Trp	Gly	Pro	Gly	Xxx	Pro	Phe	Phe	Ser	
145					150					155					160	
Phe	Leu	Xxx	Phe	Phe	Glu	Leu	Leu	Ala	Asn	Ser	Gly	Phe	Leu	Leu	Thr	
				165					170					175		
Leu	Ser	Xxx	Gly	Xxx	Gly	Glu	Val	Phe	Thr	Pro	Glu	Ala	Trp	Asp	Met	
			180					185					190			
Ala	Arg	Gly	Asp	Phe	Leu	Xxx	Phe	Leu	Phe	Pro	Thr	Glu	Glu	Leu	Gln	
		195					200					205				
Val	Ala	Lys	His	Leu	Leu	Pro	Glu	Ala	Gly							
	210					215										

<210> 621  
 <211> 389  
 <212> PRT  
 <213> homo sapiens

<400> 621

Ala	Ala	Gly	Ala	Cys	Gly	Ala	Arg	Gly	Ser	Gly	Arg	Arg	Gly	Ser	Tyr	
1				5					10					15		
Val	Pro	Glu	Val	Arg	Cys	Gly	Ala	Pro	Gly	Gly	Ala	Ala	Gly	Thr	Gly	
			20					25					30			
Ala	Pro	Arg	Ser	Cys	Cys	Cys	Gln	Thr	Asn	Pro	Gly	Pro	Pro	Ser	Ser	
		35					40					45				
Leu	Arg	Arg	Ala	Phe	Arg	Arg	Arg	Glu	Leu	Pro	Phe	Pro	Ala	Cys	His	
	50					55					60					
Glu	Ile	Gly	Leu	Gly	Ala	Glu	Ala	Gly	Ser	Gly	Pro	Pro	Pro	Ala	Pro	
65					70					75					80	
Ala	Ala	Arg	Glu	Ser	Arg	Ser	Arg	Ala	Met	Glu	Glu	Glu	Ala	Ser	Ser	
				85					90					95		
Pro	Gly	Leu	Gly	Cys	Ser	Lys	Pro	His	Leu	Glu	Lys	Leu	Thr	Leu	Gly	
			100					105					110			
Ile	Thr	Arg	Ile	Leu	Glu	Ser	Ser	Pro	Gly	Val	Thr	Glu	Val	Thr	Ile	
		115					120					125				

Ile	Glu	Lys	Pro	Pro	Ala	Glu	Arg	His	Met	Ile	Ser	Ser	Trp	Glu	Gln	
	130					135					140					
Lys	Asn	Asn	Cys	Val	Met	Pro	Glu	Asp	Val	Lys	Asn	Phe	Tyr	Leu	Met	
145					150					155					160	
Thr	Asn	Gly	Phe	His	Met	Thr	Trp	Ser	Val	Lys	Leu	Asp	Glu	His	Ile	
				165					170					175		
Ile	Pro	Leu	Gly	Ser	Met	Ala	Ile	Asn	Ser	Ile	Ser	Lys	Leu	Thr	Gln	
			180					185					190			
Leu	Thr	Gln	Ser	Ser	Met	Tyr	Ser	Leu	Pro	Asn	Ala	Pro	Thr	Leu	Ala	
		195					200					205				
Asp	Leu	Glu	Asp	Asp	Thr	His	Glu	Ala	Ser	Asp	Asp	Gln	Pro	Glu	Lys	
	210					215					220					
Pro	His	Phe	Asp	Ser	Arg	Ser	Val	Ile	Phe	Glu	Leu	Asp	Ser	Cys	Asn	
225					230					235					240	
Gly	Ser	Gly	Lys	Val	Cys	Leu	Val	Tyr	Lys	Ser	Gly	Lys	Pro	Ala	Leu	
				245					250					255		
Ala	Glu	Asp	Thr	Glu	Ile	Trp	Phe	Leu	Asp	Arg	Ala	Leu	Tyr	Trp	His	
			260					265					270			
Phe	Leu	Thr	Asp	Thr	Phe	Thr	Ala	Tyr	Tyr	Arg	Leu	Leu	Ile	Thr	His	
		275					280					285				
Leu	Gly	Leu	Pro	Gln	Trp	Gln	Tyr	Ala	Phe	Thr	Ser	Tyr	Gly	Ile	Ser	
	290					295					300					
Pro	Gln	Ala	Lys	Gln	Trp	Phe	Ser	Met	Tyr	Lys	Pro	Ile	Thr	Tyr	Asn	
305					310					315					320	
Thr	Asn	Leu	Leu	Thr	Glu	Glu	Thr	Asp	Ser	Phe	Val	Asn	Lys	Leu	Asp	
				325					330					335		
Pro	Ser	Lys	Val	Phe	Lys	Ser	Lys	Asn	Lys	Ile	Val	Ile	Pro	Lys	Lys	
			340					345					350			
Lys	Gly	Pro	Val	Gln	Pro	Ala	Gly	Gly	Gln	Lys	Gly	Pro	Ser	Gly	Pro	
		355					360					365				
Ser	Gly	Pro	Ser	Thr	Ser	Ser	Thr	Ser	Lys	Ser	Ser	Ser	Gly	Ser	Gly	
	370					375					380					
Asn	Pro	Thr	Arg	Lys												
385																

<210> 622  
 <211> 109  
 <212> PRT  
 <213> homo sapiens

<400> 622

Ala	Arg	Pro	Ala	Pro	Ala	Gly	Arg	Glu	Gly	Arg	Gly	Glu	Gly	Glu	Ala	
1				5					10					15		
Thr	Ser	Arg	Arg	Cys	Gly	Val	Gly	His	Arg	Ala	Gly	Pro	Arg	Glu	Pro	

			20					25					30			
Ala	Pro	His	Gly	Ala	Ala	Ala	Val	Arg	Pro	Thr	Pro	Gly	Pro	His	His	
		35					40					45				
His	Cys	Ala	Ala	Leu	Ser	Gly	Ala	Glu	Asn	Tyr	Arg	Ser	Arg	His	Ala	
	50					55					60					
Met	Lys	Leu	Ala	Ser	Ala	Leu	Arg	Arg	Gly	Pro	Ala	Leu	His	Pro	Leu	
	65				70					75					80	
Pro	Pro	Arg	Ala	Asn	Arg	Gly	Arg	Glu	Pro	Trp	Arg	Arg	Arg	His	Arg	
				85					90					95		
Pro	Arg	Gly	Trp	Ala	Ala	Ala	Ser	Arg	Thr	Trp	Arg	Ser				
			100					105								

<210> 623  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 623

Arg	Ser	Ala	Gly	Gly	Phe	Ser	Met	Met	Val	Thr	Ser	Val	Thr	Pro	Gly	
	1			5					10					15		
Glu	Asp	Ser	Arg	Met	Arg	Val	Met	Pro	Arg	Val	Ser	Phe	Ser	Arg	Cys	
			20					25					30			
Gly	Leu	Leu	Gln	Pro	Ser	Pro	Gly	Asp	Asp	Ala	Ser	Ser	Ser	Met	Ala	
		35					40					45				
Arg	Asp	Arg	Asp	Ser	Arg	Ala	Ala	Gly	Ala	Gly	Gly	Gly	Pro	Asp	Pro	
	50					55					60					
Ala	Ser	Ala	Pro	Arg	Pro	Ile	Ser	Trp	His	Ala	Gly	Asn	Gly	Ser	Ser	
	65				70					75					80	
Arg	Arg	Leu	Lys	Ala	Arg	Arg	Ser	Asp	Asp	Gly	Gly	Pro	Gly	Leu	Val	
				85					90					95		

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Cys	Cys	Thr	Glu	His	Arg	Trp	Pro	Ala	Ser	Met	Pro	Pro	Gln	Leu	Gln	
	1			5					10					15		
Glu	Thr	Arg	Met	Asn	Arg	Ser	Ile	Pro	Val	Glu	Val	Asp	Glu	Ser	Glu	
			20					25					30			
Pro	Tyr	Pro	Ser	Gln	Leu	Leu	Lys	Pro	Ile	Pro	Glu	Tyr	Ser	Pro	Glu	
		35					40					45				
Glu	Glu	Ser	Glu	Pro	Pro	Ala	Pro	Asn	Ile	Arg	Asn	Met	Ala	Pro	Asn	
	50					55					60					
Ser	Leu	Ser	Ala	Pro	Thr	Met	Leu	His	Asn	Ser	Ser	Gly	Asp	Phe	Ser	
	65				70				75						80	

Gln	Ala	His	Ser	Thr 85	Leu	Lys	Leu	Ala	Asn 90	His	Gln	Arg	Pro	Val 95	Ser
Arg	Gln	Val	Thr 100	Cys	Leu	Arg	Thr	Gln 105	Val	Leu	Glu	Asp	Ser 110	Glu	Asp
Ser	Phe	Cys 115	Arg	Arg	His	Pro	Gly 120	Leu	Gly	Lys	Ala	Phe 125	Pro	Ser	Gly
Cys	Ser 130	Ala	Val	Ser	Glu	Pro 135	Ala	Ser	Glu	Ser	Val 140	Val	Gly	Ala	Leu
Pro 145	Ala	Glu	His	Gln	Phe 150	Ser	Phe	Met	Glu	Lys 155	Arg	Asn	Gln	Trp	Leu 160
Val	Ser	Gln	Leu	Ser 165	Ala	Ala	Ser	Pro	Asp 170	Thr	Gly	His	Asp	Ser 175	Asp
Lys	Ser	Asp	Gln 180	Ser	Leu	Pro	Asn	Ala 185	Ser	Ala	Asp	Ser	Leu 190	Gly	Gly
Ser	Gln	Glu 195	Met	Val	Gln	Arg	Pro 200	Gln	Pro	Xxx	Gln	Glu 205	Pro	Ser	Arg
Pro	Gly 210	Ser	Ala	Asn	His	Arg 215	His	Gly	Ile						

&lt;210&gt; 625

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 625

Asn 1	Leu	Gln	Ile	Thr 5	Ser	Gly	Leu	Tyr	Pro 10	Gly	Arg	Ser	Pro	Ala 15	Cys
Ala	Leu	Lys	Phe 20	Trp	Arg	Thr	Val	Lys 25	Thr	Val	Ser	Ala	Gly 30	Asp	Thr
Gln	Ala	Trp 35	Ala	Lys	Leu	Ser	Leu 40	Leu	Gly	Ala	Leu	Gln 45	Ser	Ala	Ser
Leu	Arg 50	Leu	Ser	Leu	Trp	Leu 55	Glu	Pro	Ser	Leu	Gln 60	Ser	Ile	Ser	Phe
His 65	Leu	Trp	Lys	Asn	Val 70	Ile	Asn	Gly	Trp	Tyr 75	Leu	Ser	Phe	Gln	Arg 80
Leu	Leu	Leu	Thr	Leu 85	Ala	Met	Thr	Gln	Thr 90	Asn	Gln	Thr	Lys	Val 95	Tyr
Leu	Met	Pro	Gln 100	Gln	Thr	Pro	Trp	Ala 105	Val	Ala	Arg	Arg	Trp 110	Cys	Asn
Gly	Pro	Ser 115	Leu	His	Arg	Asn	Arg 120	Ala	Gly	Leu	Asp	Leu 125	Pro	Thr	Ile
Asp	Thr 130	Gly	Tyr	Asp	Ser	Gln 135	Pro	Gln	Asp	Val	Leu 140	Gly	Ile	Arg	Gln
Leu	Glu	Arg	Pro	Leu	Xxx	Leu	Thr	Ser	Val	Cys	Tyr	Pro	Gln	Asp	Leu

145					150					155				160	
Pro	Arg	Pro	Leu	Arg 165	Ser	Arg	Glu	Phe	Pro 170	Gln	Phe	Glu	Pro	Gln 175	Arg
Tyr	Pro	Ala	Cys 180	Ala	Gln	Met	Leu	Pro 185	Pro	Asn	Leu	Ser	Pro 190	His	Ala
Pro	Trp	Asn 195	Tyr	His	Tyr	His	Cys 200	Pro	Gly	Ser	Pro	Asp 205	His	Gln	Val
Xxx	Ile 210	Trp	Pro												

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Lys	Glu	Glu	Glu 20	Met	Gly	Cys	Asp	Gly 25	Ser	Lys	Ala	Gly	Lys 30	Val	Ser
His	Gly	Pro 35	Gln	Thr	Pro	Phe	Pro 40	Pro	Leu	Ser	Leu	Ser 45	Pro	Leu	Pro
Lys	Lys 50	Lys	Lys	Lys	Glu	Thr 55	Phe	Ile	Met	Asn	Gln 60	Gln	Gly	Phe	Ser
Pro 65	Tyr	Gln	Arg	Glu	Met 70	Trp	Lys	Glu	Leu	Lys 75	Lys	Pro	Pro	Phe	Val 80
Pro	Asn	Ser	Thr	Leu 85	Pro	Ile	Phe	Tyr	Ala 90	Thr	Gln	Thr	Leu	Ser 95	Phe
Trp	Val	Pro	Phe 100	Leu	Gln	Met	Asp	Leu 105	Leu	Arg	Arg	Ile	Ile 110	Val	Phe
His	Val	Phe 115	Ser	Pro	Gln	Val	Thr 120	Lys	Ile	Asn	Ile	Cys 125	Ile	Tyr	Asn
Leu	Tyr 130	Tyr	Cys	Tyr	Ile	Phe 135	Val	Asp	Asn	Thr	Phe 140	Arg	Trp	Cys	Trp

Val 145	Ile	Tyr	Tyr	Asn	Leu 150	Asn	Leu	Gly	Ile	Ser 155	Phe	Gly	Leu	Pro	Gln 160
Ser	Leu	Leu	Arg	Trp 165	Gly	Pro	Trp	Tyr	Gly 170	Lys	Thr	Pro	Arg	Tyr 175	Asn
Val	Thr	Ser	Pro 180	Gln	Pro	Leu	Tyr								

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<400> 631

Gly 1	Pro	Trp	Leu	Thr 5	Phe	Pro	Ala	Phe	Asp 10	Pro	Ser	His	Pro	Ile 15	Ser
Ser	Ser	Phe	Pro 20	Leu	Pro	Ala	Ala	Lys 25	Lys	Lys	Lys	Lys	Glu 30	Thr	Phe
Ile	Met	Asn 35	Gln	Gln	Gly	Phe	Ser 40	Pro	Tyr	Gln	Arg	Glu 45	Met	Trp	Lys
Glu 50	Leu	Lys	Lys	Pro	Pro	Phe 55	Val	Pro	Asn	Ser	Thr 60	Leu	Pro	Ile	Phe
Tyr 65	Ala	Thr	Gln	Thr	Leu 70	Ser	Phe	Trp	Val	Pro 75	Phe	Leu	Gln	Met	Asp 80
Leu	Leu	Arg	Arg	Ile 85	Ile	Val	Phe	His	Val 90	Phe	Ser	Pro	Gln	Val 95	Thr
Lys	Ile	Asn	Ile 100	Cys	Ile	Tyr	Asn	Leu 105	Tyr	Tyr	Cys	Tyr	Ile 110	Phe	Val
Asp	Asn	Thr 115	Phe	Arg	Trp	Cys	Trp 120	Val	Ile	Tyr	Tyr	Asn 125	Leu	Asn	Leu
Gly 130	Ile	Ser	Phe	Gly	Leu	Pro 135	Gln	Ser	Cys						

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Trp 1	Val	Lys	Gly	Arg 5	Lys	Gly	Lys	Pro	Trp 10	Ser	Ser	Asn	Pro	Ile 15	Ser
Ser	Ser	Phe	Pro 20	Leu	Pro	Ala	Ala	Lys 25	Lys	Lys	Lys	Lys	Gly 30	Asn	Val
Tyr	His	Glu 35	Ser	Thr	Gly	Phe	Gln 40	Ser	Leu	Ser	Lys	Arg 45	Asp	Val	Glu
Arg	Ala 50	Lys	Glu	Thr	Thr	Leu 55	Cys	Ser	Gln	Leu	His 60	Phe	Thr	His	Ile

00422T 5555555555





Parameter	Unit	Value	Standard Error	t-Statistic	Prob >  t	95% Conf. Interval	90% Conf. Interval
Intercept		1.0000	0.0000	1.0000	1.0000	1.0000	1.0000
Age	Years	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age squared	Years squared	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age cubed	Years cubed	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age quart	Years quart	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age quint	Years quint	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age sext	Years sext	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age sept	Years sept	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age oct	Years oct	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age non	Years non	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age dec	Years dec	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age elev	Years elev	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age decim	Years decim	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age hund	Years hund	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age thous	Years thous	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age mill	Years mill	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age bill	Years bill	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age trill	Years trill	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age quadr	Years quadr	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age quint	Years quint	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age sext	Years sext	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age sept	Years sept	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age oct	Years oct	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age non	Years non	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age dec	Years dec	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age elev	Years elev	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age decim	Years decim	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age hund	Years hund	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age thous	Years thous	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age mill	Years mill	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age bill	Years bill	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age trill	Years trill	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age quadr	Years quadr	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age quint	Years quint	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age sext	Years sext	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age sept	Years sept	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age oct	Years oct	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age non	Years non	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age dec	Years dec	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age elev	Years elev	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age decim	Years decim	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000
Age hund	Years hund	0.0000	0.0000	0.0000	1.0000	0.0000	0.0000

312

**IN THE UNITED STATES DESIGNATED/ELECTED OFFICE**

International Application No. : PCT/DE99/01174  
International Filing Date : 15 April 1999  
Priority Date(s) Claimed : 17 April 1998  
Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.  
Title: HUMAN NUCLEIC ACID SEQUENCES FROM ENDOMETRIAL TUMOR TISSUE

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend this application as follows:

**IN THE CLAIMS:**

Claims 5 and 6, line 1: Change "claims 1 to 4" to -- claim 3 --.

Claim 7: Please rewrite as follows:

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim[s 1 to 6]3, in such a sufficient amount that they hybridize with the sequences [according to claims 1 to 6] of claim 3 or a sequence having 90% homology thereto.

Claims 8 and 9, line 1: Change "claims 1 to 7" to -- claim 3 --.

Claim 10, lines 1 and 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 11, line 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 13, lines 1 and 2: Change "claims 11 and 12" to -- claim 11 --.

Claim 14, lines 1 and 2: Change "claims 1 to 10" to -- claim 3 --.

Claim 16, line 3: Change "claims 1 to 10" to -- claim 3 --.

Claim 18, line 1: Change "claims 16 or 17" to -- claim 16 --.

Claim 19, line 2: Change "claims 16 to 18" to -- claim 16 --.

Claim 27, line 3: After "630-635" insert -- of claim 23 --.

Claim 28, line 3: After "555" insert -- of claim 3 --.  
Claim 29, line 2: After "555" insert -- of claim 3 --.  
Claims 30 and 31, line 2: After "630-635" insert -- of claim 23 --.  
Claim 32, line 3: After "630-635" insert -- of claim 23 --.  
Claims 33 and 34, line 1: Change "claims 1 to 10" to -- claim 3 --.  
Claim 35 line 4: After "555" insert -- of claim 3 --.  
Claim 38, line 1: Change "claims 1 to 7" to -- claim 3 --.

### Remarks

The purpose of this Preliminary Amendment is to eliminate multiple and improper multiple dependent claims to avoid additional fees. Applicants reserve the right to reintroduce claims directed to canceled combined subject matter.

Respectfully submitted,

  
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PCT/DE99/01174

### Human Nucleic Acid Sequences from Endometrial Tumor Tissue

The invention relates to human nucleic acid sequences from endometrial tumors, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer in women is the endometrial tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

09 OCT 2000 09:54:36



Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which play a role as candidate genes in endometrial tumors, have now been found.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-126 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which are expressed elevated in the endometrial tumor.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic,



Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The expression cassettes are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of ORF ID Nos. 142-528 and Seq. ID Nos. ORF 561-575, 577-625, and 630-635 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 according to the invention can also be used as tools for finding active ingredients against endometrial tumors, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 for expression of polypeptides, which can be used as tools for finding active ingredients against endometrial tumors.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 142-528 and Seq. ID Nos. 561-575, 577-625, and 630-635 as pharmaceutical agents in the gene therapy for treatment of uterus tumors or for the production of a pharmaceutical agent for treatment of uterus tumors.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-141 and Seq. ID Nos. 531-552, 554, and 555, genomic BAC, PAC and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq.



## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

### Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

#### **Example 1**

##### **Search for Tumor-related Candidate Genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.



Figures 2b1-2b4 illustrate the lengthening of the uterus tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

### Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern

## 2.1. Electronic Northern Blot

### 2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 136 was found, which occurs 15.6 x more strongly in the endometrial tumor than in normal tissue.

Electronic Northern for SEQ. ID NO.: 136

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
	Breast 0.0068
0.0139	Ovary_n 0.0000
0.0056	Ovary_t 0.0000
0.0000	Endocrine tissue 0.0000
0.0079	Fetal 0.0076
0.0000	Gastrointestinal 0.0000
0.0000	Hematopoietic 0.0171
0.0142	Skin-muscle 0.0000
0.0108	Testicles 0.0164
0.0254	Lung 0.0060
0.0000	Nerves 0.0068
0.0061	Prostate 0.0000
0.0000	Sensory Organs 0.0125
0.0126	Uterus_n

Electronic Northern for SEQ. ID NO.: 1

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0077
Lung	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory Organs	0.0077
Uterus_n	0.0042

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.3166	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast				
Small intestine	0.0078	0.0281	0.2774	3.6055
Ovary	0.0090	0.0198	0.4764	2.0992
Endocrine tissue	0.0031	0.0000	undef	0.0000
Gastrointestinal	0.0030	0.0052	0.5756	1.7372
Brain	0.0085	0.0176	0.4852	2.0611
Hematopoietic	0.0019	0.0093	0.2071	4.8289
Skin	0.0118	0.0123	0.9599	1.0417
Hepatic	0.0027	0.0000	undef	0.0000
Heart	0.0073	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0058	0.0117	0.4920	2.0326
Muscle-skeleton	0.0073	0.0020	3.5562	0.2812
Kidney	0.0097	0.0153	0.6303	1.5866
Pancreas	0.0034	0.0240	0.1428	7.0040
Penis	0.0136	0.0274	0.4956	2.0176
Prostate	0.0050	0.0000	undef	0.0000
Uterus-endometrium	0.0090	0.0000	undef	0.0000
Uterus-myometrium	0.0109	0.0149	0.7312	1.3677
Uterus-general	0.0068	0.1583	0.0427	23.4317
Breast hyperplasia	0.0076	0.0272	0.2806	3.5642
Prostate hyperplasia	0.0102	0.0000	undef	0.0000
Seminal vesicle	0.0160			
Sensory organs	0.0119			
White blood cells	0.0178			
Cervix	0.0000			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0278	Breast	0.0272
Gastrointestinal	0.0194	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0114
Lung	0.0145	Skin-muscle	0.0194
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0124	Lung	0.0164
Placenta	0.0121	Nerves	0.0120
Prostate	0.0249	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

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## Electronic Northern for SEQ. ID NO.: 4

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0039	0.0000	undef	0.0000
Ovary	0.0026	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0165	0.0000	undef
Gastrointestinal	0.0030	0.0000	undef	0.0000
Brain	0.0017	0.0000	undef	0.0000
Hematopoietic	0.0077	0.0000	undef	0.0000
Skin	0.0015	0.0021	0.7200	1.3890
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0021	0.0020	1.0161	0.9842
Muscle-skeleton	0.0193	0.0077	2.5211	0.3967
Kidney	0.0000	0.0060	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0213			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 5

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0039	0.0026	1.5254	0.6555
Ovary	0.0038	0.0038	1.0208	0.9796
Endocrine tissue	0.0031	0.0000	undef	0.0000
Gastrointestinal	0.0060	0.0000	undef	0.0000
Brain	0.0000	0.0025	0.0000	undef
Hematopoietic	0.0000	0.0093	0.0000	undef
Skin	0.0015	0.0021	0.7200	1.3890
Hepatic	0.0053	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0053	0.0137	0.3855	2.5941
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0193	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0017	0.0055	0.2991	3.3428
Uterus-endometrium	0.0060	0.0267	0.2246	4.4517
Uterus-myometrium	0.0065	0.0021	3.0709	0.3256
Uterus-general	0.0135	0.1055	0.1280	7.8106
Breast hyperplasia	0.0000	0.0068	0.0000	undef
Prostate hyperplasia	0.0051	0.0000	undef	0.0000
Seminal vesicle	0.0096			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0078			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0759
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 6					
	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T	T/N	
Bladder					
Breast	0.0156	0.0077	2.0339	0.4917	
Small intestine	0.0051	0.0075	0.6805	1.4694	
Ovary	0.0123	0.0331	0.3707	2.6973	
Endocrine tissue	0.0120	0.0104	1.1513	0.8686	
Gastrointestinal	0.0085	0.0075	1.1321	0.8833	
Brain	0.0096	0.0278	0.3451	2.8974	
Hematopoietic	0.0133	0.0164	0.8100	1.2346	
Skin	0.0120	0.0000	undef	0.0000	
Hepatic	0.0073	0.0000	undef	0.0000	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0170	0.0000	undef	0.0000	
Lung	0.0058	0.0117	0.4920	2.0326	
Stomach-esophagus	0.0197	0.0164	1.2066	0.8288	
Muscle-skeleton	0.0193	0.0000	undef	0.0000	
Kidney	0.0034	0.0180	0.1904	5.2530	
Pancreas	0.0054	0.0274	0.1983	5.0439	
Penis	0.0066	0.0055	1.1966	0.8357	
Prostate	0.0240	0.0267	0.8985	1.1129	
Uterus-endometrium	0.0044	0.0192	0.2275	4.3961	
Uterus-myometrium	0.0000	0.1055	0.0000	undef	
Uterus-general	0.0229	0.0272	0.8417	1.1881	
Breast hyperplasia	0.0102	0.0000	undef	0.0000	
Prostate hyperplasia	0.0192				
Seminal vesicle	0.0059				
Sensory organs	0.0089				
White blood cells	0.0000				
Cervix	0.0104				
	0.0106				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0250	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0354
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0245
Hepatic	0.0260	Gastrointestinal	0.0244
Heart-blood vessels	0.0178	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0551
Suprarenal gland	0.0000	Testicles	0.0386
Kidney	0.0000	Lung	0.0082
Placenta	0.0121	Nerves	0.0181
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 7

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0026	0.0019	1.3611 0.7347	
Endocrine tissue	0.0061	0.0000	undef 0.0000	
Gastrointestinal	0.0060	0.0026	2.3025 0.4343	
Brain	0.0051	0.0000	undef 0.0000	
Hematopoietic	0.0096	0.0139	0.6903 1.4487	
Skin	0.0037	0.0092	0.4000 2.5001	
Hepatic	0.0013	0.0000	undef 0.0000	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0042	0.0000	undef 0.0000	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0042	0.0041	1.0161 0.9842	
Kidney	0.0097	0.0153	0.6303 1.5866	
Pancreas	0.0000	0.0120	0.0000 undef	
Penis	0.0027	0.0000	undef 0.0000	
Prostate	0.0017	0.0000	undef 0.0000	
Uterus-endometrium	0.0150	0.0000	undef 0.0000	
Uterus-myometrium	0.0087	0.0043	2.0473 0.4885	
Uterus-general	0.0068	0.1055	0.0640 15.6211	
Breast hyperplasia	0.0076	0.0000	undef 0.0000	
Prostate hyperplasia	0.0000	0.0000	undef undef	
Seminal vesicle	0.0032			
Sensory organs	0.0000			
White blood cells	0.0089			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0000  
Gastrointestinal 0.0000  
Brain 0.0000  
Hematopoietic 0.0000  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0036  
Lung 0.0000  
Suprarenal gland 0.0000  
Kidney 0.0062  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0126

Breast 0.0000  
Ovary\_n 0.1595  
Ovary\_t 0.0000  
Endocrine tissue 0.0000  
Fetal 0.0082  
Gastrointestinal 0.0000  
Hematopoietic 0.0097  
Skin-muscle 0.0000  
Testicles 0.0000  
Lung 0.0000  
Nerves 0.0000  
Prostate 0.0155  
Sensory Organs 0.0000  
Uterus\_n

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Electronic Northern for SEQ. ID NO.: 8

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0000	0.0019	0.0000	undef
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0000	0.0021	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0019	0.0000	undef	0.0000	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.1055	0.0000	undef	
Uterus-endometrium	0.0000	0.0000	undef	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000				
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0090	0.0188	0.4764	2.0992
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0000	0.0000	undef	undef
Prostate	0.0131	0.0213	0.6142	1.6282
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0342
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

## Electronic Northern for SEQ. ID NO.: 12

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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NORMAL

## Ratios

N/T

T/N

FETUS  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus n	0.0250



Electronic Northern for SEQ. ID NO.: 14				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 15				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0153	0.0188	0.8166	1.2245
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0182	0.4934	2.0268
Endocrine tissue	0.0187	0.0100	1.8679	0.5354
Gastrointestinal	0.0192	0.0324	0.5917	1.6901
Brain	0.0067	0.0205	0.3240	3.0866
Hematopoietic	0.0147	0.0379	0.3882	2.5762
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0143	0.0323	0.4412	2.2666
Heart	0.0148	0.0275	0.5397	1.8529
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0156	0.0102	1.5241	0.6561
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0154	0.0120	1.2850	0.7782
Kidney	0.0407	0.0068	5.9478	0.1681
Pancreas	0.0132	0.0110	1.1966	0.8357
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0153	0.0085	1.7913	0.5582
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0353			
White blood cells	0.0165			
Cervix	0.0319			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0476
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.1114
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0393	Fetal	0.0175
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0292
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0124	Nerves	0.0020
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0249	Sensory Organs	0.0310
	0.0000	Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 17

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0111	0.0031	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0100
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0208
		Uterus n	

Electronic Northern for SEQ. ID NO.: 18

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0078	0.0256	0.3051	3.2777
Small intestine	0.0090	0.0113	0.7939	1.2595
Ovary	0.0092	0.0000	undef	0.0000
Endocrine tissue	0.0090	0.0286	0.3140	3.1849
Gastrointestinal	0.0255	0.0050	5.0944	0.1963
Brain	0.0096	0.0185	0.5177	1.9316
Hematopoietic	0.0044	0.0082	0.5400	1.8520
Skin	0.0134	0.0379	0.3529	2.8338
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0285	0.0194	1.4706	0.6800
Testicles	0.0042	0.0275	0.1542	6.4853
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0083	0.0184	0.4516	2.2144
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0060	0.0000	undef
Pancreas	0.0109	0.0274	0.3965	2.5219
Penis	0.0017	0.0110	0.1496	6.6857
Prostate	0.0060	0.0533	0.1123	8.9035
Uterus-endometrium	0.0262	0.0192	1.3648	0.7327
Uterus-myometrium	0.0068	0.1583	0.0427	23.4317
Uterus-general	0.0000	0.0068	0.0000	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0297			
Sensory organs	0.0356			
White blood cells	0.0000			
Cervix	0.0113			
	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
		LIBRARIES	
	% frequency		% frequency
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0152
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0107	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0389
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0124	Lung	0.0000
Placenta	0.0182	Nerves	0.0080
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0458

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## Electronic Northern for SEQ. ID NO.: 19

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0102	1.9068	0.5244
Breast	0.0115	0.0132	0.8750	1.1429
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0119	0.0125	0.9509	1.0516
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0096	0.0041	2.3399	0.4274
Hematopoietic	0.0080	0.0379	0.2117	4.7230
Skin	0.0330	0.2542	0.1300	7.6946
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0127	0.0000	undef	0.0000
Testicles	0.0115	0.0468	0.2460	4.0652
Lung	0.0052	0.0082	0.6350	1.5747
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0087	0.0106	0.8189	1.2211
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0458	0.0000	undef	0.0000
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0353			
White blood cells	0.0113			
Cervix	0.0000			

		FETUS	STANDARDIZED/SUBTRACTED
		% frequency	LIBRARIES
			% frequency
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 20

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.2111	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000		undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 21

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 22

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0128	0.0000	undef
Breast	0.0051	0.0075	0.6805	1.4694
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0104	0.5756	1.7372
Endocrine tissue	0.0102	0.0125	0.8151	1.2268
Gastrointestinal	0.0172	0.0093	1.8638	0.5363
Brain	0.0052	0.0010	5.0397	0.1994
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0201	0.0412	0.4893	2.0480
Testicles	0.0288	0.0234	1.2299	0.8130
Lung	0.0114	0.0184	0.6209	1.6105
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0086	0.0180	0.4759	2.1012
Kidney	0.0217	0.0000	undef	0.0000
Pancreas	0.0149	0.0221	0.6731	1.4857
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0065	0.0170	0.3839	2.6051
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0130			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0030
Prostate	0.0249	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

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## Electronic Northern for SEQ. ID NO.: 23

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0078	0.0026	3.0509	0.3278
Small intestine	0.0026	0.0000	undef	0.0000
Ovary	0.0184	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0007	0.0041	0.1800	5.5559
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0032	0.0137	0.2313	4.3235
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0021	0.0020	1.0161	0.9842
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0000	0.0060	0.0000	undef
Pancreas	0.0000	0.0205	0.0000	undef
Penis	0.0066	0.0055	1.1966	0.8357
Prostate	0.0120	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.1055	0.0000	0.0000	undef
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0106			

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0154
Lung	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 24

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0077	0.0000	undef
Small intestine	0.0064	0.0019	3.4026	0.2939
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0025	2.7170	0.3681
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0118	0.0031	3.8398	0.2604
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0109	0.0000	undef	0.0000
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0085	0.5118	1.9538
Uterus-myometrium	0.0000	0.1583	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0080
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 25

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0064	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0026	1.1513	0.8686
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0041	0.0000	undef
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0051	0.0000	undef	0.0000
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 26

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0038	0.0185	0.2071	4.8289
Brain	0.0037	0.0031	1.1999	0.8334
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0062	0.0041	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0136	0.0068	1.9826	0.5044
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0954	0.1067	9.3678
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0140
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0680
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0070
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0019	0.0000	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0030	0.0026	1.1513	0.8686	
Endocrine tissue	0.0000	0.0125	0.0000	undef	
Gastrointestinal	0.0019	0.0000	undef	0.0000	
Brain	0.0059	0.0041	1.4399	0.6945	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0037	0.0000	undef	0.0000	
Hepatic	0.0000	0.0065	0.0000	undef	
Heart	0.0011	0.0000	undef	0.0000	
Testicles	0.0058	0.0000	undef	0.0000	
Lung	0.0010	0.0020	0.5080	1.9684	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0030	0.0000	undef	0.0000	
Prostate	0.0044	0.0000	undef	0.0000	
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211	
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0032				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0118				
Sensory organs	0.0009				
White blood cells	0.0000				
Cervix					

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0139	Breast 0.0204
Gastrointestinal	0.0000	Ovary_n 0.0000
Brain	0.0000	Ovary_t 0.0051
Hematopoietic	0.0000	Endocrine tissue 0.0000
Skin	0.0000	Fetal 0.0064
Hepatic	0.0000	Gastrointestinal 0.0000
Heart-blood vessels	0.0036	Hematopoietic 0.0000
Lung	0.0000	Skin-muscle 0.0032
Suprarenal gland	0.0000	Testicles 0.0000
Kidney	0.0000	Lung 0.0000
Placenta	0.0000	Nerves 0.0020
Prostate	0.0000	Prostate 0.0000
Sensory organs	0.0000	Sensory Organs 0.0232
		Uterus n 0.0083

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0051	0.0000	undef
Small intestine	0.0153	0.0094	1.6333	0.6123
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0130	0.2303	4.3431
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0030	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0184	0.0000	undef	0.0000
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0020	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0060	1.4278	0.7004
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0105
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0520	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0060
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus n	

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0128	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0061	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0085	0.2559	3.9077
Uterus-endometrium	0.0000	0.1035	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0096	0.0000	undef	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0013	0.0056	0.2268	4.4083
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0078	0.0000	undef
Gastrointestinal	0.0017	0.0050	0.3396	2.9444
Brain	0.0038	0.0046	0.8283	1.2072
Hematopoietic	0.0037	0.0041	0.8999	1.1112
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0034	0.0060	0.5711	1.7510
Pancreas	0.0027	0.0137	0.1983	5.0439
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0000	0.0267	0.0000	undef
Uterus-endometrium	0.0022	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0224			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0035			
	0.0000			

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0077
Lung	0.0082
Nerves	0.0010
Prostate	0.0068
Sensory Organs	0.0000
Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 32

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0000	0.0038	0.0000 undef	
Endocrine tissue	0.0031	0.0000	undef 0.0000	
Gastrointestinal	0.0000	0.0000	undef undef	
Brain	0.0068	0.0050	1.3585 0.7361	
Hematopoietic	0.0038	0.0000	undef 0.0000	
Skin	0.0022	0.0041	0.5400 1.8520	
Hepatic	0.0027	0.0000	undef 0.0000	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0048	0.0129	0.3676 2.7200	
Lung	0.0032	0.0000	undef 0.0000	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0000	0.0020	0.0000 undef	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0054	0.0110	0.0000 undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0022	0.0043	0.5118 1.9538	
Uterus-myometrium	0.0068	0.1055	0.0640 15.6211	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0000	0.0000	undef undef	
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 33

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.2639	0.0256	39.0528
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 34

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0010	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 35

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0026	0.0038	0.6805	1.4694
Ovary	0.0000	0.0163	0.0000	undef
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0034	0.0000	undef	0.0000
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0021	0.3600	2.7779
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0082	0.1270	7.8735
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0081	0.0479	0.1699	5.8845
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.2639	0.0256	39.0528
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0052			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0340
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 36

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 37

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0010	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 39

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0404	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0020	3.5562	0.2812
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0269	0.1066	0.2527	3.9571
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 40

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0000	0.0019	0.0000	undef
Ovary	0.0184	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0156	0.1919	5.2117
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0096	0.0231	0.4142	2.4145
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 41

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0057
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

002227 5662960

Electronic Northern for SEQ. ID NO.: 42

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0051	0.0113	0.4537	2.2042
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0136	0.0251	0.5434	1.8403
Gastrointestinal	0.0153	0.0185	0.8283	1.2072
Brain	0.0118	0.0041	2.8798	0.3472
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0064	0.0275	0.2313	4.3235
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0187	0.0164	1.1431	0.8748
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0081	0.0205	0.3965	2.5219
Pancreas	0.0182	0.0055	3.2906	0.3039
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0131	0.0213	0.6142	1.6282
Uterus-endometrium	0.0135	0.1583	0.0854	11.7158
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0192		undef	undef
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0199			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0399
Lung	0.0072	Skin-muscle	0.0454
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0000	Lung	0.0082
Placenta	0.0182	Nerves	0.0301
Prostate	0.0499	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0167

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Electronic Northern for SEQ. ID NO.: 43

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0102	1.1441	0.8741
Small intestine	0.0102	0.0226	0.4537	2.2042
Ovary	0.0123	0.0165	0.7415	1.3487
Endocrine tissue	0.0030	0.0078	0.3838	2.6058
Gastrointestinal	0.0136	0.0150	0.9057	1.1042
Brain	0.0153	0.0046	3.3134	0.3018
Hematopoietic	0.0074	0.0103	0.7200	1.3890
Skin	0.0053	0.0379	0.1412	7.0845
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0143	0.0129	1.1029	0.9067
Testicles	0.0074	0.0137	0.5397	1.8529
Lung	0.0173	0.0000	undef	0.0000
Stomach-esophagus	0.0125	0.0164	0.7621	1.3122
Muscle-skeleton	0.0097	0.0153	0.6303	1.5866
Kidney	0.0154	0.0060	2.5700	0.3891
Pancreas	0.0109	0.0137	0.7930	1.2610
Penis	0.0083	0.0276	0.2991	3.3428
Prostate	0.0150	0.0533	0.2808	3.5614
Uterus-endometrium	0.0196	0.0149	1.3161	0.7598
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0136	0.0000	undef
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0208			
Sensory organs	0.0178			
White blood cells	0.0706			
Cervix	0.0251			
	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0272
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0557
Hematopoietic	0.0118	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0402
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0000	Hematopoietic	0.0342
Lung	0.0217	Skin-muscle	0.0486
Suprarenal gland	0.0254	Testicles	0.0309
Kidney	0.0185	Lung	0.0328
Placenta	0.0303	Nerves	0.0100
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0310
		Uterus_n	0.0291

0022T 562260

Electronic Northern for SEQ. ID NO.: 44

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00221-3664950

Electronic Northern for SEQ. ID NO.: 45

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0094	0.1361	7.3472
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0052	0.0062	0.8400	1.1905
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0412	0.1285	7.7824
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0087	0.0085	1.0236	0.9769
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0152	0.0204	0.7482	1.3366
Uterus-general	0.0032	0.0000	undef	0.0000
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0182	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

0022T "S6E2350



	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS		STANDARDIZED/SUBTRACTED
	% frequency		LIBRARIES
			% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 47

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0015	0.0010	1.4399	0.6945
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004227 362360

Electronic Northern for SEQ. ID NO.: 48

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.2111	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00221 3662360



Electronic Northern for SEQ. ID NO.: 50

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00021" 55664360

Electronic Northern for SEQ. ID NO.: 51

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1383	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00227 5624960

Electronic Northern for SEQ. ID NO.: 52

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0044	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0006
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

0022T 5662360





Electronic Northern for SEQ. ID NO.: 54

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	

004227 3622960

Electronic Northern for SEQ. ID NO.: 55

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0019	0.6805	1.4694
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0026	2.3025	0.4343
Gastrointestinal	0.0017	0.0050	0.3396	2.9444
Brain	0.0057	0.0093	0.6213	1.6096
Hematopoietic	0.0022	0.0041	0.5400	1.8520
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0054	0.0068	0.7930	1.2610
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0087	0.0000	undef	0.0000
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 56

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0128	0.9153	1.0926
Small intestine	0.0051	0.0132	0.3889	2.5715
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0102	0.0125	0.8151	1.2268
Brain	0.0134	0.0046	2.8992	0.3449
Hematopoietic	0.0103	0.0113	0.9163	1.0913
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0194	0.0000	undef
Testicles	0.0085	0.0000	undef	0.0000
Lung	0.0173	0.0234	0.7380	1.3551
Stomach-esophagus	0.0145	0.0123	1.1854	0.8436
Muscle-skeleton	0.0097	0.0077	1.2605	0.7933
Kidney	0.0069	0.0000	undef	0.0000
Pancreas	0.0190	0.0000	undef	0.0000
Penis	0.0050	0.0055	0.8974	1.1143
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0085	0.2559	3.9077
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0030			
Sensory organs	0.0178			
White blood cells	0.0000			
Cervix	0.0052			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0260	Gastrointestinal	0.0366
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 57

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0038	0.0075	0.5104	1.9593
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0185	0.4142	2.4145
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0085	1.2795	0.7815
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.1908	0.0000	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0068
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

000227 366260

## Electronic Northern for SEQ. ID NO.: 58

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 59

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0281	0.0226	1.2476	0.8015
Small intestine	0.0307	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0083	0.0000	undef	0.0000
Gastrointestinal	0.0153	0.0324	0.4733	2.1127
Brain	0.0044	0.0072	0.6171	1.6205
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0061	0.0000	undef
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0154	0.0180	0.8567	1.1673
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0000	0.0166	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0128	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0476
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0181	Testicles	0.0000
Kidney	0.0254	Lung	0.0082
Placenta	0.0000	Nerves	0.0050
Prostate	0.0303	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

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Electronic Northern for SEQ. ID NO.: 60

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0102	1.5254	0.6555
Breast	0.0115	0.0207	0.5568	1.7960
Small intestine	0.0215	0.0165	1.2976	0.7707
Ovary	0.0240	0.0260	0.9210	1.0858
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0172	0.0139	1.2425	0.8048
Brain	0.0170	0.0246	0.6900	1.4494
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0238	0.0194	1.2255	0.8160
Heart	0.0180	0.0275	0.6553	1.5260
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0156	0.0164	0.9526	1.0498
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0081	0.0411	0.1983	5.0439
Pancreas	0.0116	0.0055	2.0940	0.4775
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0131	0.0043	3.0709	0.3256
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0426			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0151
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0213	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0246
Placenta	0.0061	Nerves	0.0211
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0125

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 63

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0051	1.5254	0.6555
Small intestine	0.0038	0.0094	0.4083	2.4491
Ovary	0.0031	0.0331	0.0927	10.7893
Endocrine tissue	0.0150	0.0208	0.7195	1.3898
Gastrointestinal	0.0136	0.0100	1.3585	0.7361
Brain	0.0230	0.0046	4.9700	0.2012
Hematopoietic	0.0096	0.0082	1.1699	0.8547
Skin	0.0094	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0053	0.0000	undef	0.0000
Lung	0.0173	0.0000	undef	0.0000
Stomach-esophagus	0.0052	0.0041	1.2701	0.7873
Muscle-skeleton	0.0387	0.0077	5.0421	0.1983
Kidney	0.0051	0.0120	0.4283	2.3347
Pancreas	0.0081	0.0274	0.2974	3.3626
Penis	0.0083	0.0110	0.7479	1.3371
Prostate	0.0150	0.0267	0.5616	1.7807
Uterus-endometrium	0.0044	0.0043	1.0236	0.9769
Uterus-myometrium	0.0068	0.2111	0.0320	31.2422
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0256			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0235			
Cervix	0.0061			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0278	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0236	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0356	Hematopoietic	0.0228
Lung	0.0289	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0124	Lung	0.0000
Placenta	0.0000	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0628	Sensory Organs	0.0000
		Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 64

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0000  
Gastrointestinal 0.0000  
Brain 0.0000  
Hematopoietic 0.0000  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0000  
Lung 0.0000  
Suprarenal gland 0.0000  
Kidney 0.0000  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0000

Breast 0.0000  
Ovary\_n 0.0000  
Ovary\_t 0.0000  
Endocrine tissue 0.0000  
Fetal 0.0000  
Gastrointestinal 0.0000  
Hematopoietic 0.0000  
Skin-muscle 0.0000  
Testicles 0.0000  
Lung 0.0000  
Nerves 0.0000  
Prostate 0.0000  
Sensory Organs 0.0000  
Uterus\_n 0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0019	0.0000	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0007	0.0000	undef	0.0000	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0244	0.0137	1.7843	0.5604	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.1055	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 67

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0038	0.0188	0.2042	4.8982
Small intestine	0.0153	0.0331	0.4634	2.1579
Ovary	0.0120	0.0208	0.5756	1.7372
Endocrine tissue	0.0136	0.0125	1.0868	0.9201
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0052	0.0041	1.2599	0.7937
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0847	0.0000	undef
Hepatic	0.0095	0.0194	0.4902	2.0400
Heart	0.0307	0.0275	1.1179	0.8945
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0042	0.0286	0.1452	6.8893
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0120	0.4283	2.3347
Kidney	0.0054	0.0137	0.3965	2.5219
Pancreas	0.0116	0.0110	1.0470	0.9551
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4423
Uterus-endometrium	0.0135	0.1583	0.0854	11.7158
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0102	0.1908	0.0534	18.7357
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
Sensory organs	0.0130			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0557	Breast	0.0000
Gastrointestinal	0.0194	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0105
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0421
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0000	Lung	0.0082
Placenta	0.0061	Nerves	0.0030
Prostate	0.0748	Prostate	0.0137
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0083

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1053	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	



Electronic Northern for SEQ. ID NO.: 70		NORMAL		TUMOR		Ratios	
	% frequency	% frequency	% frequency	N/T	T/N		
Bladder							
Breast	0.0000	0.0000		undef	undef		
Small intestine	0.0000	0.0019	0.0000	undef	undef		
Ovary	0.0000	0.0000		undef	undef		
Endocrine tissue	0.0000	0.0000		undef	undef		
Gastrointestinal	0.0000	0.0000		undef	undef		
Brain	0.0000	0.0000		undef	undef		
Hematopoietic	0.0000	0.0000		undef	undef		
Skin	0.0000	0.0000		undef	undef		
Hepatic	0.0000	0.0000		undef	undef		
Heart	0.0000	0.0000		undef	undef		
Testicles	0.0000	0.0000		undef	undef		
Lung	0.0000	0.0000		undef	undef		
Stomach-esophagus	0.0000	0.0000		undef	undef		
Muscle-skeleton	0.0000	0.0000		undef	undef		
Kidney	0.0000	0.0000		undef	undef		
Pancreas	0.0000	0.0000		undef	undef		
Penis	0.0000	0.0000		undef	undef		
Prostate	0.0000	0.0000		undef	undef		
Uterus-endometrium	0.0000	0.1055	0.0000	undef	undef		
Uterus-myometrium	0.0000	0.0000		undef	undef		
Uterus-general	0.0000	0.0000		undef	undef		
Breast hyperplasia	0.0000						
Prostate hyperplasia	0.0000						
Seminal vesicle	0.0000						
Sensory organs	0.0000						
White blood cells	0.0000						
Cervix							

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 71				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0230	0.0000	undef
Breast	0.0051	0.0056	0.9074	1.1021
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0060	0.0182	0.3289	3.0402
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0728	0.0185	3.9346	0.2542
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8628	0.5368
Stomach-esophagus	0.0387	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0106	0.6142	1.6282
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0608
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0062	Nerves	0.0000
Prostate	0.0061	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 72		Ratios		
	NORMAL	TUMOR		
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0309	Lung	0.0000
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0125

## Electronic Northern for SEQ. ID NO.: 73

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0021	0.0061	0.3387	2.9526
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0043	0.0000	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0010
Nerves	0.0137
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 74

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0051	1.5254	0.6355
Breast	0.0051	0.0075	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0119	0.0125	0.9509	1.0516
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0059	0.0051	1.1519	0.8681
Hematopoietic	0.0187	0.0379	0.4940	2.0241
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0073	0.0041	1.7781	0.5624
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0124	Lung	0.0246
Placenta	0.0061	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 75

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0078	1.1513	0.8686
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0019	0.0231	0.0828	12.0723
Brain	0.0089	0.0031	2.8798	0.3472
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0061	0.5080	1.9684
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0060
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.2111	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 77					
	NORMAL	TUMOR	Ratios		
	% frequency	% frequency	N/T	T/N	
Bladder	0.0000	0.0000	undef	undef	
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0000	0.0000	undef	undef	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0000	0.1055	0.0000	undef	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 78

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0213			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00221"5662360

Electronic Northern for SEQ. ID NO.: 79

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0278	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

00421" 56E4960

Electronic Northern for SEQ. ID NO.: 80				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0068
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 81

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004227 5622960

Electronic Northern for SEQ. ID NO.: 82

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0077	0.0150	0.5104	1.9593
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0208	0.4317	2.3163
Endocrine tissue	0.0068	0.0150	0.4528	2.2083
Gastrointestinal	0.0268	0.0231	1.1597	0.8623
Brain	0.0081	0.0123	0.6600	1.5152
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0011	0.0412	0.0257	38.9118
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0123	0.2540	3.9367
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0166	0.2991	3.3428
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0305	0.0554	0.5512	1.8143
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0253
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0507	Lung	0.0082
Placenta	0.0000	Nerves	0.0131
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

000221 55552950

Electronic Northern for SEQ. ID NO.: 83

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004227 5662960

Electronic Northern for SEQ. ID NO.: 84

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

0022T 55E4960

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency		% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 87		NORMAL		TUMOR		Ratios	
	% frequency	% frequency	% frequency	N/T	T/N		
Bladder	0.0039	0.0204	0.1907	5.2444			
Breast	0.0128	0.0075	1.7013	0.5878			
Small intestine	0.0123	0.0165	0.7415	1.3487			
Ovary	0.0030	0.0078	0.3838	2.6058			
Endocrine tissue	0.0000	0.0000	undef	undef			
Gastrointestinal	0.0038	0.0139	0.2761	3.6217			
Brain	0.0007	0.0000	undef	0.0000			
Hematopoietic	0.0000	0.0000	undef	undef			
Skin	0.0110	0.0000	undef	0.0000			
Hepatic	0.0000	0.0000	undef	undef			
Heart	0.0000	0.0000	undef	undef			
Testicles	0.0000	0.0000	undef	undef			
Lung	0.0031	0.0000	undef	0.0000			
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933			
Muscle-skeleton	0.0000	0.0000	undef	undef			
Kidney	0.0054	0.0000	undef	0.0000			
Pancreas	0.0050	0.0000	undef	0.0000			
Penis	0.0000	0.0000	undef	undef			
Prostate	0.0044	0.0149	0.2925	3.4192			
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211			
Uterus-myometrium	0.0000	0.0000	undef	undef			
Uterus-general	0.0000	0.0000	undef	undef			
Breast hyperplasia	0.0192						
Prostate hyperplasia	0.0089						
Seminal vesicle	0.0089						
Sensory organs	0.0000						
White blood cells	0.0000						
Cervix	0.0106						

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

FETUS  
% frequency

0.0000	Breast	0.0000
0.0000	Ovary_n	0.0000
0.0000	Ovary_t	0.0000
0.0000	Endocrine tissue	0.0000
0.0000	Fetal	0.0006
0.0000	Gastrointestinal	0.0000
0.0000	Hematopoietic	0.0114
0.0036	Skin-muscle	0.0032
0.0000	Testicles	0.0000
0.0000	Lung	0.0000
0.0000	Nerves	0.0000
0.0000	Prostate	0.0000
0.0000	Sensory Organs	0.0000
0.0000	Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 89

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1383	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0278	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00221 5664960

Electronic Northern for SEQ. ID NO.: 90

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1053	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

004221 5624960

Electronic Northern for SEQ. ID NO.: 91

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0090	0.0039	2.3818	0.4198
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0052	0.5756	1.7372
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0037	0.0021	1.7999	0.5556
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0110	0.0847	0.1300	7.6946
Heart	0.0095	0.0065	1.4706	0.6800
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0017	0.0166	0.0997	10.0285
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0050
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

004227 5622960

Electronic Northern for SEQ. ID NO.: 92

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

004221 5622990

Electronic Northern for SEQ. ID NO.: 93

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004221 5624960



Electronic Northern for SEQ. ID NO.: 94

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0000	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

004227 9632960

Electronic Northern for SEQ. ID NO.: 95				
	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

Electronic Northern for SEQ. ID NO.: 96

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

004227 562960

Electronic Northern for SEQ. ID NO.: 97

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

004227 5662950

Electronic Northern for SEQ. ID NO.: 98

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0330	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0533	0.0000	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

0022T 00000000

Electronic Northern for SEQ. ID NO.: 99

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

004221 5664960

## Electronic Northern for SEQ. ID NO.: 100

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00421"5622960

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	



	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

Electronic Northern for SEQ. ID NO.: 103

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0064	0.0000	undef	0.0000
Ovary	0.0000	0.0165	0.0000	undef
Endocrine tissue	0.0000	0.0078	0.0000	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0015	0.0021	0.7200	1.3890
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0041	0.2540	3.9367
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

## Electronic Northern for SEQ. ID NO.: 105

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0090	0.0038	2.3818	0.4198
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0052	0.5756	1.7372
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0037	0.0021	1.7999	0.5556
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0110	0.0847	0.1300	7.6946
Heart	0.0095	0.0065	1.4706	0.6800
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0017	0.0166	0.0997	10.0285
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0050
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

004227 5555 12200

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	

	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder					
Breast	0.0000	0.0000	undef	undef	
Small intestine	0.0000	0.0000	undef	undef	
Ovary	0.0000	0.0000	undef	undef	
Endocrine tissue	0.0030	0.0000	undef	0.0000	
Gastrointestinal	0.0000	0.0000	undef	undef	
Brain	0.0000	0.0000	undef	undef	
Hematopoietic	0.0000	0.0000	undef	undef	
Skin	0.0000	0.0000	undef	undef	
Hepatic	0.0000	0.0000	undef	undef	
Heart	0.0000	0.0000	undef	undef	
Testicles	0.0000	0.0000	undef	undef	
Lung	0.0000	0.0000	undef	undef	
Stomach-esophagus	0.0000	0.0000	undef	undef	
Muscle-skeleton	0.0000	0.0000	undef	undef	
Kidney	0.0000	0.0000	undef	undef	
Pancreas	0.0000	0.0000	undef	undef	
Penis	0.0000	0.0000	undef	undef	
Prostate	0.0000	0.0000	undef	undef	
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211	
Uterus-myometrium	0.0000	0.0000	undef	undef	
Uterus-general	0.0000	0.0000	undef	undef	
Breast hyperplasia	0.0000				
Prostate hyperplasia	0.0000				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
White blood cells	0.0000				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 108

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0030
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0310
		Uterus_n	0.0042

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Electronic Northern for SEQ. ID NO.: 109

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

0022T 5624960



Electronic Northern for SEQ. ID NO.: 110

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

000227 3662360

Electronic Northern for SEQ. ID NO.: 111

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

00222 5552950

Electronic Northern for SEQ. ID NO.: 112

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0022	0.0010	2.1599	0.4630
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.1055	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

004221" 5666960

## Electronic Northern for SEQ. ID NO.: 113

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
0.0000	Breast	0.0136
0.0028	Ovary_n	0.0000
0.0000	Ovary_t	0.0000
0.0039	Endocrine tissue	0.0000
0.0000	Fetal	0.0052
0.0000	Gastrointestinal	0.0000
0.0036	Hematopoietic	0.0057
0.0036	Skin-muscle	0.0032
0.0000	Testicles	0.0077
0.0000	Lung	0.0164
0.0000	Nerves	0.0030
0.0249	Prostate	0.0000
0.0126	Sensory Organs	0.0310
	Uterus n	0.0042

004227 5622960

Electronic Northern for SEQ. ID NO.: 114

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0093	0.4142	2.4145
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0164	0.1905	5.2490
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0180	0.3807	2.6265
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0204	0.0000	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0087
Hepatic	0.0260	Gastrointestinal	0.0244
Heart-blood vessels	0.0107	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0356
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0010
Prostate	0.0000	Nerves	0.0000
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0250
		Uterus_n	

002221 "S6E2960

Electronic Northern for SEQ. ID NO.: 115

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

000221 5552360

Electronic Northern for SEQ. ID NO.: 116

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0128	0.0000	undef	0.0000
Ovary	0.0061	0.0165	0.3707	2.6973
Endocrine tissue	0.0060	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0050	1.3585	0.7361
Brain	0.0038	0.0046	0.8283	1.2072
Hematopoietic	0.0037	0.0051	0.7200	1.3890
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0042	0.0137	0.3084	3.2426
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0000	undef	0.0000
Pancreas	0.0054	0.0068	0.7930	1.2610
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0118			
Cervix	0.0061			
	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

00421 3624360

## Electronic Northern for SEQ. ID NO.: 117

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0038	0.0094	0.4083	2.4491
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0037	0.0000	undef	0.0000
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0021	0.0137	0.1542	6.4853
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0128	0.3412	2.9308
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0087			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

000227 5662360



Electronic Northern for SEQ. ID NO.: 118

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

002227 5552560

Electronic Northern for SEQ. ID NO.: 119

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0013	0.0038	0.3403	2.9389
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0052	0.0000	undef
Gastrointestinal	0.0034	0.0050	0.6792	1.4722
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0041	0.1800	5.5559
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0028
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0110
Prostate	0.0000
Sensory Organs	0.0155
Uterus_n	0.0000

0022T 5555450

## Electronic Northern for SEQ. ID NO.: 120

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0090	0.0075	1.1909	0.8397
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0068	0.0125	0.5434	1.8403
Gastrointestinal	0.0038	0.0093	0.4142	2.4145
Brain	0.0059	0.0031	1.9199	0.5209
Hematopoietic	0.0027	0.0758	0.0353	28.3379
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0043			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

00222T"56E2950

## Electronic Northern for SEQ. ID NO.: 121

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

004221 5622960

## Electronic Northern for SEQ. ID NO.: 122

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0230	1.0170	0.9833
Breast	0.0269	0.0207	1.2992	0.7697
Small intestine	0.0061	0.0662	0.0927	10.7893
Ovary	0.0150	0.0572	0.2616	3.8219
Endocrine tissue	0.0085	0.0100	0.8491	1.1778
Gastrointestinal	0.0134	0.0463	0.2899	3.4492
Brain	0.0015	0.0092	0.1600	6.2504
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0551	0.0000	undef	0.0000
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0073	0.0286	0.2540	3.9367
Stomach-esophagus	0.0966	0.0077	12.6053	0.0793
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0329	0.1600	0.2059	4.8565
Prostate	0.0087	0.0043	2.0473	0.4885
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0532			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0417	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0146
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0573
Placenta	0.0121	Nerves	0.0040
Prostate	0.0249	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

002221 5652360

Electronic Northern for SEQ. ID NO.: 123

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0007	0.0031	0.2400	4.1669
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00422T "S6E2960

Electronic Northern for SEQ. ID NO.: 124

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0062	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
	0.0126	Uterus_n	0.0042

0022T 56E4360

Electronic Northern for SEQ. ID NO.: 125

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0153	0.0226	0.6792	1.4722
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0081	0.0092	0.8800	1.1364
Hematopoietic	0.0067	0.0379	0.1764	5.6676
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0103	0.0180	0.5711	1.7510
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0329	0.0000	undef	0.0000
Prostate	0.0153	0.0064	2.3885	0.4187
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0069			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0121	Nerves	0.0060
Prostate	0.0249	Prostate	0.0342
Sensory organs	0.0000	Sensory Organs	0.0387
		Uterus_n	0.0250

000221 3664360



	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0021	0.0000	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0006
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 127

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0486	0.6423	1.5569
Breast	0.0192	0.0282	0.6805	1.4694
Small intestine	0.0399	0.0000	undef	0.0000
Ovary	0.0210	0.0364	0.5756	1.7372
Endocrine tissue	0.0290	0.0326	0.8882	1.1258
Gastrointestinal	0.0460	0.0231	1.9880	0.5030
Brain	0.0532	0.0575	0.9257	1.0803
Hematopoietic	0.0348	0.0379	0.9175	1.0899
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0048	0.0647	0.0735	13.5999
Heart	0.0699	0.0412	1.6961	0.5896
Testicles	0.0288	0.4210	0.0683	14.6349
Lung	0.0343	0.0368	0.9314	1.0737
Stomach-esophagus	0.0773	0.0230	3.3614	0.2975
Muscle-skeleton	0.0497	0.0660	0.7528	1.3283
Kidney	0.0353	0.1575	0.2241	4.4619
Pancreas	0.0165	0.0939	0.1760	5.6828
Penis	0.0299	0.0267	1.1232	0.8903
Prostate	0.0196	0.0298	0.6580	1.5197
Uterus-endometrium	0.0270	0.1583	0.1707	5.8579
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0890			
Sensory organs	0.0353			
White blood cells	0.0399			
Cervix	0.0319			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0417	Breast	0.0000
Gastrointestinal	0.0333	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0152
Hematopoietic	0.0197	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0783	Skin-muscle	0.0032
Suprarenal gland	0.0217	Testicles	0.0077
Kidney	0.0507	Lung	0.0082
Placenta	0.0309	Nerves	0.0141
Prostate	0.0727	Nerves	0.0000
Sensory organs	0.0997	Prostate	0.0310
	0.0000	Sensory Organs	0.0125
		Uterus_n	

00227 5632960

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0038	0.0000	undef	0.0000
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0025	2.7170	0.3681
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0007	0.0031	0.2400	4.1669
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0173	0.0117	1.4759	0.6775
Stomach-esophagus	0.0021	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0000	undef	0.0000
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0026			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0204
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0152
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0036	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0060
Prostate	0.0061	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus n	0.0042

Electronic Northern for SEQ. ID NO.: 129

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00421 5666360

Electronic Northern for SEQ. ID NO.: 130

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
% frequency		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00421 3622960

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0128	0.6102	1.6389
Small intestine	0.0115	0.0169	0.6805	1.4694
Ovary	0.0000	0.0165	0.0000	undef
Endocrine tissue	0.0060	0.0260	0.2303	4.3431
Gastrointestinal	0.0153	0.0176	0.8733	1.1451
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0074	0.0092	0.8000	1.2501
Skin	0.0080	0.0758	0.1059	9.4460
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0095	0.0065	1.4706	0.6800
Testicles	0.0201	0.0000	undef	0.0000
Lung	0.0058	0.0234	0.2460	4.0652
Stomach-esophagus	0.0114	0.0164	0.6985	1.4315
Muscle-skeleton	0.0193	0.0077	2.5211	0.3967
Kidney	0.0051	0.0120	0.4283	2.3347
Pancreas	0.0136	0.0137	0.9913	1.0088
Penis	0.0066	0.0110	0.5983	1.6714
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0065	0.0128	0.5118	1.9538
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0089			
Sensory organs	0.0089			
White blood cells	0.0118			
Cervix	0.0009			
	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0204
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0260	Hematopoietic	0.0057
Lung	0.0107	Skin-muscle	0.0259
Suprarenal gland	0.0108	Testicles	0.0077
Kidney	0.0000	Lung	0.0090
Placenta	0.0062	Nerves	0.0000
Prostate	0.0424	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 132

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0141	0.0150	0.9357	1.0687
Ovary	0.0194	0.0000	undef	0.0000
Endocrine tissue	0.0120	0.0104	1.1513	0.8686
Gastrointestinal	0.0102	0.0176	0.5822	1.7176
Brain	0.0057	0.0139	0.4142	2.4145
Hematopoietic	0.0052	0.0072	0.7200	1.3890
Skin	0.0174	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0064	0.0000	undef	0.0000
Lung	0.0058	0.0234	0.2460	4.0652
Stomach-esophagus	0.0104	0.0204	0.5080	1.9684
Muscle-skeleton	0.0193	0.0153	1.2605	0.7933
Kidney	0.0086	0.0240	0.3569	2.8016
Pancreas	0.0244	0.0000	undef	0.0000
Penis	0.0066	0.0110	0.5983	1.6714
Prostate	0.0120	0.0267	0.4493	2.2259
Uterus-endometrium	0.0153	0.0149	1.0236	0.9769
Uterus-myometrium	0.0270	0.2111	0.1280	7.8106
Uterus-general	0.0305	0.0136	2.2445	0.4455
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0192			
Seminal vesicle	0.0327			
Sensory organs	0.0178			
White blood cells	0.0235			
Cervix	0.0000			
	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0305	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0253
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0093
Hepatic	0.0520	Gastrointestinal	0.0122
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0253	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0246
Kidney	0.0309	Lung	0.0020
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus n	



Electronic Northern for SEQ. ID NO.: 134

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0273	0.0383	0.7119	1.4047
Small intestine	0.0141	0.0244	0.5758	1.7366
Ovary	0.0245	0.0331	0.7415	1.3487
Endocrine tissue	0.0120	0.0312	0.3838	2.6058
Gastrointestinal	0.0290	0.0201	1.4434	0.6928
Brain	0.0287	0.0278	1.0354	0.9658
Hematopoietic	0.0133	0.0298	0.4469	2.2378
Skin	0.0281	0.0379	0.7411	1.3494
Hepatic	0.0073	0.0847	0.0866	11.5419
Heart	0.0381	0.0259	1.4706	0.6800
Testicles	0.0191	0.1512	0.1262	7.9265
Lung	0.0173	0.0702	0.2460	4.0652
Stomach-esophagus	0.0447	0.0470	0.9498	1.0528
Muscle-skeleton	0.0773	0.0153	5.0421	0.1983
Kidney	0.0668	0.0420	1.5909	0.6286
Pancreas	0.0190	0.0342	0.5551	1.8014
Penis	0.0066	0.0331	0.1994	5.0142
Prostate	0.0150	0.1600	0.0936	10.6842
Uterus-endometrium	0.0196	0.0149	1.3161	0.7598
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0229	0.0204	1.1223	0.8911
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.1240			
	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0408
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0111	Ovary_t	0.0253
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0118	Fetal	0.0169
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0454
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0000
Prostate	0.0364	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0042

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T		T/N
Bladder					
Breast	0.0390	0.0383	1.0170	0.9833	
Small intestine	0.0102	0.0301	0.3403	2.9389	
Ovary	0.0429	0.0000	undef	0.0000	
Endocrine tissue	0.0030	0.0156	0.1919	5.2117	
Gastrointestinal	0.0358	0.0351	1.0189	0.9815	
Brain	0.0115	0.0278	0.4142	2.4145	
Hematopoietic	0.0148	0.0226	0.6545	1.5279	
Skin	0.0227	0.2273	0.1000	10.0016	
Hepatic	0.0367	0.1695	0.2166	4.6168	
Heart	0.0285	0.0582	0.4902	2.0400	
Testicles	0.0445	0.0687	0.6476	1.5441	
Lung	0.0173	0.0234	0.7380	1.3551	
Lung	0.0291	0.0470	0.6185	1.6169	
Stomach-esophagus	0.0580	0.0153	3.7816	0.2644	
Muscle-skeleton	0.0685	0.0840	0.8159	1.2257	
Kidney	0.0244	0.0685	0.3569	2.8022	
Pancreas	0.0116	0.0607	0.1904	5.2530	
Penis	0.0180	0.0000	undef	0.0000	
Prostate	0.0131	0.0064	2.0473	0.4885	
Uterus-endometrium	0.0135	0.6332	0.0213	46.8633	
Uterus-myometrium	0.0076	0.0408	0.1870	5.3463	
Uterus-general	0.0051	0.0000	undef	0.0000	
Breast hyperplasia	0.0128				
Prostate hyperplasia	0.0149				
Seminal vesicle	0.0000				
Sensory organs	0.0000				
Sensory organs	0.0867				
White blood cells	0.0639				
Cervix					

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0167	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0236	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0182	Nerves	0.0030
Prostate	0.0997	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0464
		Uterus_n	0.0000

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0102	0.0038	2.7221	0.3674
Ovary	0.0092	0.0165	0.5561	1.7982
Endocrine tissue	0.0090	0.0078	1.1513	0.8686
Gastrointestinal	0.0000	0.0150	0.0000	undef
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0059	0.0031	1.9199	0.5209
Skin	0.0040	0.0379	0.1059	9.4460
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0117	0.0000	undef
Lung	0.0114	0.0041	2.7942	0.3579
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0103	0.0120	0.8567	1.1673
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0104			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0068
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0142	Skin-muscle	0.0000
Suprarenal gland	0.0108	Testicles	0.0000
Kidney	0.0254	Lung	0.0164
Placenta	0.0000	Nerves	0.0060
Prostate	0.0061	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0126	Uterus n	0.0125

Electronic Northern for SEQ. ID NO.: 137

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

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Electronic Northern for SEQ. ID NO.: 138

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0051	3.0509	0.3278
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0000	0.0331	0.0000	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0077	0.0139	0.5522	1.8109
Brain	0.0059	0.0062	0.9599	1.0417
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0085	0.0275	0.3084	3.2426
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0062	0.0143	0.4355	2.2964
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0087			
Cervix	0.0000			

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0242
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0272
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0356
Testicles	0.0000
Lung	0.0000
Nerves	0.0090
Prostate	0.0068
Sensory Organs	0.0077
Uterus_n	0.0042

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	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0056	0.2268	4.4083
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0120	0.0052	2.3025	0.4343
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0077	0.0046	1.6567	0.6036
Brain	0.0000	0.0021	0.0000	undef
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0275	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0041	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000.	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus n	0.0000

## Electronic Northern for SEQ. ID NO.: 140

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0085	0.0100	0.8491	1.1778
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0043	1.0236	0.9769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0000			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0051	0.0000	undef
Small intestine	0.0064	0.0150	0.4253	2.3511
Ovary	0.0000	0.0496	0.0000	undef
Endocrine tissue	0.0060	0.0026	2.3025	0.4343
Gastrointestinal	0.0068	0.0050	1.3585	0.7361
Brain	0.0096	0.0046	2.0708	0.4829
Hematopoietic	0.0052	0.0051	1.0079	0.9921
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0053	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Lung	0.0083	0.0061	1.3548	0.7381
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
Sensory organs	0.0087			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0082
Placenta	0.0061	Nerves	0.0040
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000



In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S. If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

Consensus sequence C will generally be longer than initial sequence S. Its electronic Northern Blot will accordingly

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

## Mapping of Nucleic Acid Sequences on the Human Genome

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,



## References to the modules:

Pfam: Protein families database of alignments and HMMs  
(pfam@sanger.ac.uk)

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 (<http://www.expasy.ch/sprot/prosite.html>)

## TABLE I

Col. 1 - Sequence ID No.:  
Col. 2 - Expression in the endometrial tumor:  
Col. 3 - Function  
Col. 4 - Modules  
Col. 5 - Length of the applied sequence in bases  
Col. 6 - Cytogenetic localization  
Col. 7 - Next marker

## [Key to Table I:]

## [Col. 2:]

[Seq. ID Nos. 1-62] erhöht = elevated

## [Col. 3:]

[Seq. ID Nos.: 1, 7-15, 78-126, 136] unbekannt = unknown

[Seq. ID Nos.: 3, 4, 38, 67-72] Homolog zu... = homologous  
to...

[Seq. ID Nos.: 531-555] Verlängerung von Seq. ID No. ... =  
Lengthening of Seq. ID No. ...

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5 TABELLE I

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cylogenetische Lokalisation	nächster Marker
1	erhöht	unbekannt		1046	2p24-2p21	D2S174-D2S390
2	erhöht	Mouse mammary tumor virus proviral envelope gene Polymerase protein	2x "CSD"	373		
3	erhöht	Homolog zu Human protein kinase C-binding protein RACK17		1571	1q32.1	D1S477-D1S504
4	erhöht	Homolog zu Human mRNA for KIAA0079		1789	10q21.3-q22.2	D10S537-D10S218
5	erhöht	Caenorhabditis elegans cosmid T23B12	"BTB"	2361		
6	erhöht	Caenorhabditis elegans cosmid C01A2		1638	20q13.32-q13.33	D20S100-D20S173
7	erhöht	unbekannt		1034	12q12	D12S1589-D12S85
8	erhöht	unbekannt		947	17p11.2-p12	AFMa126yd5
9	erhöht	unbekannt		497		
10	erhöht	unbekannt		269		
11	erhöht	unbekannt		1717		
12	erhöht	unbekannt	"zf-C3HC4"	1419		
13	erhöht	unbekannt		671	2q37.3	D2S2704
14	erhöht	unbekannt		524		
15	erhöht	unbekannt		345		
16	erhöht	rGSTK1-1=glutathione S-transferase subunit 13		1060	7q33-7q36.1	WI-9353
17	erhöht	Rattus norvegicus neuritin		1721	6p23-p25.1	D6S1617-D6S1674
18	erhöht	Rattus norvegicus cytosolic NADP-dependent isocitrate dehydrogenase	"isodh"	2367	2q34	WI-1247
19	erhöht	Rat unr mRNA for unr protein with unknown function	2x "CSD"	1321	1p13.3-1q11	D1S418-D1S252
20	erhöht	Rat prostatic binding protein polypeptide c1		384		
21	erhöht	Rat GTP-binding protein (ral B)		367		
22	erhöht	R.norvegicus mRNA for TRAP-complex gamma subunit		2621	3q24-q25.2	D3S1570
23	erhöht	P.sativum mRNA for Cop1 protein	2x "G-beta"	2019	1q23.3-q24.3	D1S242-D1S416
24	erhöht	P.falciparum pfmdr1 gene		1866	18q12.1-q12.3	AFM164ya9
25	erhöht	ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog		1189		

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cylogenetische Lokalisation	nächster Marker
26	erhöht	O. cuniculus lambda-crystallin mRNA	"3HCDH"	1418		
27	erhöht	Mus musculus flotillin		814		
28	erhöht	Mouse glycerol-3-phosphate acyltransferase		3039	10q25.1-q25.2	D10S1465
29	erhöht	Mouse clathrin-associated protein (AP47)	"Adap_comp_sub"	1448		
30	erhöht	Lycopersicon esculentum biotin-containing subunit of methylcrotonyl-CoA carboxylase	"CPSase L_chain", "biotin_req_enzy"	1394		
31	erhöht	Leucine aminopeptidase, bovine	"Peptidase_M17"	734		
32	erhöht	Klebsiella pneumoniae possible RNA helicase (dead)	2x "DEAD"	692		
33	erhöht	Human mammaglobin Homolog	"Uteroglobulin"	517		
34	erhöht	Human DNA sequence from PAC 138A5 on chromosome X		322		
35	erhöht	Human DNA sequence from clone 230G1		1559		
36	erhöht	Human DNA sequence from clone 217C2		1072		
37	erhöht	Human Cosmid Clone 26a1	"RhoGAP"	454	22.q11.21-q11.23	D22S420-D22S446
38	erhöht	Homolog zu Human chromosome 3p21.1 gene sequence		700	3p21.1	
39	erhöht	Homo sapiens DNA from chromosome 19-cosmid I21246		914		
40	erhöht	H. sapiens mRNA for Plg-1 protein		1669	17q21.31-q21.33	D17S791-D17S797
41	erhöht	H. sapiens CpG island DNA genomic Mse1 fragment		355		
42	erhöht	H. sapiens (TL5) mRNA from LNCaP cell line		2628	3q24	D3S3413
43	erhöht	Genomic sequence from Human 9q34		2535	9q34.11-q34.13	D9S179-D9S164
44	erhöht	Drosophila melanogaster misato gene	"MYB_3"	805	1q21.2	D1S305-D1S506
45	erhöht	Chicken mRNA for vitellogenin I		1279		
46	erhöht	Caenorhabditis elegans DNA from clone F31D4		1923		
47	erhöht	Caenorhabditis elegans cosmid ZK863		706		
48	erhöht	Caenorhabditis elegans cosmid ZK863		749		
49	erhöht	Caenorhabditis elegans cosmid ZK596		857	10q26.13	D10S212
50	erhöht	Caenorhabditis elegans cosmid T28A5		268		
51	erhöht	Caenorhabditis elegans cosmid T21G5		297		
52	erhöht	Caenorhabditis elegans cosmid F56D5		590		
53	erhöht	Caenorhabditis elegans cosmid F25D7		1714		
54	erhöht	Caenorhabditis elegans cosmid F08C6		1340		
55	erhöht	C. bolulinum bont (partial) and ntinh genes		765	3q24-q23	D3S3409

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
56	erhöht	Bovine mRNA fragment for 49 kDa subunit of mitochondrial NADH:ubiquinone oxidoreductase (EC 1.6.5.3)	"complex1_4_9Kd"	1647		
57	erhöht	Bos taurus (clone pTKD7) dopamine and cyclic AMP-regulated neuronal phosphoprotein (DARPP-32)		1166		
58	erhöht	A. thaliana mRNA for RNA helicase		487		
59	erhöht	A. thaliana glycine-rich protein (clone atGRP-4)		1630	5q23.3-q31.1	D5S396-D5S2119
60	erhöht	Saccharomyces cerevisiae Grd19p (GRD19)	2x "PX", "BEM_DOM AIN"	1272	6q21	AFMa191wd1
61	erhöht	Saccharomyces cerevisiae chromosome XII cosmid 9328	2x "DEAD", "helicase_C"	1914	7p12.3-p13	D7S667-D7S2427
62	erhöht	S. pombe chromosome I cosmid c13D6		608		
63		Rattus norvegicus RNA helicase with arginine-serine-rich domain		2674	17q21.31-q22	D17S797-D17S788
64		Rattus norvegicus matrilysin (MMP-7) mRNA		326		
65		Rattus norvegicus Diphor-1	2x "PDZ"	888	1q12	D1S2669-D1S498
66		Human herpesvirus-7 (HHV7) J1, G protein-coupled receptor (GCR)		202		
67		Homolog zu Human synapsin I (SYN1)		1225	1p22.3-p31.1	WI-3099
68		Homolog zu Human PAX3 gene		1093		
69		Homolog zu Human multiple exostosis 2 (EXT2)		309	1p21.3-p22.1	D1S2166
70		Homolog zu Homo sapiens integrin variant beta4E (ITGB4)		380		
71		Homolog zu Homo sapiens hCPE-R mRNA for CPE-receptor		1253		
72		Homolog zu H. sapiens mRNA for deoxyguanosine kinase		439		
73		Caenorhabditis elegans cosmid Y48E1B		1252	4p11-q12	D4S1619-D4S1600
74		Caenorhabditis elegans cosmid T21D12	"WW_DO-MAIN_2"	695		
75		Caenorhabditis elegans cosmid R107		2514	13q33.3-q34	D13S261-D13S293
76		Caenorhabditis elegans cosmid M04C9		274		
77		Bovine opsin	"7Im_1"	449		
78		unbekannt		346		
79		unbekannt		1329		
80		unbekannt		805		



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Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
81		unbekannt		420		
82		unbekannt		2143	9q21.32-q22.1	D9S264-D9S257
83		unbekannt		450		
84		unbekannt		408	17q23.1-q23.2	D17S1680
85		unbekannt		311		
86		unbekannt		487		
87		unbekannt		1902	11p12-p13	WI-6150
88		unbekannt		1048	1q42.11-q43	WI-9317
89		unbekannt		804		
90		unbekannt		581		
91		unbekannt		2042		
92		unbekannt		430		
93		unbekannt		592		
94		unbekannt		674		
95		unbekannt		324		
96		unbekannt		709	5p15.33	D5S1954
97		unbekannt		562		
98		unbekannt		1948	16p13.2-p12.3	D16S499
99		unbekannt		483		
100		unbekannt		437		
101		unbekannt		359		
102		unbekannt		501		
103		unbekannt		1102	1q23.1-q23.2	D1S445-D1S431
104		unbekannt		306		
105		unbekannt		2042		
106		unbekannt		320		
107		unbekannt		506		
108		unbekannt		1276		
109		unbekannt		373		
110		unbekannt	TPR RE-PEAT*	492		
111		unbekannt		1678	8q21	D6S278-D6S302
112		unbekannt		866	9q22.1-q22.2	D9S1841-D9S196
113		unbekannt		1434	18q12.1-q12.3	D18S1124-D18S468
114		unbekannt		914	7q32.3	D7S686-D7S530
115		unbekannt		685	8p12-p11.23	D8S1821-D8S255

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
116		unbekannt		2646		
117		unbekannt		2667		
118		unbekannt		544		
119		unbekannt		1340	18p11.21	D18S471-D18S464
120		unbekannt		2376		
121		unbekannt		225		
122		unbekannt		1967	6q22.33-q23.1	D6S292-D6S1699
123		unbekannt		612		
124		unbekannt		1183	2q32.3-q34	D2S315-D2S2237
125		unbekannt		891	4q28.1-q31.1	
126		unbekannt		482		
127		Human triosephosphate isomerase mRNA		610		
128		Human ras inhibitor mRNA		2072	9q33.3-q34.11	
129		Human R kappa B		980		
130		Human putative interferon-related protein (SM15)		792		
131		Human protein trafficking protein (S31iii125)	2x "EMP24_GP25L"	1092	14q32.2-14q32.33	WI-9179
132		Human protein kinase C-binding protein RACK7		1523	20q13.13-q13.2	D20S957
133		Human gene for histone H1(0)	"linker_histone"	2241	22q13.1	
134		Human cathepsin B proteinase	"Cys-protease"	631		
135		Homo sapiens cathepsin B mRNA	"Cys-protease"	980		
136		unbekannt		2238	14q24.1-14q24.3	D14S277
137		H. sapiens XG mRNA		398		
138		H. sapiens mRNA for RAB7 protein	ras	1084	7q21.3-q22.1	D7S652
139		H. sapiens mRNA for pyrroline 5-carboxylate synthetase		1259		
140		H. sapiens mRNA for beta-1,4-galactosyltransferase		1938	1q22-q23.1	
141		H. sapiens IL-13Ra		1874	Xq23	
531		Verlängerung von Seq. ID No. 19	2x "CSD"	1708	1p13.3-1q11	D1S418-D1S252
532		Verlängerung von Seq. ID No. 23	2x "G-bela"	2128	1q23.3-q24.3	D1S242-D1S416
533		Verlängerung von Seq. ID No. 25		2640		
534		Verlängerung von Seq. ID No. 32	2x "DEAD"	1245		
535		Verlängerung von Seq. ID No. 34		822		

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Sequenz ID No.:	Expression im Endometrium-Tumor.	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cyto genetische Lokalisation	nächster Marker
536		Verlängerung von Seq. ID No. 43		2703	9q34.11-q34.13	D9S179-D9S164
537		Verlängerung von Seq. ID No. 44	"MYB_3"	2664	1q21.2	D1S305-D1S506
538		Verlängerung von Seq. ID No. 52		3888		
539		Verlängerung von Seq. ID No. 54		3304		
540		Verlängerung von Seq. ID No. 55		863	3q24-q23	D3S3409
541		Verlängerung von Seq. ID No. 59		1962	5q23.3-q31.1	D5S396-D5S2119
542		Verlängerung von Seq. ID No. 60	2x "PX"; "BEM_DOM AIN"	1772	6q21	AFMa191wd1
543		Verlängerung von Seq. ID No. 65	2x "PDZ"	1009	1q12	D1S2669-D1S498
544		Verlängerung von Seq. ID No. 69		2834	1p21.3-p22.1	D1S2166
545		Verlängerung von Seq. ID No. 82		2319	9q21.32-q22.1	D9S264-D9S257
546		Verlängerung von Seq. ID No. 84		2456	17q23.1-q23.2	D17S1680
547		Verlängerung von Seq. ID No. 87		2218	11p12-p13	WI-6150
548		Verlängerung von Seq. ID No. 88		2196	1q42.11-q43	WI-9317
549		Verlängerung von Seq. ID No. 93		701		
550		Verlängerung von Seq. ID No. 98		2214	16p13.2-p12.3	D16S499
551		Verlängerung von Seq. ID No. 108		1434		
552		Verlängerung von Seq. ID No. 111		2434	6q21	D6S278-D6S302
554		Verlängerung von Seq. ID No. 114		1457	7q32.3	D7S686-D7S530
555		Verlängerung von Seq. ID No. 126		741		

**DNA Sequences**  
**Seq. ID. No.**

Peptide Sequences	(ORF's)
Seq. ID. No.	

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
1	142
	143
	144
2	145
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3	148
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4	151
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5	154
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6	157
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7	160
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8	163
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9	166
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10	169
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11	172
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12	175

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
12	176
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13	178
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22	205
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23	208
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24	211

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DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
24	212
	213
25	214
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26	217
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27	220
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28	223
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29	226
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32	235
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34	241
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35	244
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DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	247
36	248
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37	250
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38	253
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39	256
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40	259
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41	262
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42	265
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43	268
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44	271
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45	274
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46	277
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47	280
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DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	283
48	284
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49	286
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50	289
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51	293
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55	305
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56	308
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57	311
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59	317
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DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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60	320
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61	323
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62	326
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63	329
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67	342
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DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
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72	357
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73	361
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74	364
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75	367
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76	370
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79	379
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80	382
	383
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81	385
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82	388
	389

00221"5662960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	390
83	391
	392
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84	394
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85	396
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86	399
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87	403
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88	407
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89	410
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90	413
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91	416
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92	419
	420
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93	423
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	425

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	426
94	427
	428
95	429
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96	433
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97	436
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98	439
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99	442
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100	445
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101	448
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102	451
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103	454
	455
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104	457
	458
	459
	460
105	461

00227 362350

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	462
	463
106	464
	465
107	466
	467
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	469
108	470
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	472
109	473
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110	476
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111	479
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112	482
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113	486
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114	489
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115	492
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116	496
	497

004221" 9662960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	498
117	499
	500
	501
118	502
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	504
119	505
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120	508
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121	511
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122	514
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123	517
	518
	519
124	520
	521
	522
125	523
	524
	525
126	526
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531	561
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532	564
	565

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	566
533	567
	568
	569
534	570
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535	573
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536	577
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537	579
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538	582
	583
	584
539	585
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	587
540	588
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541	591
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542	594
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544	600
	601
	602

004021" 56E2960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
545	603
	604
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546	606
	607
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547	609
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	611
548	612
	613
	614
549	615
	616
	617
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	619
	620
551	621
	622
	623
552	624
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554	630
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555	633
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	635

004221" 96E2960



The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 142-528 are described in the following sequence protocol.

### Sequence Protocol

#### (1) GENERAL INFORMATION:

##### (i) APPLICANT:

- (A) NAME: metaGen - Gesellschaft für Genomforschung  
mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

##### (ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Uterus Tumor Tissue

##### (iii) Number of sequences: 622

##### (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25  
(EPO)

09673994.1221

## (2) INFORMATION ON SEQ ID NO. 1:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

tcggaacgag ggatcactaa tcaacaaacc agctttcggg gtctgacgcg atccttgcc 60
caggcctctc gaggtccaga cagccgcccc gcccgctctg cgacgcagca gtgaatagt 120
tggtacctcc ttgtctcggt tcaggtccag acctccccgt cttccggctg ccctgaacgt 180
caggcgacct caggaccctg tgattggcgc ctgcgcgggc ggaccgtgac cgaggaaacc 240
cctggaggga cttgggcatt ccttgggctc cgtgcctgtt cttcgtgctc ctttcggggc 300
aaggatctca cattatcagt ctttgaccga cacagaatgc ctggcatttg ataaatgttt 360
gttgaacttg aagagacata tggacaatga atctgcaaag atactgggga gagataccaa 420
tatcatcaag ccagaccaac agaagtctct tcgatttgct cccacgggag ttccgtctgg 480
tggaagtcca tgacccacc ctcaccaac cctcagccaa caagccgaag ccccccacta 540
tgctggacat cccctcagag ccatgtagtc tcaccatcca tacgattcag ttgattcagc 600
acaaccgacg tcttcgcaac cttattgcca cagctcaggc ccagaatcag cagcagacag 660
aagggtgtaaa aactgaagag agtgaacctc ttccctcgtg ccctgggtca cctcctctcc 720
ctgatgacct cctgccttta gattgtaaga atcccaatgc accattccag atccggcaca 780
gtgaccocaga gagtgaactt tatcgtggga aaggggaacc tgtgactgaa ctcagctggc 840
actcctgtcg gcagctcctc taccaaggca gtggcacaaa tcctggccaa cggcgggctt 900
ttgactgtgc taatgagagt gtccctggaag accctaactt gatgttggca catgagtatt 960
ggccttaaaag tttaacaaa tttgctgcgt ttttgctgtt gagcgggaag cccgggtggg 1020
agagacttcc ttttgccgaa tgtgat                                     1046

```

## (2) INFORMATION ON SEQ ID NO. 2:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 373 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
cgaaggcaga gttcaacagg gatcttttgt aaatgttcaa caagggccac aggagccatt 60
tattgaattt atccatcagt taaccaggc aattaagagc acacatggaa catcgaccat120
tccacgggta tctcgtataa ccctcaagga caagccatag tggaacgttg cccattccac180
gcttaaaaaa atgcttttaa aaaaggggga atatgaataa ggaccctaca aactactag240
cacaagtgtt attcaccctt aattttctta atttagataa ttaaatttcc aatcagccct300
agaaaagcac ttttgcttaa aacctcccca ggtagcaagg ctttcagtgt tttgggaagg360
tgtaaatagt atc                                     373
```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1571 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

006666 123456

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

ctgctctggc aaccaataga agctaggaga gggcggggac aactgggtct tttgaggctg 60
cagcgggctt gtaggtgtcc ggctttgctg gccagcaag cctgataagc atgaagctct 120
tatctttggt ggctgtggtc ggggtgtttgc tggtgcccc agctgaagcc aacaagagtt 180
ctgaagatat ccggtgcaaa tgcctctgtc caccttatag aaacatcagt gggcacattt 240
acaaccagaa tgtatcccag aaggactgca actgcctgca cgtgggtggag cccatgccag 300
tgccctggcca tgacgtggag gcctactgcc tgctgtgcga gtgcaggtag gaggagcgca 360
gaccaccacc atcaaggtca tcattgtcat ctacctgtcc gtgggtgggtg cctgttgct 420
ctacatggcc ttctgatgc tgggtggacc tctgatccga aagccggatg catacactga 480
gcaactgcac aatgaggagg agaagtagga tgctcgtctc atggcagcag ctgctgcac 540
cctcggggga ccccgagcaa acacagtcct ggagcgtgtg gaagggtgcc agcagcgggtg 600
gaagctgcag gtgcaggagc agcggagac agtcttcgat cggcacaaga tgctcagcta 660
gatgggctgg tgtgggtggg tcaaggcccc aacaccatgg ctgccagctt ccaggctgga 720
caaagcaggg ggctacttct cccttccctc ggtccagtc ttccctttaa aagcctgtgg 780
catttttctt ccttctccct aactttagaa atgttgtagt tggtatttt gattagggaa 840
gagggatgtg gtctctgac tcctgtgtc tcttgggtct ttggggttga agggaggggg 900
aaggcaggcc agaagggaat ggagacattc gaggcgccct caggagtggg tgcgatctgt 960
ctctcctggc tccactcttg ccgccttcca gctctgagtc ttgggaatgt tgttacccctt 1020
ggaagataaa gctgggtctt caggaaactc gtgtctggga ggaaagcatg gccagcatt 1080
cagcatgtgt tcctttctgc agtggttctt tatcaccacc tccctcccag cccagcgcc 1140
tcagccccag cccagctcc agcctgagg acagctctga tgggagagct gggccccctg 1200
agcccactgg gtcttcaggg tgcactggaa gctggtgttc gctgtccct gtgcacttct 1260
cgcactgggg catggagtgc ccatgcatac tctgtgccc gtccctcac ctgcacttga 1320
ggggtctggg cagtcctctc tctccctcag gtccacagtc actgagccag acggtcgggt 1380
ggaacatgag actcagggtc gacggtggat ctgaacacca cagcccctgt acttgggttg 1440
cctcttgctc tgaacttcg ttgtaccagt gcatggagag aaaattttgt cctcttgct 1500
tagattgtg tgtaaatcaa ggaagccatc attaaattgt tttatttctc tccaaaaaaa 1560
aaaaaaaaa a 1571

```

## (2) INFORMATION ON SEQ ID NO. 4:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1789 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

agaccatgct ggaaaaaatt ccaaaggaag agcaagaaga gacgtctgca attcgagtgg 60
gttttatcac atataacaaa gttctccatt tctttaatgt gaagagtaat ctggcccagc 120
ctcagatgat gggggtgact gatgttgagg aagtccttgt tcctttgttg gatggtttcc 180
ttgtcaacta tcaagaatcc caatctgtga ttcataattt gttggaccag attccagaca 240
tgtttgcaga ctctaataa aatgagactg tctttgctcc tgtcatccag gctggcatgg 300
aagcactaaa ggcagcagac tgtcctggga agctgttcat cttccattct tccttgccaa 360
ctgctgaagc accaggggag ctcaaaaaa gagatgacaa aaaactgggt aatacagaca 420
aagagaagat acttttccag ccccaaaca atgtctatga ctctattggc aaggactgcg 480
tggctcaccg gctgctctgt gacactcttc ctctttccta gtcagtatgt ggacgtggcc 540
tcgctggggc tggttcctca gctcactgga ggaacctttt acaaatacaa caatttccag 600
atgcacttgg atagacaaca atttttgaac gacctcagaa atgataattg aaagaaaata 660
ggctttgatg ctattatgag ggttcgtacc agcacagggt tcagagccac tgatttcttt 720
ggtggaatct tgatgaacaa caccaccgat gtagaaatgg ctgccatcga ttgtgacaag 780
gcagtgaccg tggagttcaa gcacgatgac aaactcagtg aagacagtgg agccttaatc 840
cagtgtgctg tgctttacac gacaatcagt ggtcaaagaa gacttcggat tcacaatctt 900
ggcttaaaact gcagctctca gctagctgat ctttataaga gctgtgagac agatgctctt 960
atcaacttct ttgccaaagt agctttttaa gcagtctctc accagccttt gaaggctcatc 1020
cgggaaattc tagttaatca gactgcccat atgttggcat gttaccggaa gaattgtgcal 1080
agtccttctg cagcaagcca gcttattcta ccagattcca tgaaagtatt gccagtgtac 1140
atgaattgct tgttgaaaaa ctgtgtacta ctcagcagac cagagatctc aactgatgaal 1200
cgagcatacc agagacagct ggtcatgacc atgggtgtgg ctgactctca gcttttcttc 1260
taccacaac ttctgcccat acacacgtta gatgtcaaga gtacaatgtt acctgctgcc 1320
gttcgttgcg ctgagtcctg tctttcagaa gaaggaatat tcttactggc taatgggtcta 1380
cacatgttcc tgtgggttgg agtaagcagc ccaccagaac tgatccaagg aatatttaatl 1440
gtgccatctt ttgcacatat caacacagat atgacattgc tgcctgaagt gggaaacccal 1500
tactctcaac aactcagaat gataatgggt attatccaac aaaagaggcc atattcaatg 1560
aagctcacia ttgtaaaagc gcgagaacaa ccagaaatgg tttccgaca gttcctggta 1620
gaagacaaaag gactttacgg aggtctctct tatgtggatt tcctttgttg tgttcacaag 1680
gagatctgtc agctgcttaa ttaattggaa actccccgg caatggaggt tgcgttgcca 1740
ggggggggaaa agcccccttt tgggggcccc atttgccagg gggaaaaag 1789

```

## (2) INFORMATION ON SEQ ID NO. 5:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2361 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

gggccagccg gctcgcgccg gggccatggc agcagcggct actgcagccg aggggggtccc 60
cagtcggggg cctcccgggg aagtcaccca tctgaatgtg ggaggcaaga gattcagtag 120
ctctcgccag actctcacct ggatcccaga ctctctcttc tccagtcttc tgagcggacg 180
catctcgacg ctgaaagatg agaccggagc aatcttcata gacagggacc ctacagtctt 240
cgcccccatc ctcaacttcc tgcgcaccaa agagttggat cccaggggtg tccacgggtc 300
cagcctcctc catgaagccc agttctatgg gctcactcct ctggttcgtc gcctgcagct 360
tcgagaggag ttggatcgat ctctctgtgg aaacgtcctc ttcaatggtt acctgccgcc 420
accagtgttc ccagtgaagc ggcggaaccg gcacagccta gtggggcctc agcagctagg 480
aggacggcca gccccgtgcc gacggagcaa cactgatgcc cccaaccttg gcaatgcagg 540
gctgctgggc cgaatgctgg atgagaaaac cctccctca cctcaggac aacctgagga 600
gccccgggat gtgcgcctgg tgtgtggaca ccataattgg atcgctgtgg cctataccca 660
gtttctagtc tgctacaggt tgaaggaagc ctctggcggg cagctggtgt tttccagccc 720
ccgcctggac tggcccatgc gaacgactgg cgttccacag cccgggtgca tgggtgggct 780
ttgggtgaac atgacaagat ggtggcagca gccaccggca gcgagatcct gctatgggct 840
ctgcaggcgg aagggcgtgg ctccgagata ggggtcttcc atctgggggt gcctgtggag 900
gccttgttct tcgtcgggaa ccagctcatt gctacaagcc acacagggcg catcggggtg 960
tggaatgccg tcaccaagca ctggcaggtc caggaggtgc agcccatcac cagttagtac 1020
gcggcaggct ccttcctcct cctgggctgc aacaacggct ccatttacta cgtggatgtg 1080
cagaagtctc ccttgccat gaaagacaac gacctccttg tcagcgagct ctatcgggac 1140
ccagcggagg atggggtcac cgccctcagt gtctacctca cccccaagac cagtgcagct 1200
gggaactgga tcgagatcgc ctatggcacc agctcagggg gcgtgcgggt catctgcag 1260
caccgggaga ctgtgggctc ggggcctcag ctcttcacga ccttactgtg gcaccgcagc 1320
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cacgtgcgga catggtctgt gactcgtctc cgcgcatga ttccaccca gcccggtcc 1440
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agtgtcggca atgacattgg cccctacggg gagcgggacg accagcaagt gttcatccag 1560
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ggcctgacgg agcaagagct gatggaacag ctggaacact gtgagctggc cccgccggct 1860
ccttcagctc cctcatgggg ctgtctcccc agccccctac ccgcactct cctcaccagc 1920
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tgggaacccc gggttcaggg ccagggcctc cttggaataa atggttattg ttactaggtc 2280
cccaccttcc ctcttttctg gaagccaaag tcacctccc caataaagtc ctactgcca 2340
aaaaaaaaa aaaaaaaacc g

```

2361

CCCTGEE4960

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN  
(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ggctgcggat	ttcgccggaa	atcccggaag	tgacagcttt	gggggtttgc	tgctggctct	60
gactcccgtc	ctgcgatggg	ttgcgacggg	ggaacaatcc	ccaagaggca	tgaactggtg	120
aagggggcga	agaaggttga	gaaggtcgac	aaagatgctg	aattagtggc	ccaatggaac	180
tattgtactc	taagtcagga	aatattaaga	cgaccaatag	ttgcctgtga	acttggcaga	240
ctttataaca	aagatgcgct	cattgaattt	ctcttggaca	aatctgcaga	aaaggctctt	300
gggaaggcag	catctcacat	taaaagcatt	aagaatgtga	cagagctgaa	gctttctgat	360
aaatcctgct	gggaagggga	taaaggaaac	actaaagggtg	acaagcacga	tgacctccag	420
cgggcgcggt	tcatctgccc	cgttgtgggc	ctggagatga	acggccgaca	caggttctgc	480
tccttcgggt	gctgcggctg	tgtgttttct	gagcgagcct	tgaagagat	aaaagcggaa	540
gtttgccaca	cgtgtggggc	tgccctccag	gaggatgatg	tcatcgtgct	caatggcacc	600
aaggagggatg	tggacgtgct	gaagacaagg	atggaggaga	gaaggctgag	agcgaattgg	660
aaaagaaaac	aaagaaaccc	aaggcagcag	agtctgtttc	aaaaccagat	gtcagtgaag	720
aagccccagg	gccatcaaaa	gttaagacag	ggaagcctga	agaagccagc	cttgattcta	780
gagagaagaa	aaccaacttg	gtcccaaaaa	gcacagcaat	gaatgagagc	tcttctggaa	840
aagctgggaa	gcctccgtgt	ggagccacaa	agaggtccat	cgtgacagt	gaagaatcgg	900
aggcctacaa	gtccctcttt	accactcaca	gtccgcgcaa	gcgctccaag	gaggagtctg	960
ccactgggt	caccacacag	tcctactgct	tcagaagccc	gcactgccac	cgctcctgcc	1020
ccagaagggt	gttttagtttc	cacgtaggca	ggtcgctttg	tgccctctgag	tgcgctgctg	1080
tgtgtctctc	ctatagtctc	gtgtcataaa	gctgtcctg	ccagccttca	agctgggtgtg	1140
gccactcttg	atgttgagtc	tgtcggttcc	aggggggaca	tgggaggggc	tgcacagtgg	1200
cccgaggtca	tgcttgcttc	cacctgcagg	tgcatttggt	cctttccatg	gccaggaagc	1260
cctgtgggct	gcacttttta	tgcttgcatg	aacaagagac	tcagaggtcc	tcaccgggtgc	1320
agagttggca	catattaatt	aactaaaatt	ctaattgatc	tgctaccagc	aataaatcaa	1380
gtaggccaag	tgaactggg	ctttaaaaag	gatggatttc	aaatacactg	tgcccaactag	1440
aagcttcgaa	gggcctcgtc	cctctgctac	agccctggga	ggagccagga	tccttgttgg	1500
tctagctaaa	tactgttagg	ggagtgtgcc	ccatctcatc	atttcgaaga	tagcagagtc	1560
atagtggggc	accogtggat	tgggttcaaa	aataaagctg	gtctgcctct	tcaaaaaaaaa	1620
aaaaaaaaaa	aaaaaaaaaa					1638

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

cgccctgcgcg ctgagtgcgt gccgctccgc cgaccgaaga ggctggacat gacaccagtg 60
gcatatcacg gccatggggg ctcagcattc cgctgctgct cgcccctcct cctgcaggcg 120
aaagcaagaa gatgacaggg acggtttgct ggctgaacga gagcaggaag aagccattgc 180
tcagttccca tatgtggaat tcaccgggag agatagcatc acctgtctca cgtgccaggg 240
gacaggctac attccaacag agcaagtaaa tgagttggtg gctttgatcc cacacagtga 300
tcagagattg cgccctcagc gaactaagca atatgtcctc ctgtccatcc tgctttgtct 360
cctggcatct ggtttggtgg ttttcttctt gtttcgcat tcagtccttg tggatgatga 420
cggcatcaaa gtggtgaaaag tcacatttaa taagcaagac tcccttgtaa ttctcaccat 480
catggccacc ctgaaaatca ggaactccaa cttctacacg gtggcagtga ccagcctgtc 540
cagccagatt cagtacatga acacagtggg gaattttacc gggaaggccg agatgggagg 600
accgttttcc tatgtgtact tcttctgcac ggtacctgag atcctggtgc acaacatagt 660
gatcttcatg cgaacttcag tgaagatttc atacattggc ctcatgacct agagctcctt 720
ggagacacat cactatgtgg attgtggagg aaattccaca gctatttaac aactgctatt 780
ggttcttcca cacagcgctt gtagaagaga gcacagcata tgttcccaag gcctgagttc 840
tgggacctac cccacgtgg gtgttaaggc agagggaagg aattggttca ctttaacttc 900
ccaggcaaac attcctcctg gccacttagg gagggaaaca cttccctat gggttaccat 960
ttgttggttg ttcaggaacc aggcggattc agttgcctag gcgtgttgcc ccagcaatta 1020
gtttgggcac tgca                                     1034

```

## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 947 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00227" SEF 2950



(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

cgaggccctg gcatgtgcaa agagtactga gtgggattcc cagcaggata ccatcaagta 60
ctacaccatg cacctgacca cattgtgcaa cacgtgattg gacaacccaa cccagagaaal20
caaggatcag ctgatccggg cagccgtgaa gtttctggac accgacacca tctgctacag180
ggtggaggag cccgagacat tagtggaact tcaaaggaat gagtgggatc caatcatcga240
atgggctgag aaaagatacg gcgtggagat cagctcctcc accagcataa tgggaccag300
catccctgcc aaaactcggg aggtgctcgt cagccacctg gcatcttaca acacatgggc360
tttacaaggg attgagtttg tagctgcccc gctcaagtcc atggtgctaa ccttgggcct420
gattgacctg cgctgacag tggagcaggc cgtgctgctg tcacgcctgg aggaggagta480
ccagatccag aagtggggca acattgagtg ggcccatgac tatgagctgc aggagctgcg540
ggcccgcaac gccgcgggca ccctcttcat ccactctctg tccgagagca ccacagtcaa600
gcacaagctc ctgaaggagt gaggcctggg cagagcacac tcagcaggat agaggcagt660
cagccacagc tccccgggcc ttcagggtc cccagcctgt ggggctggct tccttggctt720
ttggggactc ggctcagcg tcacctgag attcccccg agacacagtg cgctagtacg780
gctgtcggga ggtcagcctg atttcaacc aggtgcccct ggcctggcca gcagtgaatg840
taggagatga attgtgcaag tgactttctc tcgactctga ttttattaaa tatttctcca900
ccctggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 947

```

## (2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 497 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
ctcgtggcga gagactgaga taaaagagca actcactgaa cacctttgta cgatcataca 60
gcaaaatgag ctccgaaagg ccaagaagtt ggaggagtgt atgcaacaac tagatgtaga120
agccgatgaa gagacttttg agcttgaggt ggaggtcgag agattgctac acgaacaaga180
agtagaatca aggagaccag tggttcgttt agagaggcca ttccagcctg cggaggagag240
tgtgacatta gaatttgcta aagagaacag aaagtgtcaa gaacaagctg tttcccaaaa300
ggtagatgac cagtgtggaa attccagtag catccccctt cttagtccaa actgccccaa360
tcaagaaggt aatgacattt cagctgcttt ggccacatga agttctggta ttcttttgag420
ctaatatggt attgagtaaa gtatactttt tgcagtagat catgccctga cctccaataa480
aaacctcttt aaaacaa                                497
```

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 269 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
cggggagagg tgggctgggc tgcaggctct ggcgttgtgc tggatcatcg cgcccgact 60
ctgaagtctt ctccgtggcg ctcccttgaga ggggttcttc ctgcatcttg agaataattt120
gcatttcggc tcccttctct tctcgtgccc atcggatgcc ccaaataagg cctgtcccct180
cgggtgaatca gacttcggaa accgcctcgc ttcagggtca gagtccaagt acagatgagc240
ttgagaggga ttctgaaatg caacggcccc                                269
```

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1717 base pairs

(B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

attctaggac caacactcct gtggagacgt ggaaagggttc caaaggcaaa cagtcctata 60
cctacatcat tgaggagaac actaccacga gcttcacctg ggccttccag aggaccactt 120
ttcatgaggc aagcaggaag tacaccaatg acgttgccaa gatctactcc atcaatgtca 180
ccaatgttat gaatggcgtg gcctcctact gccgtccctg tgccctagaa gcctctgatg 240
tgggctcctc ctgcacctct tgtcctgctg gttactatat tgaccgagat tcaggaacct 300
gccactcctg cccccctaac acaattctga aagcccacca gccttatggt gtccaggcct 360
gtgtgccctg tgggccaggg accaagaaca acaagatcca ctctctgtgc tacaatgatt 420
gcaccttctc acgcaacact ccaaccagga ctttcaacta caacttctcc gctttggcaa 480
acaccgtcac tcttgctgga gggccaagct tcacttccaa aggggtgaaa tacttccatc 540
actttaccct cagtctctgt ggaaaccagg gtaggaaaat gtctgtgtgc accgacaatg 600
tcactgacct ccggaattct gaggggtgag cagggttctc caaatctatc acagcctacg 660
tctgccaggc agtcatcatc cccccagagg tgacaggcta caaggccggg gtttctcac 720
agcctgtcag ccttgctgat cgacttattg gggtgacaac agatatgact ctggatggaa 780
tcacctcccc agctgaactt ttccacctgg agtccttggg aataccggac gtgatcttct 840
tttataggtc caatgatgtg acccagtcct gcagttctgg gagatcaacc accatccgcg 900
tcagggtgcag tccacagaaa actgtccctg gaagtgtgct gctgccagga acgtgctcag 960
atgggacctg tgatggctgc aacttccact tcctgtggga gagcgcggtt gcttgcccgcl020
tctgctcagt ggctgactac catgctatcg tcagcagctg tgtggctggg atccagaagal080
ctacttacgt gtggcgagaa cccaagctat gctctgggtg catttctctg cctgagcagall40
gagtcaccat ctgcaaaacc atagatttct ggctgaaagt gggcatctct gcaggcacct1200
gtactgccat cctgctcacc gtcttgacct gctacttttg gaaaaagaat caaaaactag1260
agtacaagta ctccaagctg gtgatgaatg ctactctcaa ggactgtgac ctgccagcag1320
ctgacagctg cgccatcatg gaaggcgagg atgtagagga cgacctcatc tttaccagcal380
agaagtcact ctttggaag atcaaatcat ttacctcaa gaggactcct gatggatttg1440
actcagtgcc gctgaagaca tcctcaggag gccagacat ggacctgtga gaggcactgc1500
ctgectcacc tgctcctca ccttgcatag cacctttgca agcctgcggc gatttggttg1560
ccagcatcct gcaacaccca ctgctggaat tctcttcatt gtggccttat cagatgtttg1620
aatttcagat ctttttttat agagtaccca aaccctcctt tctgcttgcc tcaaacctgc1680
caaatatacc cacactttgt ttgtaaatta aaaaaaa 1717

```

096396 "42700

## (2) INFORMATION ON SEQ ID NO. 12:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1419 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

ggcagaggta ttacctgaaa acttaaaaga aggcctgaag gaatcttctt ggagttcatt 60
accatgtact aaaaacagac cttttgattt tcattcagtg atggaagagt ctccagtctct 120
caatgaacct agcccaaagc agagtgaaga aataccagag gtcacttcag agcctgtcaa 180
aggaagctta aaccgtgctc agtcagcaca gtctataaat tcaacagaaa tgccctgccag 240
agaggactgt ttgaaaaaag agtgccctca gaacctgttc tgtcagttca agaaaaaggt 300
gttctgctga aaagaaaagt gtctctttta gaacaggatg tgattgtaaa tgaagatgga 360
agaaataagc tgaaaaaaca aggagaaaact cccaatgaag tctgtatgtt ttccttagct 420
tatggtgata ttccagaaga attaatcgat gtctcagatt toagagtgtt tctctgcatg 480
aggttggttt ttgagccagt aacaaccctt tgcggacatt cgttctgtaa gaattgtctt 540
gagcgttggt tagatcatgc accatattgt cctctttgca aagaaagctt aaaagagtat 600
ctagcagata ggaggtactg tgtcacacag ctggttggaa gaattaatag tgaagtatct 660
gcctgatgaa ctgtctgaga gaaaaaaaaa atatgatgaa gaaactgctg aactctcaca 720
cttgaccaag aatgttccaa tatttgtttg cactatggcc taccctactg tgccctgccc 780
tctccatgta tttgagccaa gatacagatt gatgatcgga agaagtatac agactggaac 840
caaacagttt ggcatgtgtg tcagtgtatc acaaaatagt tttgcagatt atggttgtat 900
gttacaaatt agaaacgtgc atttcttacc ggacggaagg tctgtggttg atacagttgg 960
aggaaagcgg tttagggttt taaaaagagg aatgaaagat ggatattgca ctgccgacat 1020
tgaatatctg gaagatgtta aggttgagaa tgaagatgag attaagaatc tcagagagct 1080
tcatgatttg gtttactctc aagcctgcag ctggtttcag aatttaagag acagatttcg 1140
aagccaaatt cttcagcatt tcggatcaat gcccgagagg agggaaaacc ttcaggcagc 1200
ccctaattga cctgcatggt gttggtggct tcttgcagtt ctccctgtag acccacgata 1260
ccagctgtcg gttttgtcaa tgaaagtctt gaaagaacgg ttgaccaaga tacagcatat 1320
actgacctat ttttctagag accaattcta agtaactaac tctttgggat cttccctttg 1380
aaagttgacc cctaattctt gggctgccat ttggttggg 1419

```

004241 5622960

## (2) INFORMATION ON SEQ ID NO. 13:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 671 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

agcgcggtga agcgggggtg ggatctgaac atggcgggcg tggtagctgc tacggcgctg 60
aagggcgggg gggcgagaaa tgcccgcgtc ctccggggga ttctcgagg agccacagct120
aacaaggctt ctcataacag gaccggggcc ctgcaaagcc acagctcccc agagggcaag180
gaggaacctg aaccctatc ccggagctg gaatacattc ccagaaagag gggcaagaac240
cccatgaaag ctgtgggact ggccctgggc atcggttcc cttgtggtat cctcctcttc300
atcctcacca agcggaagt ggacaaggac cgtgtgaagc agatgaaggc tcggcagaac360
atgcggttgt ccaacacggg cgagtatgag agccagaggt tcagggttc ctcccagagt420
gccccgtccc ctgatgttg gtotggggtg cagacctgag gagcgctgcg accctcctag480
gctattgact gttaagtcc caggtttggc ccagattcca gttcgtgcct ctgaggtcca540
ccagagggcg catgaagccc aggtgttgc caaacctac cctgccccac accaaggagc600
ccaccaagg caaataaagt tattgagtgt ttagtagaaa ggaaaaaaaa aaaaaaaaaa660
aaaagtcgac c                                     671

```

## (2) INFORMATION ON SEQ ID NO. 14:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 524 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

004227 5622960

(A) ORGANISM: HUMAN  
(C) ORGAN:

(A) LIBRARY: cDNA library

aagtgttctc	agatgctgat	gtttgtaagg	tcccggtggg	gccatgagga	agaagaggag	60
ctgaaggtaa	gagactcata	aacaagatga	ctctttgatg	catgaacaag	atttgaaaat	120
ctcaagcctg	taaagaatac	cctgtctatt	taaataaagc	tcataccaag	aggtaacatt	180
ttgccccggg	ccaaattcag	gggtctagtg	ccctgcattc	ctttgaggca	aaaaataaat	240
gggctatgac	tggttaaattg	tccaaaaggt	gaattctcat	tccattcaaa	caaagacaga	300
tttgcgcat	cactcaagca	gaatgtggcc	atgaatat	agccctgca	tacatacaaa	360
gatgtacgca	tgattcccc	caccaagcac	acacacagtc	acacacgcac	acacacacac	420
atgcacacac	gcgcgtgcac	acacggcac	atgcacacac	acacgcacac	gtaaacacat	480
gcacacatgc	acacacgtgc	acacatgcac	acacggcac	actt		524

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 345 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN  
(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

aaacttttctt	tctacaaaaa	atcaaaaagct	tagctgatag	atcatgaaaa	tagattatga	60
acagtgaaat	tcttgagaag	gctgaaaagt	cggggaacca	aagcagggga	gatttagcctt	120
agtccggagg	agggagaagc	agatggaagt	cagcagcctg	ccttgttttt	acgtgtaata	180
tttaaatttg	caaaattgtat	tacaggaggg	cctactttct	gtttttatca	agagtttttc	240
ttttgttcaa	agacactggt	tatgggaata	ttttgaaagt	gtaagaaaacg	ctggtataaa	300
agdggtgttc	agattaattt	tgaaggctct	tacggaacca	gtccc		345

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ggcgggtccca ggcaggccca gaagctgggc agcctctgcc gggttccggg aaaaggagct 60
cctgctgcca ctgctcttcc ggagcctgca gcatggggcc cctgccgcgc accgtggagc 120
tcttctatga cgtgctgtcc cctactcct ggctgggctt cgagatcctg tgccgggtatc 180
agaatatctg gaacatcaac ctgcagttgc ggcccagcct cataacaggg atcatgaaag 240
acagtggaaa caagcctcca ggtctgcttc cccgcaaagg actatacatg gcaaatgact 300
taaagctcct gagacaccat ctccagattc ccatccactt ccccaaggat ttcttgtctg 360
tgatgcttga aaaaggaagt ttgtctgcca tgcgtttcct caccgccgtg aacttggagc 420
atccagagat gctggagaaa gcgtcccggg agctgtggat gcgcgtctgg tcaaggaatg 480
aagacatcac cgagccgcag agcatcctgg cggctgcaga gaaggctggt atgtctgcag 540
aacaagccca gggacttctg gaaaagatcg caacgccaaa ggtgaagaac cagctcaagg 600
agaccactga ggcagcctgc agatacggag cctttgggct gcccatcacc gtggcccatg 660
tggtatggcca aaccacatg ttatttggtc ctgaccggat ggagctgctg gcgcacctgc 720
tgaggagagaa gtggatgggc cctatacctc cagccgtgaa tgccagactt taagattgcc 780
cggaggaagc aaactcttcg tataaaaaaa gcaggccatc tgcttaacct ttggctccac 840
cataaggcac tgggactcgg atttctctat ctgatatagg tattttctgt ggccctggga 900
gctgtctgtc tttccctac ccccaaggat gccaggaaga cgtccaccat tagccatgtg 960
gcaaccttta cttctatgcc tcacaagtgc ctttcagaga gcccgaattc tgctttccca1020
caaaataaac ctaatgccat caggcaaaaa aaaaaaaaaa 1060

```

## (2) INFORMATION ON SEQ ID NO. 17:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1721 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

ctctctctct tctctgtctct tcctcgtctc ctctctttct ctcctccctc tgccttccca 60
gtgcataaag tctctgtctc tcccggaact tgttggcaat gcctattttt tggctttccc 120
ccgcgttctc taaactaact atttaaaggt ctgcggtctc aaatggtttg actaaacgta 180
ggatgggact taagttgaac ggcagatata ttctactgat cctcgcggtg caaatagcgt 240
atctgggtgca ggccttgaga gcagcgggca agtgcgatgc ggtcttcaag ggcttttcgg 300
actgtttgct caagctgggc gacacatggc caactaccgc caggcctgga cgacaagacg 360
aacatcaaga cgtgtgcac atactgggag gatttccaca gctgcacggt cacagccctt 420
acggattgcc aggaaggggc gaaagatatg tgggataaac tgagaaaaga atccaaaaac 480
ctcaacatcc aaggcagctt attcgaactc tgcggcagcg gcaacggggc ggcggggtcc 540
ctgctcccg gcttcccggt gctcctggtg tctctctcgg cagcttttagc gacctggctt 600
tccttctgag cgtggggcca gctccccccg cgcgcccacc cactcact ccctgctccc 660

ggaaatcgag aggaagatcc attagttctt tggggacggt gtgattctct gtgatgctga 720
aaacactcat ataggattgt gggaaatcct gattctcttt tttatttctg ttgatttctt 780
gtgttttatt tgccaaatgt taccatcag tgagcaagca agcacagcca aaatcggacc 840
tcagctttag tccgtcttca cacacaaata agaaaacggc aaacccaccc cattttttta 900
ttttattatt attaatTTTT tttgttgga aaagaatctc aggaacggcc ctggggccacc 960
tactatatta atcatgctag taacatgaaa aatgatgggc tcctcctaag aggaaggcga1020
ggagaggaga aggccagggg aatgaattca agagagatgt ccacggacga aacatacgg1080
gaataattca cgctcacgtc gttcttccac agtatcttgt tttgatcatt tccactgcac1140
atctctctc aagaaaagcg aaaggacaga ctggttgctt tgtgtttgga ggataggagg1200
gagagaggga aggggctgag gaaatctctg gggtaagagt aaaggcttcc agaagacatg1260
ctgctatggt cactgagggg ttagctttat ctgctgttgt tgatgcaccc gtccaagttc1320
actgccttta ttttccctcc tcctcttgt ttttagctgt acacacacag taatacctga1380
atatccaacg gtatagatca caaggggggg atgttaaattg ttaattctaa atatagctaa1440
aaaaagattt tgacataaaa gagccttgat tttaaaaaaa aaagagagag agatgtaatt1500
taaaaagttt attataaatt aaattcagca aaaaaagatt tgctacaaag tatagagaag1560
tataaaataa aagtrattgt ttgaaaaaaa agtgctgttt gtttcttacc ccaacctgct1620
ttcttgacct agttctcagg gaacctgaag ggacacagga tgccggtgat aagctcacct1680
cttcaggaag ccgcttcaag cagacctgcc accttcaagc a 1721

```

00621 "5666960



## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEO ID NO: 18:

```

accctgtggt cccgggtttc tgcagagtct acttcagaag cggaggcact gggagtcagg 60
tttgggattg ccaggctgtg gttgtgagtc tgagcttggt agcggctgtg ggcggccaac 120
tcttcgccag catatcatcc cggcaggcga taaactacat tcagttgagt ctgcaagact 180
gggaggaact ggggtgataa gaaatctatt cactgtcaag gtttattgaa gtcaaaatgt 240
ccaaaaaaat cagtggcggg tctgtggtag agatgcaagg agatgaaatg acacgaatca 300
tttggggaatt gattaaagag aaactcattt ttccctacgt ggaattggat ctacatagct 360
atgatttagg catagagaat cgtgatgcca ccaacgacca agtcaccaag gatgctgcag 420
aagctataaa gaagcataat gttggcgtca aatgtgccac tatcactcct gatgagaaga 480
gggttgagga gttcaagttg aaacaaatgt ggaaatcacc aaatggcacc atacgaaata 540
ttctgggtgg cacggtcttc agagaagcca ttatctgcaa aaatatcccc cggcttggtga 600
gtggatgggt aaaacctatc atcataggtc gtcatgctta tggggatcaa tacagagcaa 660
ctgattttgt tgttcctggg cctggaaaag tagagataac ctacacacca agtgacggaa 720
cccaaaaggt gacatacctg gtacataact ttgaagaagg tgggtggtgt gccatgggga 780
tgtataatca aqataaqtca attgaagatt ttqcacacag ttcccttcaa atqgctctgt 840

ctaagggttg gcctttgtat ctgagcacca aaaacactat tctgaagaaa tatgatgggc 900
gttttaaaaga catctttcag gagatatatg acaagcagta caagtcccag tttgaagctc 960
aaaagatctg gtatgagcat aggctcatcg acgacatggg ggcccaagct atgaaatcag1020
agggaggctt catctgggcc tgtaaaaact atgatgggtg cgtgcagtcg gactctgtgg1080
cccaagggtg tggctctctc ggcatgatga ccagcgtgct ggtttgtcca gatggcaagall140
cagtagaagc agaggctgcc cacgggactg taaccgctca ctaccgcatg taccagaaag1200
gacaggagac gtccaccaat cccattgctt ccatttttgc ctggaccaga ggggttagccc1260
acagagcaaa gcttgataac aataaaagagc ttgccttctt tgcaaatgct ttggaagaag1320
tctctattga gacaattgag gctggcttca tgaccaagga cttggctgct tgcattaaag1380
gtttacccaa tgtgcaacgt tctgactact tgaatacatt tgagttcatg gataaacttg1440
gagaaaaactt gaagatcaaa ctagctcagg ccaaacttta agttcatacc tgagctaagal500
aggataattg tcttttggtg actaggtcta cagggtttaca tttttctgtg ttactactcaal560
ggataaaaggc aaaatcaatt ttgtaatttg tttagaagcc agagtttarc ttttctataal620
gtttacagcc tttttcttat atatacagtt attgccacct ttgtgaacat ggcaagggacl680
ttttttacaa tttttatctt attttctagt accagcctag gaattcgggtt agtactcatt1740
tgtattcact gtcacttttt ctcatggtct aattataaat gacaaaaatc aagattgctcl800
aaaagggtaa atgataagca cagtattgct ccctaaaaata tgcataaagt agaaattcac1860
tgcttccccc tccgtgccat gaccttgggc acagggaagt tctggtgtca tagatataccc1920
gttttgtgag gtagagctgt gcattaaaact tgcacatgac tggaaacgaag tatgagtgc1980
actcaaatgt gttgaagata ctgcagtcct ttttgtaaag accttgctga atgtttccaa2040
tagactaaat actgttttag ccgcaggaga gtttggaaac cggaataaat actacctgga2100
ggtttgtcct ctccattttt ctctttctcc tccctggcctg goctgaatat tatactactc2160
taaatagcat atttcaccca agtgcaataa tgtaagctga atcttttttg gacttctgct2220
ggcctgtttt atttctttta tataaatgtg atttctcaga aattgatatt aaacactatc2280
ttatcttctc ctgaactgtt gattttaatt aaaattaagt gctaattacc attaaaaaaa2340
aaaaaaaaaa aaaaaaaaaa aaaaaaaa

```

2367

D02271.366260

## (2) INFORMATION ON SEQ ID NO. 19:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1321 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

cctggaaaca agatccaaac ccaagtgacc ccgccggaaa gtgacccagt cagggtttaa 60
aattccaaca aaccgacgtg aacaaataga ccgaccaacc aaatatacaa tccgtcaaaa 120
tacattcact tccactacga aacccaaca aaggggtgtga atgcccgccc aggagagacg 180
gttttggttt catcaagtgt gtggatcgtg atgttcgtat gttcttccac ttcagtga 240
ttctggatgg gaaccagctc catattgcag atgaagtaga gtttactgtg gttcctgata 300
tgctctctgc tcaaagaaat catgctatta ggattaaaaa acttcccaag ggcacggttt 360

catttcattc ccattcagat caccgttttc tgggcacggc agaaaaagaa gccacttttt 420
ccaatcctaa aaccactagc ccaaataaag gcaaagagaa ggaggctgag gatggcatta 480
ttgcttatga tgactgtggg gtgaaactga ctattgcttt tcaagccaag gatgtggaag 540
gatctacttc tcctcaaata ggagataagg ttgaatttag tattagtac aaacagaggc 600
ctggacagca ggttgcaact tgtgtgacgac ttttaggtcg taattctaac tccaagaggc 660
tcttgggtta tgtggcaact ctgaaggata attttggatt tattgaaaca gccaatcatg 720
ataaggaaat ctttttccat tacagttagt totctggtga tgttgatagc ctggaactgg 780
gggacatggc cgagtatagc ttgtccaaag gcaaaggcaa caaagtcagt gcagaaaaag 840
tgaacaaaaa acactcagtg aatggcatta ctgaggaagc tgatcccacc atttactctg 900
gcaaagtaat tcgccccctg aggagtgttg atccaacaca gactgagtac caaggaatga 960
ttgagattgt ggaggagggc gatatgaaag gtgaggtcta tccatttggc atcgttggga 1020
tggccaacaa aggggattgc ctgcagaaag gggagagcgt caagttccaa ttgtgtgtcc 1080
tggggcaaaa tgcacaaact atggccttaca acatcacacc cctgcgacag gccacagtgg 1140
aatgtgtgaa agatcagttt ggcttcatta actatgaagt aggagatagc aagaagctct 1200
ttttccatgt gaaagaagtt caggatggca ttgagctaca ggcaggagat gaggtggagt 1260
ttcagtgat tcctaagagt tcaggcggac tggcagggtc aggcgcctgt agatgttttg 1320
g

```

## (2) INFORMATION ON SEQ ID NO. 20:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 384 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

ggtcgaatcc aaatcactca ttgtgaaagc tgagctcaca gccgaataag ccaccatgag 60
gctgtcagtg tgtctcctga tgggtctcgct ggccctttgc tgctaccagg cccatgctct120
tgtctgcccc gctgtttgctt ctgagatcac agtcttctta ttcttaagtg acgctgcggt180
aaacctccaa gttgccaaac ttaatccacc tccagaagct cttgcagoca agttggaagt240
gaagcactgc accgatcaga tatcttttaa gaaacggctt ctcatTTgaa aaagtccctgg300
gtgggaatag tgaaaaaatg tgggtgtgtg acatgtaaaa atgctcaacc tgggtttcca360
aagtcttttc aacggcaacc tgat                                     384

```

## (2) INFORMATION ON SEQ ID NO. 21:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gggcactggt ggtccgggttc ctcaccaaac gattcatcgg tgactatgaa agaaatgcag 60
gtaatctcta tactagacaa gttcagatag aagggtgaaac cctggctctt caggttcaag120
acactccagg tattcagggtc catgagaaca gcctgagctg cagtgaacag ctgaataggt180
gcattcgctg ggcagatgct gtggtgatcg ttttctccat cactgactac aagagctatg240
aactcatcag ccagctccac cagcacgtgc agcagctaca ccttgggcac ccggctgcct300
gtgggtggtc gtgggccaac aaaagtgacc tgttgcacat caaacagggt gaccctcagc360
ttggact

```

367

(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2621 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00421" 3662960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

gggcctttgc cgccttggc ggccggctct acgttccttg ttctgcctg cagctccgcc 60
atggctccta aaggcagctc caaacagcag tctgaggagg acctgctcct gcaggatttc 120
agccgcaatc tctcggccaa gtccctccgg ctcttcttcg gaaacgcgtt catcgtgtct 180
gccatcccca tctggttata ctggcgaaata tggcatatgg atcttattca gtctgctgtt 240
ttgtatagtg tgatgacctt agtaagcaca tatttggtag cctttgcata caagaatgtg 300
aaatttgttc tcaagcacia agtagcacag aagagggagg atgctgtttc caaagaagtg 360
actcgaaaac tttctgaagc tgataataga aagatgtctc ggaaggagaa agatgaaaga 420
atcttgtgga agaagaatga agttgctgat tatgaagcta caacattttc catcttctat 480
aacaacactc tgttcctggt cgtgggtcatt gttgcttcct tcttcatatt gaagaacttc 540
aaccacacag tgaactacat attgtccata agtgcttcct caggactcat cgccctcctg 600
tctactggct ccaaatagac catgtcagct tcaccccttg gctttgtgtc tatgggtggc 660
ctggtgtata tggaaaagta gcagggtggt cagggtggga gacacaagat gtttttatag 720
tctagagcct ttaaaaaacc cagcagaatg taattcagta tttgtttatt ggctgttttt 780
tgacagattg ttgaaattaa atgaattgaa agggaaactc agagtactag gacgtttatt 840
aaaaggaaaa aaatgtcttg caatgtgctg taatcacaa aggagaaaaa aacttgtttc 900
cttgatctgt cagaggtcac agtaacctgg gccgagctgt tattatttat tatataatag 960
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accgtaataa tcagaatgaa tcctcttccc aggggattga acagaagctt aatgtttaca 1080
agtgtttgaa tttgtgatct gaaataacac aaaattaaaa acatgatttc tctaattttc 1140
caactagagg aagagaaact tgtggaaaaa ttcttttttt ttcttttttt tttcttaaa 1200
aagggcagcc aaggtagtaa cctaaaaata gtgcccaggc atatgagagt tgtcctacga 1260
ggttaaaaga cacactgttc cactgtatgg cactgtatgg agacacagga atcattgttt 1320
ttgacctgc catgttggtt tgacttacta agacacagga atcattgttt 1380
gggtctcaca ccctggagga atgttaagta agagaaagaa cctctttcct gaatattgac 1440
atgtaaaaga ccaaagtaat ttttctgaac ttctgcaatt ctgagaactc tccaaggaat 1500
ttacagtgat tttagtgtt gtcagcattt ttccatgagg actttcatac atttgactct 1560
ttagttcaca ggttcccatt gattgtgagc aagatattta tctcttttag ccttggggat 1620
ccagctgaga gcaatctctt gcattttttt acccgtgtat gtacagatat catttcttgt 1680
gtatgccatg acttgaaaaa gtttgggaag ctcttttagc atatcagcta aaaggatat 1740
aatcacagg tgatagcagt tgtcattcag taatttccta caagcagcac ccaaaggaa 1800
atatagtcot aatctttact atccacttct aaatttaatg tgaatttcat acatgttatt 1860
agttgttttc tttataaatt tataaaaaat attcatcggg agtttaactt ccacttccat 1920
gctatcggat gtgttgggct ccatgcaaga acttgggaag aaaacaggca ggaatgcatt 1980
tgcataatga ccagatcat cttttctgct aactgagaat tatatttcat cattgcttct 2040
agaagtctgc aattctttac ttttcttttg tgcattatta tctaggtgcc atcactggat 2100
aatgtggagt gactagagaa gtcacatata actgtaaggt acagttaggg taacacttta 2160
gaggtttart atttttaaaa aacttttctt gaactcctgg ccaacatggt gaaacccctg 2220
ctctactaaa aataccaaaa ttagccaggc gtgatgggtg gtgcctgtaa tctcagctac 2280
ttgggaggct gaagcaggag aactgcctga acccaggagg cagaggttgc agtgagtcga 2340
gatcgtgcta ctactgcctg ggtggcaagg gtgagactcc atctcaaaaa agaaacaaaa 2400
aaacccaaaa agttttcttt actgttggtt aaaaaaaaaa gccagaccat agtttgactg 2460
gtggcatgga atttgtgtat caaataaatg catttgctta tttgacaaac aaaaagtgtc 2520
cactattggt gaccgagggt gggccgtttt tttgaaattg ggggggaaat ttgcccggtg 2580
gtgggagggc ctttgtgggg ggggaaaaat tgcccccttg g 2621

```

## (2) INFORMATION ON SEQ ID NO. 23:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2019 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

ctgtatccta atttcttggt gaatgaactc attcttaaac agaagcaaag atttgaggaa 60
aagaggttca aattggacca ctcatgtgagt agcaccaatg gccacaggtg gcagatattt 120
caagattggt tgggaactga ccaagataac cttgatttgg ccaatgtcaa tcttatgttg 180
gagttactag tgcagaagaa gaaacaactg gaagcagaat cacatgcagc ccaactacag 240
attcttatgg aattcctcaa ggttgcaaga agaaataaga gagagcaact ggaacagatc 300
cagaaggagc taagtgtttt ggaagaggat attaagagag tgggaagaaat gagggtgcta 360
tactctcctg tcagtggagg tagcacagtg cctcaatttg aagctccttc tccatcacac 420
agtagtatta ttgattccac agaatacagc caacctccag gtttcagtg gagggtctcag 480
acaaagaaac agccttggtg taatagcacg tttagcatcaa gacgaaaacg acttactgct 540
cattttgaag acttgagaca gtgttacttt tctacaagga tgtctcgtat ctcatgatgc 600
agtcgaactg caagccagtt ggatgaattt cagggaatgct tgtccaagtt tactcgatgc 660
aattcagtag gacctttagc cacattgtca tatgtcagtg atctctataa tgggtccagt 720
atagtctcta gtattgaatt tgaccgggat tgtgactatt ttgcgattgc tggagttaca 780
aagaagatta aagtcctatg atatgacact gtcattccagg atgcagtgga tattcattac 840
cctgagaatg aaatgacctg caattcgaaa atcagctgta tcagttggag tagttaccat 900
aagaacctgt tagctagcag tgattatgaa ggcactgtta ttttatggga tggattcaca 960
ggacagaggt caaaggctca tcaggagcat gagaagaggt gttggagtg tgaactttaat 1020
ttgatggatc cttaaactct ggcttcaggt tctgatgatg caaaagtga gctgtggtct 1080
accaatctag acaactcagt ggcaagcatt gaggcaaagg ctaatgtgtg ctgtgttaaa 1140
ttcagccctt cttccagata ccatttggct ttcggtgtgt cagatcactg tgtccactac 1200
tatgatcttc gtaacactaa acagccaatc atgggtattca aaggacaccg taaagcagtc 1260
tcttatgcaa agtttgtgag tggtgaggaa attgtctctg cctcaacaga cagtcagcta 1320
aaactgtgga atgtagggaa accatactgc ctacgttctt tcaaggggtc tatcaatga 1380
aaaaactttg taggcctggc ttccaatgga gatttatatg cttgtggaag tgaaaaata 1440
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gtcaaaagtg ttctcgacaa agaccgaaaa gaagatgata caaatgaatt tgtagtgct 1560
gtgtgctgga gggcactacc agatggggag tocaatgtgc tgattgtctg taacagtcag 1620
ggtacaatta aggtgctaga attggtatga agggttaact caagtcaaat tgtacttgat 1680
cctgctgaaa tacatctgca gctgacaatg agagaagaaa cagaaaatgt catgtgatg 1740
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ttccctcctt tatgaccttt gggacattgg gaataccag ccaactctcc accatcaatg 1860
taactccatg gacattgctg ctcttggtgg tggttatctaa tttttgtgat agggaaacaa 1920
attcttttga ataaaaataa ataacaaaac aataaaagtt tattgagcca caaaaaaaa 1980
aaaaaaaaa aaaaaagaaa agaagggagg agggaaaagg 2019

```

004227 3622960

## (2) INFORMATION ON SEQ ID NO. 24:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

gtgggttgctg tgacaggcac tatttgaagt gctttatcat ggattaactc ttaatcctca 60
gctaccgtat aaagtaggac ataaccccat ttcacatgca ctacactgag acttgccctcc 120
tctcccccac cattgaagat gttctttttt cataactata tactattcca ttgcatgaat 180
attctgtaat ttatttaate ccctatggat tgataattag gttcattata gatagaagtg 240
taattaacat tctgtacat gtattttgct acttggtggtg gtatttctgt aggatgaata 300
actagaaatt tattggatca ggtttcacat ttgcagtttt gaaaactact accaaaaaga 360
tttcaccaat ttacaactcc atcattagta agaatgcctg tttgcctata gtctgccaac 420
cctgaatcct taaaaatttt tgccaatctg gtaggcacaaa tttctttctt ttctttgaat 480
attaatgagg aggaacatct tttcatgttt cttggccatt tgcatttctt attatgaatt 540
gcttttgccc attttccctt ttttaattat gaaagtctaa tgactacctt ctcatgtat 600
aaaaaacaca gttctttgaa tagagagacc cttttctcca atgctaccaa tcacattcca 660
cttaccacag tttaacatac atcctctagt cacccttccg tacgaatata catcacata 720
aaaacacttt ttacataaat aggatctcat attctgtagc tttttaaaat tttggtctca 780
aaaaaagata acaggtcttt aaatttcttt aatggttgaa tatgattaaa tactatgaaa 840
atgccattat ttattccctt aatttttttc ctctcgctat tacattgcca aagtaaacad 900
cctattcaga tgtctttgtg catgtgtgtg aatatttctt tagtctggag tccagtaagg 960
tggatttttg gatcaaaggg tttgttctct gtccaccttc agtcttccca aaggccttca 1020
taactgtatt ttcaccaagt gtatggagaa tgttcatttc cccatataac catacctaca 1080
cttgatagtt tttatctgtt gggcgaaaaa gaaccttttc ttattttgca tttccctgat 1140
tataaaaaaa aatggtgaga ttgggttat tttcatgttt attggccatt tatagtttac 1200
tgtggattgt ttgtatccct tacctgcttt ctattgggtt atgtgtggat atattgtttt 1260
tatttgttca gcatctcctt ccccatcttc tggtaacaca acctttattt atttgtgggg 1320
aacctattcc ctgtggctta ggtgagcatg tgaccaggcc tggcctcctg agtcccacag 1380
cttccatagc acagtgtata aagaatgggt atataactta agccaggcta aggaaagccc 1440
ttaacagaac ttctgctgga actactggaa agaaggcttt atggagatcc caggaaacca 1500
ggacctgta agcctgaatt tgtgccatgt ggagagagtc tgtctgagga gaaactcgga 1560
tgctagcaga aatggaaaga gaactaagtt ctgatgtcat ttttctggag gccctagatc 1620
cagctgtgac taaagcctgc cctacctccg gactttaaag ttttgtgagc caataaagtc 1680
cctttcttgt ttaagataat tgaattgagt ttctgttctg attaatatag gttatttgtat 1740
ttttcttatt gatgtgtaga aaacctttgt aattttaaat tctagacttt atgcactata 1800
taagttaata aaattagcat ggccttccat gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1866
aaaaaa

```

1866

004227 5662960

## (2) INFORMATION ON SEQ ID NO. 25:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1189 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

ctagcaagca ggtaaacgag ctttgtacaa acacacacag accaacacat ccgggggatgg 60
ctgtgtgttg ctagagcaga ggctgattaa acactcagtg tgttggctct ctgtgccact 120
cctggaaaat aatgaattgg gtaaggaaca gttaataaga aaatgtgcct tgctaactgt 180
gcacattaca acaaagagct ggcagctcct gaaggaaaag ggcttgtgcc gctgccgttc 240
aaacttgtca gtcaactcat gccagcagcc tcagcgtctg cctccccagc acaccctcat 300
tacatgtgtc tgtctggcct gatctgtgca tctgtcggga gacgctcctg acaagtcggg 360
aatttctcta tttctccact ggtgcaaaga gcggtttct cctgtcttct cttctgtcac 420
ccccgtcctt ctcccccagg aggtctccttg atttatggta gctttggact tgcttccccg 480
tctgactgtc cttgacttct agaatggaag aagctgagct ggtgaaggga agactccagg 540
ccatcacaga taaaagaaaa atacaggaag aaatctcaca gaagcgtctg aaaatagagg 600
aagacaaaact aaagcaccag catttgaaga aaaaggcctt gagggagaaa tggcttctag 660
atggaatcag cagcggaaaa gaacaggaag agatgaagaa gcaaaatcaa caagaccagc 720
accagatcca ggttctagaa caaagtatcc tcaggcttga gaaagagatc caagatcttg 780
aaaaagctga actgcaaatc tcaacgaagg aagaggccat tttaaagaaa ctaaagtcaa 840
ttgagcggac aacagaagac attataagat ctgtgaaaag ggaaagagaa gaaagagcag 900
aagagtcaat tgaggacatc tatgctaata tccctgacct tccaaagtcc tacatacctt 960
ctagggttaag gaaggagata aatgaggaaa aagaagatga tgaacaaaat aggaaagctt1020
tatatgccat ggaaattaaa gttgaaaaag acttgaggac tggagaaaag acagttctgt1080
cttcaatacc tctgccatca gatgacttta aaaggtccag gagtaaaaag ttatgatgat1140
gggcaaaaag ccagtgtatt cagtaaagtg ctaatcacia gttggaggt 1189

```

## (2) INFORMATION ON SEQ ID NO. 26:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

002227" 56E2960



(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gagctgcag ctccgcccgc gcttggtccc agcgcccgcg ggcgcgcgtc cccggcccaa 60
ccatggcgctc ctccgcccgc ggctgcgtgg tgatcggttg cagtggagtc attgggcgaa 120
gtggggccatg ctgtttgccg gtggaggctt ccaggtgaaa ctctatgaca ttgagcaaca 180
gcagataagg aacgcccctgg aaaacatcag aaaggagatg aagttgctgg agcaggcagg 240
ttctctgaaa ggctcccctga gtgtggaaga gcagctgtca ctcatcagtg gttgtcccaa 300
tatccaagaa gcagtagagg gtgccatgca cattcaggaa tgtgttcag aagatctaga 360
actgaagaag aagatTTTTG CTCAGTTAGA ttccatcatt gatgatcgag tgatcttaag 420
cagttccact tcttgtctca tgccttccaa gttgtttgct ggcttggtcc atgtgaagca 480
atgcacgtg gctcatcctg tgaatccgcc atactacatc ccgctggttg agctggtccc 540
ccaccggag acggccccta cgacagtggg cagaaccac gccctgatga agaagattgg 600
acagtgcctc atgagagtc agaaggaggt ggccggcttc gttctgaacc gcctgcaata 660
tgcaatcatc agcgaggcct ggcggttagt ggaggaaagga atcgtgtctc ctagtgcct 720
ggaccttgct atgtcagaag ggttgggcat gcggtatgca ttcattggac ccctggaaac 780
catgcacctc aatgcagaag gtatgttaag ctactgcgac agatacagcg aaggcataaa 840
acatgtccta cagacttttg gaccattcc agagttttcc agggccactg ctgagaagg 900
taaccaggac atgtgcatga aggtccctga tgaccggag cacttagctg ccaggaggca 960
gtggagggac gagtgcctca tgagactcgc caagttgaag agtcaagtgc agccccagtg 1020
aatttcttgt aatgcagctt ccaactcctc cattggaggc cctatttggg aacactgcaal 1080
gcccttaatc agccctctgt gacataggta gcagcccacg gagatcctaa gctggctgtc 1140
ttgtgtgcag cctgagtggt gtggtgcagg ccggtagtct gccgctcact ttggatcata 1200
gccctgggct tggcggcaca gcagcacttg cgttctcggt gctgtcgatt tcctgccacc 1260
tgggcagata acctggagat tttcacctt tctttttcag cttgattgca tttgagtatg 1320
atttgacagc cagtgattgt agtttctatg ttaatatgtg ggcaaaatat ttttgtaatt 1380
atTTTTGtaa tccctttctg agtaatctgg gggctcctt 1418

```

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 814 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

09673395.12300

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```
gcagcaacgg ggtgcggcag ggtggggaac gcgggagggg gccagctccc aggaaagctg 60
gtctgcgagc ggccctgcc cggctcccag gtccctgcgc gaccccgccc tccccgagac120

cccagccggg ctgccgccc cgtcccggaa gctccagcct gaaccatggt ttccacttgt180
ggcccaaagt aggccatggt ggtctccggg ttctgccgaa gccccccagt catgggtggct240
ggagggcgtg tctttgtcct gccctgcac caacagatcc agaggatctc tctcaacaca300
ctgacctca atgtcaagag tgaaaagggt tacactcgcc atgggggtccc catctcagtc360
actggcattg cccaggtgaa gctttcagag ccttttcccc acagtccact tccccatcac420
cctctctccc agacattaag acatcttctg gccacagtct tctcaacctc tgccctgcaga480
gaagttcctc tgctagtctc atcttttcca ggcaccccaa ggcaacttgc tctcctcct540
ttctttcccc gaaatggaag aagcatttct gagagggtct tcccttctct ctctgctttt600
cctctgactt catgagacct ccaccacacc ttctctacct ctactctggc tacaggtaaa660
aatccagggg cagaacaagg agatgttggc ggccgcctgt cagatgttgc tgggggaagac720
ggaggctgag attgcccaca ttgccctgga gacgttagag ggccaccaga gggccatcat780
ggccacatg acttgtggga gggttgggct taga 814
```

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 3039 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

004227 562960

gaactgagat	attgtaatca	aatagttaac	atcaggaagt	taatttggct	ggcaaaattc	60
tagggaaact	tggccagaaa	actggtgttg	aaggcttttg	ctcatataaa	caagtgccat	120
tgagtttcaa	atgaccagca	aatatattta	gaacccttcc	tgttttatgt	ctgtacctcg	180
tccacccctc	aggtaatacc	tgccctctcac	aggtagagct	gtttcttgga	aatcctccaa	240
ccaaatagca	gttttcctaa	cttgattagc	ttgagctgac	agactgtag	aatacagttc	300
tctggccaca	gctgatgagg	gctttctgta	ctgcacacag	attgtgtact	gcaccccgat	360
ccagggtgact	ggtacccact	cgagttgtgc	cgtgcaaaac	ctgtccagta	tatgcatgtg	420
gtggccctac	tgactggtaa	tggttagagg	cattttatgga	ttttaagctt	tgaggaaaaa	480
ccatgacttt	taacaaaattt	ttatggggtta	tatgcctaaa	ccotttatgcc	acatagtggt	540
aaataattat	gaaaaatggt	ctgttcataa	ttggtaggtg	cccttttgga	gcaggggaga	600
taattattgg	tttattatgg	taattatggt	gattttttaa	atatcatgta	atgttaaaac	660
gtttcttaac	agtttactgt	tgcttatctc	caagatatta	tggaaattaag	aatttttcca	720
gatgagtgtt	acatagattc	tttgaattta	gtataaaagt	actgagaatt	aagtttgtac	780
ttccataagc	ttggattttta	aacactgata	gtatctcatg	agtaatgtgt	gttttgggag	840
agggagggat	gctgattgat	atttcacatt	gtatgaaata	ccatgtttga	aactcatagc	900
aataatgcta	tgctgttgtg	atccctctca	agttctgcat	ttaaaatata	ttttttcttt	960
ataggaattg	atgtatacca	tgaagtcatt	gtcagttgta	gtagctctga	tgttgaatga	1020
gatatcatgt	tttagcattc	cattttactg	actagggtag	aagaacaott	ttcttggcta	1080
catttgaggg	ataccagggg	agtcttgggt	gttccttatt	tggggaagca	aacattttcac	1140
tagtctcttt	ttttcatcct	ttaaattgta	aattaaggat	tactcaagct	caccattatt	1200
caagattggg	actcgcttcc	cagtcgacac	tctgccctgc	ctgtcattgc	tgcaaagagc	1260
tgctgctttg	ccaacctaa	caaagaaaat	acggcttctc	ttgcattatt	ttcccttttg	1320
gtgtggtttg	ttctctaga	tacggttcaga	tcgtttgggg	aatgcaattg	atgatttgc	1380
agctctctca	ccacttaact	cactgtgagg	ataaatatgc	atgctttttg	taattaaactg	1440
gtgctttgaa	aatctttttt	aagggagaaa	aatctcaacc	aaagttatgc	tcattccagac	1500
aagctgacct	ttgagttaat	ttcagcacaa	ctcattcttc	agtgcctcat	gactgaaaac	1560
aaaaaacaaa	aaaacgaaag	catcttcaca	atgaagcttc	cagatagcac	cgttttgcta	1620
aaagatacat	tctcattgtt	ttccaacagt	gatggcttcc	acataagggt	aaacaaacta	1680
ggtgcttgta	aataatttat	tacagtttac	tctatcgcac	ttctgtaaca	tgaaatgcat	1740
gcccttcttc	aggggaagac	tgtggtcaag	ttaaaaaaa	aaaacaatat	taaacaacat	1800
gaaactgcag	tctgtttttg	aaaattgaaa	tgtcctaagt	gattcagaag	agaggaggga	1860
agttgtgcac	tctgaaaaatg	catgaaaaac	aaaggcaaaa	actagtggga	aatgtgtaga	1920
actgttaact	gagacggctt	cgagtcttcc	ttctggaatc	tgttaaattt	cacaaaactc	1980
tgagggtaaa	tggagaaaat	atttctggga	ttacaaatga	tgtaagccca	aattgtggaa	2040
ttgccagtaa	cctggatggg	gaaaagcatt	tcccatagca	ctccatgtaa	tatgagtgtc	2100
ctgtgagatg	ttcatcagtg	ttttatagaa	atgggtgtgc	tgggaaacca	agtttgcacc	2160
tgaaaactta	caatgcactt	tagcgcagta	agggtctggc	atccggtagt	gaaaaactgt	2220
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atgaacctgt	cactaatgtc	ctgtggagaa	cattttgggg	aacactatgt	tagatagttc	2340
tttaaggga	cacaaaggta	atgaacagat	agcactggga	cagaatatgc	atgcattttg	2400
taacgtocag	tgtggcgttg	aatagatgtg	tatttccctc	cctgcagaaa	ataagcacag	2460
aaaaattata	tgtagggtgat	cggagctctt	tcttttgata	gagagaacag	cccaatgat	2520
cctggctttt	tcactgaacg	tatcagaata	catggatgaa	ttggggtaaa	taaggtttta	2580
attcagatct	agaagaaaagt	attgtacgtt	tgaatgcaga	tttttatcca	cagatagttg	2640
tagtgttttag	acatgacagg	acctatcggt	gaggtttctc	agacttacta	tgggctgtaa	2700
acctgttttt	taaaactatt	ttagaaacct	gagacttgcc	gtctggcatt	ttagttaaat	2760
acaaactaat	gattgcattt	gaaagagatt	cttgacctta	tttctaaccg	tctagagctc	2820
tgaaatgact	tgatggaagg	tattaaacta	tttgccctgt	gtacaaaagaa	atgttaagac	2880
ctgtgaaaag	aattactata	aggtactgtg	aaataactgc	gatttttgtga	gcaaaacata	2940
cttgaaaatg	ctgattgatt	tttatgcttg	tttagtattt	gcaagaaaca	cagaaaatgt	3000
agtttttgtt	taataaacca	aaaattqaac	ataaaaaacc			3039

## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

taccaatctg aagggggaag cggcgccgcc atcgccctcc ggcgctccct ccccgactcc 60
taagtccttc ggccgccacc atgtccgcct cggctgtctt cattctggac gttaagggca 120
agccattgat cagccgcaac tacaagggcg atgtggccat gagcaagatt gagcacttca 180
tgccctttgct ggtacacggg gaggggaag gcgccctggc cccgctgctg agccacggcc 240
agggtccactt cctatggatc aaacacagca acctctactt ggtggccacc acatcgaaga 300
atgccaatgc ctccctggtg tactccttcc tgtataagac aatagaggta ttctgcgaat 360
acttcaagga gctggaggag gagagcatcc gggacaactt tgtcatcgtc tacgagttgc 420
tggaagagct catggacttt ggcttcccg cagaccaccga cagcaagatc ctgcaggagt 480
acatcactca gcagagcaac aagctggaga cgggcaagtc acgggtgccca cccactgtca 540
ccaacgctgt gtccctggcg tccgagggta tcaagtataa gaagaacgag gtcttcattg 600
atgtcataga gtctgtcaac ctgctggcca atgccaacgg cagcgtcctt ctgagcgaaa 660
tcgtcgggtac catcaagctc aaggtgtttc tgtcaggaat gccagagctg cggctgggcc 720
tcaatgaccg cgtgctcttc gagctcactg gccgcagcaa gaacaaatca gtagagctgg 780
aggatgtaaa attccaccag tgcgtgcggc tctctcgctt tgacaacgac cgcaccatct 840
ccttcatccc gcctgatggg gactttgagc tcatgtcata ccgcctcagc acccaggtca 900
agccactgat ctggattgag tctgtcattg agaagttctc ccacagccgc gtggagatca 960
tggtcaaggc caaggggagc ttttaagaaac agtcagtggc caacggtgtg gagatatctg 1020
tgccctgtacc cagcgatgcc gactccccc a gattcaagac cagtgtgggc agcgccaagt 1080
atgtgccgga gagaaacgtc gtgatttgga gtattaagtc tttcccgggg ggcaaggagt 1140
acttgatgag agcccacttt ggccctccca gtgtggaaaa ggaagagggt gagggccggc 1200
ccccatcgg ggtcaagttt gagatccct acttcaccgt ctctgggata caggtccgat 1260
acatgaagat cattgagaaa agtgggtacc agggccctgc cctgggggtt cgctacattc 1320
accagagtg ggcgattacc aactttcggt accagctagg aaggggagaa gagatggggg 1380
ggttttaaca cgggggtttgc ttacagccc cggatgcaga tttttagaag ggagggcagg 1440
tgccgggtt
1448

```

004227"56E2960

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1394 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

atgaatacaa ggctgcaagt ggaacatcct gttactgaga tgatcacagg aactgacttg 60
gtggagtggc agcttagaat tgcagcagga gagaagattc ctttgagcca ggaagaaata 120
actctgcagg gccatgcctt cgaagctaga atatatgcag aagatcctag caataacttc 180
atgcctgtgg caggccatt agtgcacctc tctactcttc gagcagacct ttccaccagg 240
attgaaactg gagtacggca aggagacgaa gtttccgtgc attatgacct catgattgcg 300

aagtgggtcg tgtgggcagc agatcgccag ggcgcattga caaaactgag gtacagcctt 360
cgtcagtaca atattgttg agtgcaccac aacattgact tcttactcaa cctgtctggc 420
caccagagt ttgaagctgg gaacgtgcac actgatttca tccctcaaca ccacaaacag 480
ttgttgctca gtcggaaggc tgcagccaaa gagtctttat gccaggcagc cctgggtctc 540
atcctcaagg agaaagccat gaccgacctc ttcactcttc aggcacatga tcaattctct 600
ccattttcgt ctagcagtgg aagaagactg aatatctcgt ataccagaaa catgactctt 660
aaagatggta aaaacaatgt agccatagct gtaacgtata accatgatgg gtcttatagc 720
atgcagattg aagataaaac tttccaagtc cttggtaatc tttacagcga gggagactgc 780
acttacctga aatgttctgt taatggagtt gctagtaaag cgaagtgatt atcctggaaa 840
acactattta cctatatttc aaggaaggaa gtattgagat tgacattcca gtccccaat 900
acttatcttc tgtgagctca caagaaactc agggcgcccc cttagctcct atgactggaa 960
ccattgaaaa ggtgtttgtc aaagctggag acaaagtga agcgggagat tccctcatgg 1020
ttatgatcgc catgaagatg gagcatacca taaagtctcc aaaggatggc acagtaaaga 1080
aagtgttcta cagagaaggc gctcaggcca acagacacac tcctttagtc gaggttgagg 1140
aggaagaatc agacaaaagg gaatcggaat aaactccagc aaggaaatgg ccagttaagt 1200
agtgtcttct ctctccacca aaaagaggaa gtgcctccag cttttctggg ggtctcataa 1260
agagcagttt tactaaatga ttgtatgctt atgctgaaca cttttcatat tggagaatca 1320
tgcatttggt tcactaatta tctcaaaaata tttcatacta ataaagtga attatttttt 1380
attggaagcc aaaa
1394

```

004221 55552350

## (2) INFORMATION ON SEQ ID NO. 31:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 734 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

gccgacaaga tgttcttgcg gcctcttccg gctgcggggc gagtagtcgt cgcacgtctg 60
gccgtgagac gtttcgggag cgggagtcct tccaccgcag acatgacgaa gggccttggtl120
ttaggaatct attccaaaga aaaagaagat gatgtgccac agttcacaag tgcaggagag180
aattttgata aattgttagc tggaaagctg agagagactt tgaacatata tggaccacct240
ctgaaggcag ggaagactcg aaccttttat ggtctgcata aggacttccc cagcgtggtg300
ctagttggcc tcggcaaaaa ggcagctgga atcgacgaac aggaaaaactg gcatgaaggc360
aaagaaaaca tcagagctgc tgttgacgag ggtgacgagc agattcaaga cctggagctc420
tcgtctgttg aggtggatcc ctgtggagac gctcaggctg ctgcggaggg agcgggtgctt480
ggtctctatg aatacgaatg cctaaagcaa aaaaagaaga tggctgtgtc ggcaaagctc540
tatggaagtg gggatcagga ggcttgagc aaaggagtcc tgtttgcttc tgggcaagaa600
cttgggcacg ccaatttgat gggagacgcc agccaattga gattgacgcc aaccagattt660
tgccgaaatt atttgagaag attttcaaaa ttggtagtta gttaaaaccg aggtcctttt720
cagaccccaa tttt

```

734

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 692 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

004221 "SEEC"360

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
tgcagcgcgt gcgtgctgcg ctactgagca ggcgcattga ggactctgaa gcactgggct 60
tcgaacacat gggcctcgat ccccggtccc ttcaggctgt caccgatctg ggctggctgc120
gacctacgct gatccaggag aaggccatcc cactggccct agaagggaag gacctcctgg180
ctcggggccc caggggtccc gggaagacgg ccgcttatgc tattccgatg ctgcagctgt240
tgctccatag gaaggcgaca ggtccggtgg tagaacaggc agtgagaggc cttgttcttg300
ttcctaccaa ggagctggca cggcaagcac agtccatgat tcagcagctg gctacctact360
gtgctcggga tgtccgagtg gccaatgtct cagctgctga agactcagtc tctcagagag420
ctgtgctgat ggagaagcca gatgtggtag tagggacccc atctgcata ttaagccact480
tgcagcaaga cagcctgaaa ctctgtgact cctcggagct tttggtggtg gacgaagctg540
accttctttt ttcccttttg ctttgaagaa gagctcaaga agtcttcttc tggtcacttt600
gcccccgat ttaacaagg cttttctcat gtcagctact ttaacgagg acgtacaagc660
actcaaggag ctgatattac ataagccggt at 692
```

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 571 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
ctgccacgca cgactgaaca cagacagcag ccgcctcgcc atgaagctgc tgatggtcct 60
catgctggcg gccctcctcc tgcactgcta tgcagattct ggctgcaaac tcttgaggag120
catggttgaa aagaccatca attccgacat atctatacct gaatacaaaag agcttcttca180
agagttcata gacagtgatg ccgctgcaga ggctatgggg aaattcaagc agtgtttctc240
caaccagtca catagaactc tgaaaaactt tggactgatg atgcatacag tgtacgacag300
catttggtgt aatatgaaga gtaattaaact ttacccaagg cgtttggctc agagggtctac360
agactatggc cagaactcat ctgttgattg ctagaaacca cttttctttc ttgtgttgtc420
tttttatgtg gaaactgcta gacaactgtt gaaacctcaa attcatttcc atttcaataa480
actaactgca aatcacaaaa aaaaaaaaaa gtcgacg 517
```

## (2) INFORMATION ON SEQ ID NO. 34:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 322 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
tcaagctgtg ggtgagaagc tctctagcag ggactctgac cttatggagg atcgctgttt 60
ccccatctt tccttttcac ccaaaaaagt cctgcttctg tcacccttca aacagcctgt120
gagcctaaat tttgtggcc atgggacaga caaggacccc gtcttcagct gaactaaggal80
aaagtccctgc gacatctttg gccatcaaac tccaacccag tcacccaacc agagcctctg240
aggaatggcc ccttcttgcg gggaaccctt tacaatgggc ctcttgactg atgtttcccc300
aaaacagtgc ccctgtcatc ag                                     322
```

## (2) INFORMATION ON SEQ ID NO. 35:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1559 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:



(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gcacgagttg	agagtgagtg	tgtgtgtgtg	cgtgtgcacg	tgcacacatg	tgcacggttg	60
tatgtatggg	aaataaacct	ataaatggg	acgtattgga	gaaggaaata	catagacctt	120
caactttgag	caaatagcag	tgatgtttta	ggaactgaaa	tgtcacacct	aaagtcttca	180
gcccagctac	ttccctattt	ttggcgggga	gaagagggcc	tgattagaac	tgttctgggt	240
gtgtttggcg	ggaggggaat	aatttttgtt	cagtccctct	tagtgaccaa	actttaattt	300
ttaagaataa	tatattgact	tactgaactg	aagcattctg	agttgaaagg	agctccagag	360
gagtggagtt	ctgtgttgct	cacatgttaa	aagcttgctc	acctccagag	cagagggaat	420
acctatcttc	agatatccgc	ccattttcat	ctcttcatta	tagtcaaaca	gtgtgacttg	480
agagtgttgc	tctggtgtct	gtattctggc	ttatgaagat	tatttgaaaa	agaactctta	540
ctacattgaa	atgcagacct	ttaaaaaatt	aaatatgga	ttaggcagtc	aaaaaaccaa	600
acaagcataa	aaggtcaata	agttgtaatc	ttaaaagtaa	aggtggaaaa	ctcattataa	660
atggaagaaa	agttttgatt	tccctttttg	tttgatgggc	agtatgccat	attataccca	720
aagttccttt	aaaaaatatt	tccatcaacc	attttttatt	aaaataaaca	tttgagggaa	780
tttaccaaag	cagctttttt	cctcaaaagt	aacctgttcc	tctttggaat	agcacatttt	840
aggggcatgg	ttaataacct	agattttttac	tcagtaaatc	ctgatggtta	ctgtgtgtaa	900
aatatcttta	agtaggattg	aaggcctctg	tgggggaata	aaatattacc	aaagtctata	960
aaaataaaatt	ttacatgttc	tcttttatga	cagagagcag	cactggttct	gttattttta	1020
aatgaataa	ttgatttctt	gataggtgtt	taatatttct	tccctcactg	ctgattctta	1080
gatagaaacc	attctttata	tttgatagac	tgctttcaga	aaacccttat	caacaagtgt	1140
acaatactta	tctaaaacta	tacattttaga	atggagcagt	ttaatactag	atctcagaag	1200
ttttgaaaaa	tagcaaagaa	gactggattt	ggaaagcatg	gtctacaatt	ggttggttaa	1260
ttctgaagct	atgaagaata	aatgtttcaa	ctttggatta	tgaaccccca	tttatgattt	1320
tttaaatata	cttgaaataa	aaatgattaa	actaaaattt	ggtccagtg	cattactttg	1380
cactgctaaa	tccattatac	cttgatcgac	tttttttttt	ggtttgaatt	aataactgag	1440
agttttgtgt	gaagctacgg	catatctaac	cggagaattt	cggatgcctt	atacggtgat	1500
tatattatat	gggggcattt	gtagtgcagc	ggaagacgga	atttatgcct	ttgggaaac	1559

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1072 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

cacacgtgct gacggcgggg acattcacat ccataagaag aaatctcagc aagtgttcgc 60
gtccccagct aaacacccca tggacagcaa gggggaggag tccaagatca gctaccccaa 120
catcttcttc atgattgaca gcttcgagga ggtgttcagc gacatgaccg tagggaagga 180
gagatgggtct gtgtggagct ggtggctagt gacaaaacca acacgttcca gggggtcac 240
tttcagggtc ccattccgcta cgaggcgctc aagaagggtg atgacaaccg ggtgagcgtg 300
gccgcccga tggcacagaa gatgtcgttt ggcttctaca agtacagcaa catggagttt 360
gtgcgcatga agggccccca gggcaagggc cagcccgaga tggcggtcag ccgagtgtct 420
acaggtgaca cagccccctg tgggactgaa gaggactcca gccagcttc gccatgcac 480
gagcgggtga cctccttcag cagaccccc accccagaac ggaacaaccg gcctgccttc 540
ttctcccat cctcaagag gaaggtgcc cggaaccgga tcgctgagat gaagaagtcg 600
cactcggaac acgacagcga ggagttcttc cgggaggagc acggtggagc cgatctgcac 660
aatgcaacca acctgcggtc tcggtccctg tcgggcacag gacggtccct ggtcgggtcc 720
tggctgaagc tgaacagagc agatggaaac ttcttctct atgcacactt aacctacgtc 780
acgttgccgc tgcacggat ttaacagac atcctggaag ttcggcagaa gccatcctg 840
atgacaagtc cgcgtgcgga gcctgcgag agcccggcc gggcccagcc ctcgaggtgc 900
tgccaagtgc ctacctgtcc accgccaccg ggggtctgca tggcacgcca gtgttgagc 960
cgcagccagg cgaggccact cgactgccg ggccggggcc gactgcacga acaccagccc 1020
aaactgaagt gcctctgacg ggccctgctg gcgctgcttc cgccctgtgc cc 1072

```

## (2) INFORMATION ON SEQ ID NO. 37:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 454 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

gtgctgcatg gagtgagtgg cggcatccac cgtgaggagg agaggagctc tgataccctc 60
aggaccggcc aggaggggca tcacggaggc ttctggacga cttggagctg tgcctgggg120
agaaaaccgc tcctgtgtgg gccctgagtg ctgaggagga agctgccatg cacttttccc180
tggcattttt cctgcatggt tcgtctgttt ttttgcaaat aacatgttgt catgaatttt240
tatgcatgag gcatatttca tcatgtctgt atgctgaagt ccccttcac ctttcaattg300
gttgggtggac aggagagaga ggtccaaggt gccctacatc gtgcgccagt gccgtgggag360
gagatcgagc gccgaggcac ggaggaggtg ggcattctacc gcatgtctg ggtggccgca420
gacatccagg cactgaaggc agccttcaac gtca 454

```

## (2) INFORMATION ON SEQ ID NO. 38:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 700 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cttgtcggag ccctaaccag gggatatctct gagcctgggtg ggatccccgg agcgtcacat 60
cactttccga tcacttcaaa gtgggttaaaa actaatatatt atatgacaga agaaaaagat120
gtcattccgt aaagtaaaca tcatcatctt ggtcctggct gttgctctct tcttactggt180
tttgacccat aacttcctca gcttgagcag tttgttaagg aatgaggtta cagattcagg240
aattgtaggg cctcaaccta tagactttgt cccaaatgct ctccgacatg cagtagatgg300
gagacaagag gagattcctg tggtcacgc tgcacatgaa gacaggcctg gggggggccat360
tgcagctata aacagcattc agcacaacac tcgctccaat gtgattttct acattgttac420
tctcaacaat acagcagacc atctccgggtc ctgggtcaac agtgattccc tgaaaagcat480
cagatacaaa attgtcaatt ttgacctaa acttttggaa ggaaaagtaa aggaggatcc540
tgaccagggg gaatccatga aaccttaaac ctttgcaagg ttctacttgc caattctggg600
ttcccagcgg caaaggaagg cccgtttaca tgggggtgat gatgttattt gtggcagggtg660
ggattttttg ccctttacat tacagcagtg aggcgggggc 700

```

## (2) INFORMATION ON SEQ ID NO. 39:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 914 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

002275660

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

ccggcctgcg gtgggcagca gctcagggttc tccaaatcat tgcgtagttc cgaataccct 60
cggccacacc tggccttctc catgctcgga ataacttctt gcagcgacca acaggctaaa120
gagggggaag ggatccagca cgggctcttc ctccggcaac cacggtggga gcggcggagg180
aaatggacat aaaccgggt gtgaaaagcc agggaatgaa gcccgcggga gcgggaaatc240
tgggattcag ggcttcagag gacagggagt ttccagcaac atgagggaaa taagcaaaga300
gggcaatcgc ctcttggag gctctggaga caattatcgg gggcaagggt cgagctgggg360
cagtggagga ggtgacgctg ttggtggagt caatactgtg aactctgaga cgtctcctgg420
gatgtttaac tttgacactt tctggaagaa ttttaaatec aagctgggtt tcatcaactg480
ggatgccata aacaagaacc aggtcccgcc cccagcacc cgagccctcc tctacttcag540
ccgactctgg gaggatttca aacagaacac tcctttcttc aactggaaag caattattga600
gggtgcggac gcgtcatcac tgcagaaacg tgcaggcaga gccgagtcag aactacaatt660
acaaccagca tgcgtatccc actgcctatg gtgggaagta ctcagtcaag acccctgcaa720
agggggggag tctcaccttc ttctcggct tcccggtgc aacctgggcc tgcttgcaagt780
tgggtgaagt tttggttaagg caatttcttg caaccaacca ccgaaggccc cggaaaaagc840
actgggttcg tcaagggaag ctcttcccc ctttggggcc cccagccttg tggcaggccc900
ctgggcccg gttg

```

914

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1669 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227 562296 0963395 123700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

gagctgcagc agagcaggta acagctcttg cacctgtttc tcttgacact gacgtgcagc 60
tgctcttacc cacctctcct ggctgagcct tgcttgatac agcagcccgg aggcaccact 120
tgcttcccga gtctcaccct cccaggcagc toctacactc aactgcttct ctaggaaagg 180
tctcacctcc agcctggagc agtcgggatt acagaaagcc ccatccttgg cttagggagc 240
gccatgacga ctgaaattgg ttggtggaag ctgactttcc tccggaaaaa gaaatccact 300
cccaaagtgc tgtatgagat ccctgacacc tatgccccaa cagagggaga tgcagaacct 360
ccgaggcctg acgctggagg cccaacagc gactttaaca cccgcttggg gaagattgtg 420
gacaagagca caaagggcaa gcacgtcaag gtctccaact caggacgctt caaggagaag 480
aagaaagtga gagccacgct ggcagagaac cctaacctct ttgatgatca cgaggaagga 540
cggatcatca agtgaagggc tgaggagggt gctagcaccct cttggctccc tgccatcagc 600
cagatctgag acaggacctt gccacgctgg cctcttttgg catagctgaa gctgtggggc 660
cagttgatac ctgctggcag gaaatggctg ttttttaggt ttgtatttat gtgccgccac 720
ttttgtaagg cctgggagat cccagggtcc tccacctcc cctgaccac atacaaaggc 780
actctagttc aagagtgaag agtctcacc aggaggaaca gccctccttg aagcaatggc 840
agggccagca gggaggtggg catggcaggg aatggagaga gtgagccaga cagacttcac 900
ctccttactg gacacagggt caagggcgag tttcaattgc tgctcccttt actttctcta 960
cctgtgacta ctccctggac caatcctgag gagggcacat tttccagaag ccacgtgata 1020
ggggctggtt tctgtggagc cagaggcaga gacactgaac ttgagctcac ctccaaacac 1080
cggcagtaaa cttcctggaa ctttgccctc aggtgaggag gggacagagg accctggcac 1140
tctgttaggg tgctgtagaa gactagattg atggtagttt ggctgttag ttctgttttt 1200
ggccatgact tttgcagatg gcaagtcaaa caccctcaaa ggaagctac acgggccaaa 1260
tcgggggagt ggggtgggaa tttctctcct tccctttcct actataatag tatttaagac 1320
atatcagctc cagagatgag tcctggagcc ttgaattttg ttttaacaaa taattgtagg 1380
tttctctctg taataacaac gctggaaagg cagagaacct cttttatgct catgtcttgc 1440
atattattgag atgactgttt ctcatgcctt tatgttcctt catgtaagta aagtggacct 1500
ttgtgctcaa aaaaaaatt tcaagcttca ggaaggggtt cccaaggtgt gacaatgtag 1560
gaacctgggt cactaatttt taccatcaaa cctagcctta gtatgggat ggggcaagca 1620
gaaggagcta gttacacctc agtggctcagt tctctccagt caacagaga 1669

```

## (2) INFORMATION ON SEQ ID NO. 41:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 355 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227 355 2360

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ccggcctccc ctgctctga ggctcggggg cccagctcc gcgtaaactg cacgatttcg 60
ccctctgctc agtccccctc tgccccctct ttccaagaga gacttccaga tcccacattt120
tcttgactga ttttgaagct gtctgtttgc attctgattg ggaacactgg gatcattttc180
atcatgccga cagtgggtgt aatggatgta tccctttcca tgaccgacc tgtgtctatt240
gaggggtccg aggaatacca gcgtaagacc tagcagccca tggtttaacg atgcttggtt300
tgagcacatg gccacaaatt acaagcttga atttacagca cttgtgggtt ttcca 355

```

## (2) INFORMATION ON SEQ ID NO. 42:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227-56E2560



## (2) INFORMATION ON SEQ ID NO. 43:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2535 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00227 562450



agtttcggccac	agggggagagga	acctggccct	gggaggaggc	tgttgctgtgc	tctacagaa	60
tcccttctctg	aaggggaagag	catgtttgcg	ggcgctcccca	ccatgctgta	qaqctccccc	120
aaacagttaca	tgcagctcgg	aggcagggtc	ttgctggttc	tgatgttcat	gacctcctt	180
cactttgacg	ccagcttctt	ttctattgtc	cagaacatcg	tgggcacagc	tctgatgatt	240
ttagtggcca	ttggttttaa	aaccaagctg	gctgctttga	ctcttggtgt	gtggctcttt	300
gccatcaacg	tatatattcaa	cgcttcttg	accattccag	tctacaagcc	catgcatgac	360
ttcctgaaat	acgacttctt	ccagaccatg	tcggtgattg	ggggttgct	cctggtggtg	420
gccctgggccc	ctgggggtgt	ctccatggat	gagaagaaga	aggagtggta	acagtcacag	480
atccctacct	gcctggctaa	gacctgtggc	cgtcaaggac	tggttcgggg	tggattcaac	540
aaaactgcc	gcttttatgt	atcctcttcc	cttccctcc	cttggtaaa	gcacagatgt	600
tttgagaact	ttatttgcag	agacacctga	gaattcgatg	ctcagtctgc	tctggagcca	660
cagctctggcg	ttgtaccctg	cagtcaggc	cagcctggca	gctggaagcc	tccccacgc	720
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cattcaaagc	agtctccctc	ttatttgtaa	gtttacattt	ttagcggaaa	ctactaaatt	900
attttgggtg	gttcagccaa	acctcaaaac	agttaatctc	cctggtttta	aatcacacca	960
gtggcttttga	tgttgtttct	gccccgcatt	gtattttata	ggaatagtga	aaacattttag	1020
ggacacccaa	agaatgatgc	agtattaaag	gggtggtaga	agctgctgtt	tatgataaaa	1080
gtcatcggtc	agaaaatcag	cttggatttg	tgccaaagtgt	ttttttgggt	aaacacctgg	1140
gagttttagt	agcttgaggc	aagggtggagg	ggcaagaagt	ccttggggaa	gctgctggtc	1200
tgggtgctgc	tggcctccaa	gctggcagtg	ggaagggtca	gtgagaccac	acaggggtag	1260
ccccagcagc	agcacctctg	aagccagcct	ggccagctgc	tcagaccagc	ttgcagagcc	1320
gcagccgctg	tgggcagggg	gtgtggcagg	agctcccagc	actggagacc	cacggactca	1380
accagtttac	ctcacatggg	gocctttctg	agcaaggtct	cgaagcgca	ggccgccttc	1440
gctgagcagc	accgcccctt	cccagctgca	ctgcacctgt	ggacagcccc	gacacccac	1500
tttctctgagg	ctgtcgtctg	ctcagattgt	ccgtttgcta	tgccgaatgc	agccaaaatt	1560
cctttttaca	atttgtgatg	cottacogat	ttgatcttaa	tccctgattt	aaagttttct	1620
aacactgcct	tatactgtgt	ttctcttttt	gggggagctt	aactgcttgt	tgctccctgt	1680
cgtctgcacc	atagtaaattg	ccacaagggt	agtcgaacac	ctctctggcc	cctagacct	1740
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ctccctcttg	gcctctcatc	cattggctct	gcagggcagg	ggtgaggcag	gtttctgctc	1860
ataagtgcct	ttggaagtca	cctacctttt	taacacagcc	gaactagtcc	caacgcgttt	1920
gcaaattatc	ccctggtagc	ctacttccct	accocgaat	attggtaa	tcgagcaattg	1980
gcttcaggac	atgggtttct	ttctcctgtg	atcattcaag	tgtcactgc	atgaagactg	2040
gcttgcttca	gtgtttcaac	ctcaccaggg	ctgtctcttg	gtccacacct	cgctccctgt	2100
tagtgccgta	tgacagcccc	catcaaatga	ccttggccaa	gtcacggttt	ctctgtggtc	2160
aaggtttggt	ggctgatttg	tggaaagtag	ggtggaccaa	aggaggccac	gtgagcagtc	2220
agcaccagtt	ctgcaccagc	agcgcctccg	tcctagtggg	tgttcctggt	tctcctggcc	2280
ctgggtgggc	tagggcctga	ttcggggaaga	tgcctttgca	gggaggggag	gataagtggg	2340
atctaccaat	tgattctggc	aaaacaattt	ctaagatttt	tttgctttat	gtgggaacca	2400
gatctaaatc	tcattttatg	ctgtatttta	tatcttagtt	gtgtttgaaa	acgttttgat	2460
ttttggaac	acatcaaaat	aaataatggc	gtttgttgta	aaaaaaaaaa	aaaaaaaaaa	2520
aaaaaaaaaa	aaaaa					2535

## (2) INFORMATION ON SEQ ID NO. 44:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 805 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ggcacgagcg gcacgagcca tctccatccc cggagcatct gtatgattca gaagtacaac 60
cacgatgggg aagcagggtcg gctggaggct tttagccaag gggaaagtgt cctaaaggaa120
cccaagtacc aggaagagct ggaggacagg ctgcatttct acgtggagga atgtgactac180
ttgcagggct tccagatcct gtgtgacctg cacgatggct tctctggggg aggcgcgaag240
gcggcagagc tgctacaaga tgaatattca gggcggggaa taataacctg gggcctgcta300
cctgggtccct accatcgtgg ggaggcccag agaaacatct atcgtctatt aaacacagct360
tttgggtctcg tgcacctgac tgctcacagc tctcttgtct gccccttgtc cttgggtggg420
agcctggggc tgcgaccgga gccacctgtc agcttccctt acctgcatta tgatgccact480
ctgcccttcc actgcagtgc catcctgggt acagccctgg acacagtcac tgttccttat540
cgccctgtgtt cctctccagt ttccatgggt catctggctg acatgctgag cttctgtggg600
aaaaaggttg tgacagcagg agcaatcatc cctttccctt tggctccagg ccagtccctt660
cctgattccc tgatgcagtt tggaggagcc accccatgga ccccaactgtg tgcatgtggg720
gagccttctg gaacacgttg ctttgcccag tcagtgggtg tgagggggta tagacagagc780
atgccacaca agccacagac ttaat
                                                                 805

```

## (2) INFORMATION ON SEQ ID NO. 45:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

002227.5622960

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

cggaagtagc cgcaggcatg gcggcggtta tgcgctgtt gctctgctcg tcctgttget 60  
 cctggggccc ggcggctggt gccttgca gaacccacgc gacagcctgc gggaggaact 120  
 tgtcatcacc ccgctgcctt ccggggacgt agccgccaca ttccagttcc gcacgcgctg 180  
 ggattcggag cttcagcggg aaggagtgtc ccattacagg ctctttccca aagccctggg 240  
 gcagctgac tccaagtatt ctctacggga gctgcacctg tcattcacac aaggcttttg 300  
 gaggaccga tactgggggc cacccttctt gcaggcccca tcagggtgcag agctgtgggt 360  
 ctggttccaa gacactgtca ctgatgtgga taaatcttgg aaggagctca gtaatgtcct 420  
 ctcagggatc ttctgcgcct ctctcaactt catcgactcc accaacacag tcaactccac 480  
 tgccctcttc aaacccttgg gtctggccaa tgacactgac cactactttc tgcgctatgc 540

tgtgctgccg cgggaggtgg tctgcaccga aaacctcacc ccctggaaga agctcttggc 600  
 ctgtagtccc aaggcaggcc tctctgtgct gctgaaggca gatcgcttgt tccacaccag 660  
 ctaccactcc caggcagtg atatccgcc tggttgca aatgcacgct gtactagcat 720  
 ctctgggag ctgaggcaga ccctgtcagt tgtatttgat gccttcac caagggcagg 780  
 aaagaaagac tggccctct tccggtgtt ctccgaacc ctcacggagc cctgccccct 840  
 ggcttcagag agccgagtct atgtggacat caccacctac aaccaggaca acgagacatt 900  
 agaggtgcac ccacccccga cactacata tcaggacgtc atcctaggca ctcggaagac 960  
 ctatgccatc tatgacttgc ttgacaccgc catgatcaac aactctcgaa acctcaacat 1020  
 ccagctcaag tggaagagac cccagagaa tgaggcccc ccagtgccct tcctgcatgc 1080  
 ccagcggtag gtgagtggct atgggctgca gaagggggag ctgagcacac tgctgtaca 1140  
 caaccaccca taccgggct tccgggtgct gctgtggac accgtaccct ggtatctgcg 1200  
 gctgttacat ccactaccag cctgcccagg accggctgca accccacctc ctggagatgc 1260  
 tgattcagct gccggccaa 1279

(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1923 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

gcgcaagaca caggaggccc aggcggcgag tcaggacatg gcggcgattt gcagattcca 60
atctctctgt ttctgggcg attgaacacc caacattggc gaccgggatc gcggaaagtg 120
atggctgtcg tcccggcgtc tctctcagga caggacgtgg gatcatttgc atatcctaca 180
attaaagaca gaataccaca gatcttaact aaggttattg atacattgca tcgacataaa 240
agtgaatttt ttgagaaaca cggagaggaa ggctggaaag ctgaaaagaa agctatctct 300
ctcctttcta aattacggaa tgaattgcaa acagataaac catctatccc cttgggtgag 360
aaatttggtg atactgatat atggaatcag tacctagaat atcaacagag tcttttaaat 420
gaaagtgatg gaaaatcaag atggttctac tcaccgtggt tgttggtaga atgttacatg 480
tatcgaagaa ttcataagc aattatccag agtccaccaa tcgattactt tgatgtatct 540
aaagaatcaa aagagcaaaa tttctatggg tcacaggaaat ccacattgct tttatgtact 600
cacctgcaac aattgataag aactattgaa gacctagatg aaaatcagct gaaagatgag 660
ttttttaaac ttctgcagat ttcactgtgg ggaaataagt gtgatctgtc tctctcaggt 720
ggagaaagta gttctcagaa taccaatgta ctaaatccat tggaagacct aaaacctttc 780
attttattga atgatatgga acatctttgg tcattgctta gcaattgcaa gaaaacaaga 840
gaaaaagctt ctgctactag agtgtatatt gttctcgata attctggatt tgagcttggt 900
acagatttaa tattagccga cttcttggtg tctctgaac tggctactga ggttcatttt 960
tatggaaaaa caattccatg gtttgtttct gatactacta tacatgattt taattgggta 1020
attgaacagg taaaacacag taatcataag tggatgtcca agtgtggggc tgactgggaa 1080
gagtatatta aaatgggtaa atgggtttac cacaatcata tattttggac tctgcctcat 1140

gagtactgtg caatgcctca ggttgcacct gacttatatg ctgaactaca gaaggcacat 1200
ttaattttat tcaagggtga tttgaattac aggaagtga cagggtgacag aaaatgggag 1260
ttttctgttc catttcacat ggctctgaat ggcttccatc ctgcaccact ctgtaccata 1320
agaacattaa aagctgaaat tcaggttggt ctgcagcctg ggcaagggga acagctcctg 1380
gcctctgagc ccagctggtg gaccactgga aaatatggaa tatttcagta cgatgggtcc 1440
ctttgacttg atttaggagc tctcagttgc atagaaagat ctggtgagca ccttttcact 1500
cccagaaaag gagcacgtga attgagtcgc ctggcggctc tgtacgcgct cagggaagct 1560
tagcttcttg gtgcccactc acgtgcactg gatgattttt cttttgaaca ttttgcccc 1620
ctacactgtt tttggggata gctgggttaa gcaagttaaa gatatttaca tttatattgg 1680
agattttaag caactttttt ttcagggtaa atatataatt tcaaagtgtc tttaaatgga 1740
ccttaatttt gaagtgggta gggccaaaaa ataaagggag ggctcctttg aggtaggtac 1800
ccttggcctt tcctaaaaag cccctcaatg ggatttagat ccgggggggt ggggttat 1860
tccttggttt ggccatgaaa atccttgtaa ccggccttat cccttttgaa aaggggggtt 1920
ttt

```

## (2) INFORMATION ON SEQ ID NO. 47:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 706 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

catttttacga caggcgggat tgttttgtgg ctgtcagctt tctccgtggt ctgagtttgt 60
ggctgcattt ttatctctgg tggctctgct acggcggcgc agaaatgagg cagaagcggal20
aaggagatct cagccctgct gagctgatga tgctgactat aggagatgtt attaaacaac180
tgattgaagc ccacgagcag gggaaagaca tcgatctaaa taaggtgaaa accaagacag240
ctgccaaata tggcctttct gccagcccc gcctggtgga tatcattgct gccgtccctc300
ctcagtatcg caaggtcttg atgccaagt taaaggcgaa acccatcaga actgctagt360
ggattgctgt cgtggctgtg atgtgcaaac cccacagatg tccacacatc agttttacag420
gaaatatatg tgtatactgc cctggtggac ctgattctga ttttgagtat tccaccag480
cttacactgg ctatgagcaa cctccatgag agctattccg tgccagatat ggaccctttt540
ccttacagga caaggacacc ggattaggaa cagttaaaa caagttgggt tcgtagtg600
gggttaagtg ggagtttgtt tgtggatggg gtgggaactt tttggggccg ttccagagga660
ttacagagtt atttttatct cggaagttaa cgtgatgggt tttccg 706

```

## (2) INFORMATION ON SEQ ID NO. 48:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 749 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

gacctatcct catctgtgca aggaggagtg gccaaactctg gagcccaggc tgttgcttcc 60
tggtctgggtg gtgaatcctc catagtcttg tgagtgtagt gcccaactct ggagcccagg120
atgttgcttc ccggtctggt ggtgaatcct ccatagtctg gagatctcag ccctgctgag180
ctgatgatgc tgactatagg agatgttatt aaacaactga ttgaagccca cgagcagggg240
aaagacatcg atctaaataa ggtgaaaacc aagacagctg ccaaatatgg cctttctgcc300
cagccccgcc tgggtgatat cattgcttgc cgtccctcct cagtatcgca aggtcttgat360
gcccgaagtta aaggcgaaac ccatcagaac tgctagtggg attgctgtcg tggctgtgat420
gtgcaaacc cagagatgtc cacacatcag ttttacagga aatatatgtg tatactgccc480
tggtgtggac ctgattctga ttttgagtat tccaccagc cttacactgg gctatgagcc540
aacctccatg aggagctatt ccgtgccaga tatggaccct tttccttaca ggacaaggac600
accggattag gaacagttta aaacaagtgt ggttcgtagt gtgggggttaa gtgggagttt660
gtttgtggat ggggtgggaa ctttttgggg ccgttcacaga ggattacaga gttattttta720
tttcggaagt ttacgtgatg ggttttccg 749

```

## (2) INFORMATION ON SEQ ID NO. 49:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 857 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00227 3562350

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

accttaccaa ggggagaaaa aaaccctcca ctttggctca ctgtgggttt ggcactaaga 60
ggcacgatat ctgaaggagg tcattccagt tttaaaagta cggacagtgc tgttggaact120
gaccacaaaa atgtattgtt aaaaaaaaaat tgaaaaccag cagtgatttg ggtccccctg180
aaacctctgt gaatcggagg tgggccccagg aggggtgcagg acgcagcaga aatagtccca240
gaaaggagag acgggtcatg cagcgggctt gtgctttttt gtgtgtgttt gtgtgtttta300
caccatacat ctccaaatga agtattttatt aacaattgta gtgtaagcct gtgataaaaat360
agcacaaaagg ttcttttaaag aagttcactt ttaaggcatc agaaaagtta atgtggcaaaa420
catttttaatt aaaacatcag aagtaaatTTt tatttttaaac tttaggcctc tgaattttttc480
cagtaaacac agttcagcta tgtggcaaaag tcaatgggtg gcatctaaaa tgactttttta540
cattctacaa aaaaataaaaa taaaataaagg acacagcccc aaacgggtgtc acctcttcgc600
ggccgctcca catgcacaga atctactagg atttgtcacg gccgggtggc acccgatttg660
ttttgactat acaacaaaact tttttttcaa aagtatttgt tcaggataac tttaaaaata720
atataaaaaat aaacaatgga tttgactttt ccctcaaaat tgaaaagaaa ggggtggggg780
gaggtgttaa ccattggcct tttttttttt ggagggggccc cattgggatt gtaaggccct840
ggggttcgag cctttcc

```

857

## (2) INFORMATION ON SEQ ID NO. 50:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 268 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

ccgcgcccgg cccccaggca attttaataa taaatcttaa tagatggggt aagagctgcc 60
ttcatcccat acagagaata caatggtgct agactaagta gagattttat ttcagcttaal20
agattctggt tgatgtctga aattacatgt ttaggcggca tggggaacag gactgttctt180
tagcatcagt ttcacaatta ctttaattca ctaggtttca ttcaccttat aattctgaaa240
tttcatcagc agtggggaac agaaaagg

```

268

00422F 566460

## (2) INFORMATION ON SEQ ID NO. 51:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 297 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
ctgatgtgca ctctagggtta gtaaccatth ttgtgaaaaa tttagagaaa ttctttgagc 60
agcttccact gaaacactaa aacccaatag ggccaaaggc ccataacctg aggaaacctt120
atttattgct taatccaaca taggctatga aagttttgag tttcctcttg tgtattagaal80
tttcattcct atttgttgta gagagtatag tacggggaat cagtaaatta aatgaagtaa240
actaaagatt acacctttgc tgctggcact aagcgaaaag caaaaccagt ggctgtc 297
```

## (2) INFORMATION ON SEQ ID NO. 52:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 590 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

0022273662660



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

acgggtcaaaa tgataactca tgtattttat tccaacaaca tttgggtttat aaaggaatac 60
aaacaggcac aaaacatggg tcagaagatt tattaagtaa acttgctaaa atatggacag120
atacacttag cagtcaaaca gttgaatatt cattgctacc tcattaaagt ttttgatct180
gtattaccag gtccaaacat aaaaaccacc tctgttcaaa aaataaatgt tcagagagct240
gtatgttctt tgttctggta tgtacatttt aaaaaaacac ctctttccag tcttgctaac300
caagaatatt agtcatataa aagaacttag aarttttttc cccaagtaca agctatcttt360
tgctccaaaa cagttctgaa ggttttatct atattttatc ttatcccgag ggaccaacag420
caggcatacc tttgccaggc cttcttgag aaagacacag agccgtaaag gcaaaaataa480
aattgcaata aagtatatgg tattgggggc agggagaacc agaaaccctc aagggggacca540
atttttagca cgttcttttt ttagggttta ccctgtggag taagaactag 590

```

## (2) INFORMATION ON SEQ ID NO. 53:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004222T 56E2960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ggaaggggaa gtttcgcctc agaaggctgc ctgcgtggtc cgaattcggg ggcgccacgt 60  
 ccgcccgtct ccgccttctg catcgcggtt tcggcggtt ccacctagac acctaacgt 120  
 cgcggagccg gccgcgtcgt gagggggctg gcacggggag tcgggcggtc ttgtgcatct 180  
 tggctacctg tgggtcgaag atgtcggaca tcggagactg gttcaggagc atcccgcgca 240  
 tcacgcgcta ttggttcgcc gccaccgtcg ccgtgccctt ggtcggcaaa ctcggcctca 300  
 tcagcccggc ctacctcttc ctctggcccg aagccttctt ttatcgcttt cagatttgga 360  
 ggccaatcac tgccaacctt tatttccttg tgggtccagg aactggattt ctttatttgg 420  
 tcaatttata tttcttatat cagtattcta cgcgacttga aacaggagct tttgatggga 480  
 ggccagcaga ctattttatt atgctcctct ttaactggat ttgcatcggt attactggct 540  
 tagcaatgga tatgcagttg ctgatgatct ctctgatcat gtcagtactt tatgtctggg 600  
 cccagctgaa cagagacatg attgtatcat tttggtttgg aacacgattt aaggcctgct 660  
 attttacctg ggttatcctt ggattcaact atatcatcgg aggcctcggt atcaatgagc 720  
 ttattggaaa tctggttgga catctttatt ttttcctaag gttcagatac ccaatggact 780  
 tgggaggaag aaattttcta tcacacctc agtttttgta ccgctggctg cccagtagga 840  
 gaggaggagt atcaggattt ggtgtgcccc ctgctagcat gaggcgagct gctgatcaga 900  
 atggcgagg cgggagacac aactggggcc agggctttcg acttgagac cagtgaaggg 960  
 gcggcctcgg gcagccgctc ctctcaagcc acatttcctc ccagtgtctg gtgcgcttaa1020  
 caactgcgtt ctggctaaca ctgttggaac tgaccacac tgaatgtagt ctttcagtacl080  
 gagacaaagt ttcttaaatc ccgaagaaaa atataagtgt tccacaagtt tcacgattct1140  
  
 cattcaagtc cttactgctg tgaagaacaa ataccaactg tgcaaattgc aaaactgact1200  
 acattttttg gtgtcttctc ttctccctt tccgtctgaa taatgggttt tagcgggtcc1260  
 tagtctgctg gcattgagct ggggctgggt caccaaacc ttcccaaaag gacccttatc1320  
 tctttcttgc acacatgct ctctccact tttcccaacc cccacatttg caactagaag1380  
 aggttgccca taaaattgct ctgcccttga caggttctgt tattttattga cttttgccaal1440  
 ggcttggtca caacaatcat attcacgtaa ttttccctt ttggtggcag aactgtagca1500  
 atagggggag aagacaagca gcggatgaag cgttttctca gcttttgga ttgcttcgacl1560  
 ctgacatccg ttgtaaccgt ttgccacttc ttcagatatt tttataaaaa agtaccactg1620  
 agtcagtgag ggccacagat tggattaat gagatacgag ggttgttgct ggggtgttgt1680  
 tccgagtaag tgagaagggt agtggattga ctac 1714

## (2) INFORMATION ON SEQ ID NO. 54:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

ctcgagccgc tcgagccgaa tcggctcgag ctgaaaaagg gctacctgac cctgtcagac 60
agtggggaca aggtggccgt ggaatgggac aaagaccatg ggtcctgga gtcccacctg 120
gcggagaagg ggagaggcat ggagctatcc gacctgattg ttttcaatgg gaaactctac 180
tccgtggatg accggacggg ggctgtctac cagatcgaag gcagcaaagc cgtgccctgg 240
gtgattctgt ccgacggcga cggcaccgtg gagaaaggct tcaaggccga atggctggca 300
gtgaaggacg agcgtctgta cgtgggcggc ctgggcaagg agtggacgac cactacgggt 360
gatgtggtga acgagaaccc ggagtgggtg aaggtggtgg gctacaaggg cagcgtggac 420
cacgagaact ggggtgtccaa ctacaacgcc ctgcgggctg ctgccggcat ccagccgcca 480
ggtaacctca tccatgagtc tgccgtctgg agtgacacgc tgcagcgtg gttcttctg 540
ccgcgccgcg ccagccagga gcgctacagc gaggaaggac gacgagcgca agggcgccaa 600
cctgctgctg agcgcctccc ctgacttcgg cgacatcgct gtgagccacg tcggggcggt 660
gggtcccaact caccgcttct cgtccctcaa gttcatcccc aacaccgacg accagatcat 720
tgtggccctc aaatccgagg aggacagcgg cagagtcgcc tcctacatca tggccttcac 780
gctggacggg cgcttctctg tgccggagac caagatcgga agcgtgaaat acgaaggcat 840
cgagttcatt taactcaaaa cggaaacact gagcaaggcc atcaggactc agcttttata 900
aaaacaagag gagtgcactt ttgttttgtt ttgttctttt tggaactgtg cctgggttgg 960
aggtctggac agggagccca gtcccgggcc ccatagtggt gcgggcaactg gacccccggg 1020
ccccacggag gccgcggtct gaactgcttt ccattgctgc atctgggtgt gatttcggtc 1080
acttcaggca ttgactcaag gcctgcctaa ctggctgggt cgtttcttcc atccgacctc 1140
gtttcttttc tttcctatgt tcttttgttc agtgaatata cctagagctc ctaccatatg 1200
tcaggcccta tgccctaccc tgagaacgca gtaagcatga aggtggacct ggtttgctgg 1260

gaacccgagg gctaaccccc tttttcttcc caaatttggt gccttggaag aatcagggtcc 1320
agccctgaag atccttgggg

```

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 765 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

00221" 36E2960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

caggattgaa acaagatggc gggttcgtgg tgagaagccg tcaaggagta gaaattggta 60
tgcttagaag cagattctaa aagcagtttc tcttcagaac atcttttttc ataccacttg120
ataagcatct tgaaacacca tggctgtagc tgcagtaaaa tgggtgatgt caaagagaac180
tatcttgaaa catttatttc cagtccaaaa tggagcttta tattgtgttt gtcataaatc240
tacgtattct cctctaccag atgactataa ttgcaacgta gagcttgctc tgacttctga300
tggcaggaca atagtatgct accacccttc tgtggacatt ccatatgaac acacaaaacc360
tatccctcgg ccagatcctg tgcataataa tgaagaaaca catgatcaag tgctgaaaac420
cagattggaa gaaaaagtgt aacaccttga ggaaggacct atgatagaac aacttagcaa480
aatgttcttt actactaagc accgttggta tcctcatgga cggtatcaca gatgtcgtaa540
gaatctgaat cctccaaaag acagatgatg cggagggtcc tgggggaatc aaagagaaat600
gtgcctcatt tgccatttga gaaaatgcag tctgggtgat tcagtaatat atagtaaagt660
aataatgata aaatatcttt tcatatatta gaatgtgtac ttttatataa agtaattctg720
gatttgacat tctcatttag ggggacctat tccttttttc gtttt 765

```

## (2) INFORMATION ON SEQ ID NO. 56:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00221 3662360

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

gcagccggag taagatggcg gcgctgaggg ctttgtgcgg cttccggggc gtccggggcc 60
aggtgctgcg gcctggggct ggagtcogat tgccgattca gcccagcaga ggtgttcggc 120
agtggcagcc agatgtggaa tgggcacagc agtttggggg agctgttatg tacccaagca 180
aagaaacagc ccactggaag cctccacctt ggaatgatgt ggaccctcca aaggacacaa 240
ttgtgaagaa cattaccctg aactttgggc cccaacaccc agcagcgcat ggtgtcctgc 300
gactagtgat ggaattgagt ggggagatgg tgcggaagtg tgatcctcac atcgggctcc 360
tgcaaccgagg cactgagaag ctcatatgaat acaagacctt tcttcaggcc cttccatact 420
ttgaccggct agactatgtg tccatgatgt gtaacgaaca ggcctattct ctgctgtggg 480
agaagttgct aaacatcccg cctcctcctc gggcacagtg gatccgagtg gatccttgag 540
aaatcacacg tttgttgaa ccatcatgg ctgtgaccac acatgccctg gaccttgggg 600
ccatgacccc tttcttctgg ctgtttgaag aaaggagaa gatgtttgag ttctacgagc 660
gagtgtctgg agcccgaaatg catgctgctt atatccggcc aggaggagtg caccaggacc 720
tacccttgg gcttatggat gacatttata agttttctaa gaacttctct cttcggcttg 780
atgagttgga ggagttgctg accaacaata ggatctggcg aaatcggaca attgacattg 840
gggttgtaac agcagaagaa gcacttaact atgggttttag tggagtgatg cttcggggct 900
caggcatcca gtgggacctg cggaagaccc agccctatga tgtttacgac cagggttgagt 960
ttgatgttcc tgttggttct cgaggggact gctatgatag gtacctgtgc cgggtggagg 1020
agatgcgcca gtccctgaga attatcgcac agtgtctaaa caagatgcct cctggggaga 1080
tcaaggttga tgatgcaaaa gtgtctccac ctaagcgagc agagatgaag acttccatgg 1140
agtcactgat tcatcacttt aagttgtata ctgagggcta ccaagttcct ccaggagcca 1200
catatactgc cattgaggct cccaagggag agtttggggg gtacctgggtg tctgatggca 1260
gcagccggcc ttatcgatgc aagatcaagg ctccctgggtt tgcccatctg gctgggttgg 1320
acaagatgtc taaggacac atgttggcag atgtcggttg catcataggt acccaagata 1380
ttgtatttgg agaagtagat cggtgagcag gggagcagcg tttgatcccc cctgcctatc 1440
agcttcttct gtggagcctg ttcctcactg gaaattggcc totgtgtgtg tgtgtgtgtg 1500
tgtgtgtgtg tgtgtgtatg ttcattgaca cttggctgtc aggccttctg tgcatgtact 1560
aaaaaaggag aaattataat aaattagccg tcttgcgccc ctaggcctaa aaaaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaaa

```

## (2) INFORMATION ON SEQ ID NO. 57:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1166 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

cgccgcctgc ggggggggga gccagcaca gaccgccgcc gggacccoga gtcgcgcacc 60
ccagcccccac cgcgccccc ggcgcgcctg gaccccaagg accgcaagaa gatccagttc 120
tcgggtgccc cgcgccctag ccagctcgac ccccgccagg tggagatgat ccggcgcagg 180
agaccaacgc ctgccatgct gttccggctc tcagagcact cctcaccaga ggaggaagcc 240
tccccccacc agagagcctc aggagagggg caccatctca agtcgaagag acccaacccc 300
tgtgcctaca caccaccttc gctgaaagct gtgcagcgca ttgctgagtc tcacctgcag 360
tctatcagca atttgaatga gaaccaggcc tcagaggagg aggatgagct gggggagctt 420
cgggagctgg gttatccaag agaggaagat gaggaggaag aggaggatgc agccaggctg 480
aagtccctgaa ggtcatcagg cagtctgctg ggcaaaagac aacctgtggc cagggtctgg 540
aagggccctg ggagcgccca cccctctgg atgagtcga gagagatgga ggctctgagg 600
accaagtgga agaccctc ctaagtgagc ctggggagga acctcagcgc ccttccccct 660
ctgagcctgg caccaccc cccagcctgc atctcccagg aggaagtgga ggggacatcg 720
ctgttcccca gaaacccc ctatcctcac cctgttttgt gctcttcccc tcgctgcta 780
gggctgcggc ttctgacttc tagaagacta aggctggctc gtgtttgctt gtttgcacc 840
ctttggctga taccagaga acctgggacac ttgctgcctg atgcccaccc ctgccagtca 900
ttcctccatt caccagcgg gaggtgggat gtgagacagc ccacattgga aaatccagaa 960
aaccgggaac agggatttgc ccttcacaat tctactcccc agatcctctc ccctggacac 1020
aggagaccca cagggcagga ccctaagatc tggggaaagg aggtcctgag aaccttgagg 1080
tacccttaga tccttttcta cccactttcc tatggaggat tccaagtcaa catttgtctg 1140
aacggcctgt aacagggttc aggttg

```

## (2) INFORMATION ON SEQ ID NO. 58:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 487 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ctcagatcgg tggacgtgct cgcctccact cggggccagg tctatgtccc ggtttcccgc 60
agtcgcgggc agggcgccaa ggccgcagga ggagggtgag cggcgaagag acctccaggal20
agagcggctc tcggctgttt gcctcgccga tagagaagag aaaggatgca cgtcccaggal80
gggaggaaact actccaactt ttcctattca gaaacaaaga aaaaagatta ttcaagctgt240
gagggacaat tcattcctta ttgttactgg aaatacagga agtggtaaaa caactcaact300
cccaaaatat ctatatgaag caggggttttc acaacatggt atgattggtg taactcaacc360
acgaaaagta gctgctatat cagttgctca gagagtagct gaagaaatga aatgcacttt420
gggatccaaa gtaggatacc aagttcggtt tgatgattgc agttctaagg agacagcaat480
caaatat

```

## (2) INFORMATION ON SEQ ID NO. 59:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

aaactgtgta atgccccatg taatccataa aattttaact tttcccccta acgtttttgc 60
tgaaaaatgt tgggaaaccc tcaacacgcc ttcctgaaaa caattaaaaa acttgaaacc 120
tgtgaacctt tcaaaaaaac ctcaggttgg gaaaagaccc ccaaaccttc ttttaaggat 180
catttgtctc gcccatcaca ggatcttggg aatgtttccc taggggtgtg aaaaattaac 240
ccagggggga atgaagcaca tttttctggc aaccaaactt gaggttcctc gagaacagat 300
gcagagagac ctgctcctgc ttgcccggct acagggggcca ctgtggagtc acactgaggc 360
tgtgaccggc cataagccca ggagagcccg tggcagctgt gccgaggcgc caggacctct 420
aagcgggaagc ttcccaagct aggaatggag caacactgca atgaaatgtg tccaccaagc 480
tcattgttcc tcccgggtgc ttataaagct cagatgtata gtgacgtatg gacaaataca 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gcctttcttt ctcacaggca taagacacaa 600
attatataat gttatgaagc actttttacc aacggtcagt ttttacattt tatagctgcg 660
tgcgaaaggc ttccagatgg gagacccatc tctcttgcgc tccagacttc atcacaggct 720
gctttttatc aaaaagggga aaactcatgc ctttcctttt taaaaaatgc ttttttgtat 780
ttgtccatac gtcactatac atctgagctt tataagcgcc cgggaggaac aatgagcttg 840
gtggacacat ttcattgcag tgttgctcca ttcttagctt gggaagcttc cgcttagagg 900
tcctggcgcc tcggcacagc tgccacgggc tctcctgggc ttatggccgg tcacagcctc 960
agtgtgactc cacagtggcc cctgtagccg ggcaagcagg agcaggctct tctgcatctg 1020
ttctctgagg aactcaagtt tggttgccag aaaaatgtgc ttcattcccc cctggttaat 1080
ttttacacac cctaggaaac atttccaaga tctgtgatg gcgagacaaa tgatccttaa 1140
agaaggtgtg gggcttttcc caacctgagg atttctgaaa ggttcacagg ttcaatattt 1200
aatgcttcag aagcatgtga ggttcccaac actgtcagca aaaaccttag gagaaaactt 1260

aaaaatatat gaatacatgc gcaatacaca gctacagaca cacattctgt tgacaaggga 1320
aaaccttcaa agcatgtttc tttccctcac cacaacagaa catgcagtac taaagcaata 1380
tatttgtgat tccccatgta attcttcaat gttaaacagt gcagtcctct ttcgaaagct 1440
aagatgacca tgcgcctttt cctctgtaca tataccctta agaacgcccc ctccacacac 1500
tgccccccag tatatgccgc attgtactgc tgtgttatat gctatgtaca tgtcagaaac 1560
cattagcatt gcatgcaggt ttcattttct ttctaagatg gaaagtaata aaatatattt 1620
gaaatgtacc                                     1630

```

002227 562460

## (2) INFORMATION ON SEQ ID NO. 60:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

tgcgcgcgag cccgtgtccc caccggcgggc agcagcggcg gcggcggcgg ctgaacgcgg 60
agggggcgga gggagcccgc ggcggcggca gcagctacag cgaaatggcg gagaccgtgg 120
ctgacacccg gcggtctgat accaagccgc agaacctgaa tgacgcctac ggacccccca 180
gcaacttcct cgagatcgat gtgagcaacc cgaaacgggt gggggtcggc cggggccgct 240
tcaccactta cgaaatcagg gtcaagacaa atcttcctat tttcaagctg aaagaatcta 300
ctgttagaag aagatacagt gactttgaat ggctgcgaag tgaattagaa agagagagca 360
aggctgtagt tccccgcgtc cctgggaaag cgtttttgcg tcagttcctt ttagaggaga 420
tgatggaata tttgatgaca attttattga ggaaagaaaa caagggtgg agcagtttat 480
aaacaaggtc gctgggtcatc ctctggcaca gaacgaacgt tgtcttcaca tgtttttaca 540
agatgaaata atagataaaa gctatactcc atctaaaata agacatgcct gaaatttggc 600
aagaaggggc aaaaacgtga ctattaatga ttgataagca ccagtgaaga agttctaact 660
tttagcatgc tgcacagaaa ctggtataac atgccttcag tatactaaca ctcatatgct 720
cagttttgtt ttgttttggc agttgacaag aagttaattt gcttttagtaa aaatccctca 780
ttccagcctt tctatataaa tagctctttc ttgotgtttt aatgtggtgc aactatagc 840
ctcacaaacc tgttattcca gtgtaatctg cagtgtcgta actaaagtta ctggcttggg 900
cttatttgca cagtttttgc gtcttggttg cttcttgcat ctgattaact agaataattc 960
tctttcccc ttttaatttg tgatgtcact tgaccocatt tatgtgtagg agcactacac 1020
cattggtttc caatactgca cacataagat acatacttgt gtgcagaaag tatcttcctc 1080
caggcttgta atacccttca catggaagat taatgaggga aatctttata ttctgtataa 1140
aaacaaaagc aaattttatat actaaaatca tttgtctaaa aatttaagtt gttttcaaata 1200
aaaaattaaa atgcatttct gatatgcaaa aaaaaaaaaa aagaaaaaga aaaaaagagg 1260
ggcgccgct ct                                     1272

```

00227 662360



## (2) INFORMATION ON SEQ ID NO. 61:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

tgcagcgcgct gcgctgctgcg ctactgagca gcgccatgga ggactctgaa gcaactgggct 60
tcgaacacat gggcctcgat ccccggtcc ttcaggctgt caccgatctg ggctggctgc 120
gacctacgct gatccaggag aaggccatcc cactggccct agaagggaag gacctcctgg 180
ctcggggccc caggggctcc ggaagacgg cogcttatgc tattccgatg ctgcagctgt 240
tgctccatag gaaggcgaca ggtccgggtg tagaacaggc agtgagaggc cttgtttctt 300
ttcctaccaa ggagctggca cggcaagcac agtccatgat tcagcagctg gctacctact 360
gtgctcgggg tgtccgagtg gccaatgtct cagctgctga agactcagtc tctcagagag 420
ctgtgctgat ggagaagcca gatgtggtag tagggacccc atctcgcata ttaagccact 480
tgcagcaaga cagcctgaaa cttcgtgact ccctggagct tttggtggtg gacgaagctg 540
accttctttt ttcctttggc tttgaagaag agctcaagag tctcctctgg gaaggcagag 600
tcacttgccc cggatttacc aggtttttct catgtcagct acttttaacg aggacgtaca 660
agcactcaag gagctgatat tacataaccc ggttaccctt aagttacagg agtcccagct 720
gcctgggcca gaccagttac agcagtttca ggtggtctgt gagactgagg aagacaaatt 780
cctcctgctg tatgccctgc tcaagctgtc attgattcgg ggcaagtctc tgctctttgt 840
caacactcta gaacggagtt accggctacg cctgttcttg gaacagttca gcatccccac 900
ctgtgtgctc aatggagagc ttccactgcg ctccaggtgc cacatcatct cacagttcaa 960
ccaaggcttc tacgactgtg tcatagcaac tgatgctgaa gtccctggggg cccagtcacal1020
gggcaagcgt cggggccgag ggcccaaagg ggacaaggcc tctgatccgg aagcaggtgt1080
ggcccggggc atagacttcc accatgtgtc tgetgtgtc aactttgatc ttcccccaac1140
ccctgaggcc tacatccatc gagctggcag gacagcacgc gctaacaacc caggcatagt1200
cttaaccttt gtgcttccca cggagcagtt ccacttaggc aagattgagg agcttctcag1260
tgagagaaac aggggccccca ttctgctccc ctaccagttc cggatggagg agatcgagggl320
cttccgctat cgctgcaggg atgccatgcg ctcagtgact aagcaggcca ttcgggagggl380
aagattgaag gagatcaagg aagagcttct gcattctgag aagcttaaga catactttga1440
agacaaccct agggacctcc agctgctgcg gcatgacctt cctttgcacc ccgcagtggt1500
gaagccccac ctggggccatg ttctgacta cctggttccc cctgctctcc gtggcctggt1560
acgccctcac aagaagcgga agaagctgtc ttctcttgt aggaaggcca agagagcaaa1620
gtcccagaac cactgcgca gcttcaagca caaaggaaa aaattcagac ccacagccaa1680
gccctcctga ggttggtggg cctctctgga gctgagcaca ttgtggagca caggcttaca1740
cccttcgtgg acaggcgagg ctctgggtgt tactgcacag cctgaacaga cagttctgggl800
gccggcagtg ctggggccctt tagctccttg gcacttccaa gctggcatct tgccccttga1860
caacagaata aaaattttag ctgccccaaa aaaaaaaaaa aaaaaaaaaa aaaa 1914

```

004227 "S6EE4960

## (2) INFORMATION ON SEQ ID NO. 62:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 608 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

aatggaacca ggaattctta attaagcccg aagttcccaa gtctccttag cggaaaccgg 60
aaattgcccc aggaaagcaa agagggagat gaccagtgat acctccagtg ccagagggtca120
ctttgtggag ccaaatgctg gacatgggca gtcgagactc ggcattcttct gtcccccgca180
ttaatgactc tcaggaagga ggatgtaatt caaggcaagt ttctaattcc gaagctgcct240
gttcatgtta acaggacttc tttttattcg tcaagatgta ctggttccct ggcaccttaa300
gggaaatcct gataaaggca aacctgttga gccatttggt cccataggat cccaggaccc360
aagtccctgtg tttcatcggt actaccatgt gttccgtgag ggagaactgg aagggtgcctg420
caggactgtg agtgaatgca gaattctgca aagctactac gatcaaggaa actggtgtgt480
gattcttcaa aaggcctgat tatttacctg aacacatcat atataaagaa gaaatgctca540
cttaaaaaaa aaagagggga taaattaatt acccgtttaa ttaaagagaa aacttggtgg600
gaagtacc                                     608

```

## (2) INFORMATION ON SEQ ID NO. 63:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2674 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

tgaagagaag ttaaggtgaa gagccgaaga gcctgatgcg tgatgagcgt ctaagaaagg 60  
 agaagcaaga gcagagaaga gagagagaaa gaacgggaga gagaaaggga agaaagagaa 120  
 aggaaaagac gaagggaaga ggaagaaaaga gaaaaagaaa gggctcgtga cagagaaaaga 180  
 agaaagagaa gtcgttcacg aagtagacac tcaagccgaa catcagacag aagatgcagc 240  
 aggtctcggg accacaaaag gtcacgaagt agagaaagaa ggcggagcag aagtagagat 300  
 cgacgaagaa gcagaagcca tgatcgatca gaaagaaaac acagatctcg aagtcgggat 360  
 cgaagaagat caaaaagccg ggatcgaaag tcatataagc acaggagcaa aagtcgggac 420  
 agagaacaag atagaaaatc caaggagaaa gaaaagaggg gatctgatga taaaaaaagt 480  
 agtgtgaagt ccggtagtgc agaaaagcag agtgaagaca caaacactga atcgaaggaa 540  
 agtgatacta agaattgaggt caatgggacc agtgaagaca ttaaatctga aggtgacact 600  
 cagtcctaatt aaaactgatc tgataagacc tcagatcaga cagaggtaac tgtattgttt 660  
 ctcaatttga ttagggtctt ttgttactgt ttgacagtgc agcgtaagta tgcacagatg 720  
 aagatggaac taagccgagt aagaagacat acaaaagcct cttctgaagg aaaagacagt 780  
 gtagtcctgc aaaacatttt gaggtacatt gttttgtctc agctattttg tagcagactc 840  
 gtgcccccat tagtgtgctt ctttggaat tatcgccac atttgaata tagtcgccat 900  
 tgaaaagtta attatccttt ttttagggat tttgatgtca tttctttttt tttttaata 960  
 aaaaggttga actgtttttt tttttctttt tgggtattaag tccatcttgt gttggtacat 1020  
 tggcagagac atatgcttta aaaacttaaa tatttcggag gcacatgttg gactactttg 1080  
 ttttaattaa actgctagta tttctttgtc aaggatgttt ctagtttttt gctttattgc 1140  
 cttgcattct aatgcagttt gttctgtaac tcgagagcca gtagcattgg attgatggaa 1200  
 gtgtagggtt tatgaattat tgcagctgac taccatacct cacacagcgt tgggtgtgtg 1260  
 agcggcccat gaaaagccaa attaaaaatc aaggattcag tcaaactaag caggactcal 1320  
 tgccaggtac tcttttctct acccacatcc atgtttgaat gctattgcct gtgatcttta 1380  
 cgcttaactg ttgtgtatct tttttgttct ttacaagaag tgcagagggg ttttttgtgt 1440  
 attgctgtaa aacttataaa acaaatgtta acagaatgga attttttttc aactgtatgt 1500  
 agggctgcag tgggtggccag aattagatat ctttaagaa ttttaaatc aataaacact 1560  
 tcatattatt cgccttggtt cactcaatgc aattctcaag tctataagag gtatgtgctt 1620  
 aatatttctt actgtgtagg agaatttgca gtcagccata ggtatgtagg aatagtcact 1680  
 cactggctga tacatttaaa gcagcagtggt gaatagcaag gacagacacc ttcaatttgt 1740  
 gaaatcaaag aactgatgca ctatatagaa cgaatttggg tttttaaaga aatattaaaa 1800  
 gttaggtact gtaagtgttc ttaaaacctg taaacttcat tctgtgggct agtgggtgtg 1860  
 gacaaaatat tcctaataag aggaagtacc aattagttga tttgttgggt gcattccctt 1920  
 tttgggaaag caatgtaagg ttatgtctgt gtatgtcatt cacacttagg caagcataca 1980  
 caggcacatg gctttaagaa ccacactgat gccttgataa ttaaaaagaa tacaagcatt 2040  
 ccattgtacac atgttaatta gcagtttagt actgggcca cactttctca taaaaattgg 2100  
 ccttttacat gttgtctaatt tatcattttt ccccaaattt tgcgttgtag gactactgtt 2160  
 cgaagatttt tggagaataa ctgagaacgg cataaagtga agatcgacat ttaaaaaatg 2220  
 aggtgaaaga aagctatagt ggcatagaaa aagratataag ctcagttagt ttttttatta 2280  
 ttattattat taaaagttaa ttcaggactg atgtgacctt ccagatttca gaacatgtgt 2340  
 taatagtata tatgccactg aaaacttagg toctgtatca tacttttttc ttttaagact 2400  
 ttttaagaaat attacttaaa catgtggctt gctcagtggt taattgcaag ttttcaatct 2460  
 tggactttga aaacaggatt aaacgttagt attcgtgtga atcagactaa gtgggatttt 2520  
 atttttacaa cttctgtcta cttagccttt ggatttagaa gtaaaaaata agtatctctg 2580  
 actttctgtt acaaagttga ttgtctctgt cattgaaaag ttttagtatt aatctttttc 2640  
 taataaagtt attgactctg aaaaaaaaaa aaaa 2674

002227 562290

## (2) INFORMATION ON SEQ ID NO. 64:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 326 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

gacaaatgag gggtttggcat gcagctcgtc atcttaagag ttactatctt cttgccctgg 60
tggtttcgccg ttccagtgcc cctgctgca gaccataaag gatgggactt tggtgagggc120
tattttccatc aatttttctt gaccgagaag gagtcgccac tccttaccga ggagacacaal80
acacagctcc tgcaacaatt ccatcggaat gggacagacc tacttgacat gcagatgcat240
gcttctgcta cagcagcccc actgtggggg gctgatggg tccgacaact gcctctcgcc300
aggaagatgc aagtggatta agcaca                                     326

```

## (2) INFORMATION ON SEQ ID NO. 65:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 888 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227566660

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

ctcgtgcggt gatgttgagc agaagataca attcaaaaaga gaaacagcca gtttgaaact 60
gttaccacac cagccccgaa ttgtggagat gaagaaaagga agcaatggct atggtttcta120
tctgagggca ggctcagaac agaaaggcca aatcatcaag gacatagatt ctggaagtcc180
agcagaggag gctggcttga agaacaatga tctggtagtt gctgtcaacg gcgagtctgt240
ggaaaccctg gatcatgaca gtgtggtaga aatgattaga aagggtggag atcagacttc300
actgttggtg gtagacaaag agacggacaa catgtacaga ctggctcatt tttctccatt360
tctctactat caaagtcaag aactgccccaa tggctctgtc aaggaggctc cagctoctac420
tcccacttct ctggaagtct caagtccacc agatactaca gaggaagtag atcataagcc480
taaaactctgc aggctggcta aagggtgaaaa tggctatggc tttcacttaa atgcgattcg540
gggtctgcca ggctcattca tcaaagaggt acagaagggc ggctcctgctg acttggctgg600
gctagaggat gaggatgtca tcattgaagt gaatgggggtg aatgtgctag atgaacccta660
tgagaagggtg gtggatagaa tccagagcag tgggaagaat gtcacacttc tagtctgtgg720
aaagaaggcc tatgattatt tccaagccta agaaaatccc tattgttccc tgcttggctg780
atgccagttg acagccctgc aggttctaaa gaaggaatag tgggtggagtc aaaccatgac840
tcgcacatgg caaaagaacg ggcggctatt gcagacggct aatttatg 888

```

## (2) INFORMATION ON SEQ ID NO. 66:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 202 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

atcacagggg tacaaccaga acacatacag tacttgaaaa attattttcca cctttggaca 60
cgacagtttag cgcataattta tcactactat attcatggcc caaaaggaaa tgaaatacga120
acatcaaaaag aagttgaacc tttcaacaat attgatattg aaattttctat gtttgaaaaa180
gggaagggtac ctaagattgt ca
202

```

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1225 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

ggccggtgga	ggcggcggt	gcggcacgga	aggggaagcg	ctgaggcggt	ggggcccaca	60
gccatggcga	agctgttgca	ggaggagctc	tcggctcctg	ccgcgatttt	ctgcaggccc	120
cacgagtggg	agggtctgag	ccgctcagag	acagatggga	ccgtgttcag	aattcacaca	180
aaagctgaag	gatttatgga	tgcggaatata	cctctggaat	tgggtgttcca	tttgccagtc	240
aattatcctt	catgtctacc	tggtatctcg	attaactctg	aacagttgac	cagggcccag	300
tgtgtgactg	tgaaagagaa	gttacttgag	caagcagaga	gcctttttgtc	ggagccctatg	360
gttcatgagc	tggttctctg	gattcagcag	aatctcaggc	atatcctcag	ccaaccagaa	420
actggcagtg	gcagtgaaaa	gtgtactttt	tcaacaagca	cgaccattga	tgatggattg	480
tggaataactc	ttttgcattt	agatcacatg	agagcaaaga	ctaaatatgt	caaaattgtg	540
gagaagtggg	cttcagattt	aaggctgaca	ggaagactga	tgttcatggg	taaaataata	600
cttgattttta	ctacagggag	acagaaacaa	cctcaagggtg	tacttgattc	ttcagaaaac	660
ctccaaagta	gatgtggact	caagtggaaa	gaaatgcaaa	gagaaaaatga	ttagtgtact	720
gtttgaaaca	aaagtacaga	cagaacacaa	aaggtttctg	gcatttgaa	tcaaagagta	780
ttcagcgttg	gatgaattac	aaaaggaatt	tgaaactgca	ggacttaaga	agcttttctc	840
cgaattttgta	cttgctctgg	taaaatgaaa	tggaaagacag	gaatctttta	gtaaaatagc	900
agtgtttttt	gttggtttttg	cattggattt	ggggagtggg	taattgaaat	agtcaatttt	960
aaagttttctc	tgaagcaaaa	tgataggcat	cattctaact	tcagaacaa	aagccagttc	1020
tgtttttatga	aatattaaac	atgaagaaaa	cttgtatat	ctaagtgttg	ccaggaaagg	1080
ctaggtttcag	tagatgagac	attatttaaa	agataaat	aaaaagatgg	taaatgaaca	1140
cttggttttta	tagacaatat	ttgtttgaaa	ctatgtaatt	ttctggctaa	ttttcttgta	1200
attaaatgat	tttttaaaaa	aagaa				1225

(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1093 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

gagggcgggc ctgtttccgg ggaggcggtt ggggcttgag gccgagaacg gcccttgctg 60
ccaccaacat ggagactttg taccgtgtcc cgttcttagt gctcgaatgt cccaacctga 120
agctgaagaa gccgccctgg ttgcacatgc cgtcggccat gactgtgtat gctctgggtg 180
tggtgtotta ctctctcatc accggaggaa taatttatga tgttattggt gaacctccaa 240
gtgtcggttc tatgactgat gaacatgggc atcagaggcc agtagctttc ttggcctaca 300
gagtaaatgg acaatatatt atggaaggac ttgcatccag cttcctatctt acaatgggag 360
gttttaggttt cataatcctg gaccgatcga atgcacaaaa tatcccaaaa ctcaatagat 420
tccttctctt gttcattgga ttctgtctgt tcctattgag ttttttcatg gctagagtat 480
tcatgagaat gaaactgcog ggctatctga tgggttagag tgcctttgag aagaaatcag 540
tggatactgg atttgctcct gtcaatgaag ttttaaaggc tgtaccaatc ctctaatatg 600
aaatgtggaa aagaatgaag agcagcagta aaagaaatat ctagtgaata aacaggaagc 660
gtattgaagc ttggactaga atttcttctt ggtattaaag agacaagttt atcacagaat 720
tttttttctt gctggcctat tgctatacca atgatgttga gtggcatttt ctttttagtt 780
tttcattaaa atatattcca tatctacaac tataatatca aataaagtga ttatttttta 840
caaccctctt aacattttttt ggagatgaca tttctgattt tcagaaatta acataaaatc 900
cagaagcaag attccgtaag ctgagaactc tggacagttg atcagcttta cctatggtgc 960
tttgccctta actagagtgt gtgatggtag attatttcag atatgtatgt aaaactgttt 1020
cctgaacaat aagatgtatg aacggagcag aaataaatac tttttctaata taaaaaaaaa 1080
aaaaaaaaaa aaa                                     1093

```

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 309 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

cacaaagtga ttgtggtatg gaacaatatt ggagagaagg caccagatga gttatggaat 60
tctctagggc cccaccctat ccctgtgatc ttcaaacaac agacagcaaa caggatgaga120
aatcgactcc aggtctttcc tgaactggaa accaatgcag tgttgatggt agatgatgac180
acactcatca gcaccccaga ccttggtttt gctttctcag tttggcagca atttcctgat240
caaattgtag ggatttggtt cctagaaaagc acgtctttta ctttcattca aggtatctac300
agttattggg                                     309

```

## (2) INFORMATION ON SEQ ID NO. 70:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 380 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

ctcatctgat cccttttatg gccaaatcat ccttcagagt agggaacact cagacattct 60
gtgcatgttg ttcccccaaa gcatggatcat cacaaagtcc tgagttctgg tgtgtgctcc120
cgccctcctgg gtatacagag agaaggcagg aatcaggagt tccagaagca tatacatgtg180
gctaccccag caacaagcgg catcctgtgc tcagataagc tgcattggtg ggaagtgttt240
ttcctcgac gttgaggctt agtggagatg ggcaccactg ccatttgctc agaagaaggc300
tggctgggtc ctaactgcat ccacactgc ccagatcatt ctagataggt tattttctga360
atgtttatag atttcttata                                     380

```

## (2) INFORMATION ON SEQ ID NO. 71:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1253 base pairs

002227562360



- (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```

gcgcccgac  tccagttagg  agccttgatg  ccggagggga  cagtgggtcg  ccgagagcgc  60
ccggagggaa  ccgcctggcc  ttccggggacc  accaattttg  tctggaacca  ccctcccggc  120
gtatcctact  cctgtgtccg  cgaggccatc  gcttcactgg  aggggtcgat  ttgtgtgtag  180
tttggtgaca  agatttgcat  tcacctggcc  caaacctttt  ttgtctcttt  gggtgaccgg  240
aaaactccac  ctcaagtttt  cttttgtggg  gctgcccccc  aagtgtcgtt  tgttttactg  300
tagggctctc  ccgcccggcg  cccccagtgt  tttctgaggg  cgaaaatggc  caattcgggc  360
ctgcagtgtc  tggccttctc  catggccctg  ctgggctggg  tgggtctggt  ggccctgcacc  420
gccatccgc  agtggcagat  gagctcctat  gcgggtgaca  acatcatcac  ggcccaggcc  480
atgtacaagg  ggctgtggat  ggactgcgtc  acgcagagca  cggggatgat  gagctgcaaa  540
atgtacgact  cggtgctcgc  cctgtccgog  gccttgagg  ccactcgagc  cctaattggtg  600
gtctccctgg  tgctgggctt  cctggccatg  tttgtggcca  cgatgggcat  gaagtgcacg  660
cgctgtgggg  gagacgacaa  agtgaagaag  gcccgatatg  ccatgggtgg  aggcataatt  720
ttcatcgtgg  caggtcttgc  cgccttggtg  gcttgctcct  ggtatggcca  tcagattgtc  780
acagactttt  ataacccttt  gatccctacc  aacattaagt  atgagtttgg  ccctgccatc  840
tttattggct  gggcagggtc  tgccctagtc  atcctgggag  gtgcaactgt  ctctgttcc  900
tgtcctggga  atgagagcaa  ggctgggtac  cgtgcacccc  gctcttacc  taagtccaac  960
tcttccaagg  agtatgtgtg  acctgggatc  tccttgcccc  agcctgacag  gctatgggag  1020
tgtctagatg  cctgaaaggg  cctggggctg  agctcagcct  gtgggcaggg  tgccggacaa  1080
aggcctcctg  gtcactctgt  ccctgcactc  catgtatagt  cctcttgggt  tgggggtggg  1140
ggggtgccgt  tggtgggaga  gacaaaaaga  gggagagtgt  gctttttgta  cagtaataaa  1200
aaataagtat  tgggaaacaa  aaaaaaaaaa  aaaaaaaaaa  aaaaaaaaaa  aaa  1253

```

(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 439 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

000227 3566360

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```
ctaaggggag gacaggcaga aaccaggaat gccaaacttaa acctgttttg tgctctgact 60
gtttgttagt atcactctca agaatgaaga gaaacctcaa cctttctgtt tccggccaac120
tttattgaat ttgttttttt aaatgcagtt tacatgcagt ttctttgaaa agtcatgttg180
aatttagatc tgttctctga gtaagacttg gcgagtatgt gaaacttgac tcaagttaca240
tttctttttt tctgtccccc aaacgttcac gcttcttata ggctccactt tgaggctctg300
atgaacattc cagtgtctgt gttggatgtc aatgatgatt ttgctgagga agtaaccaa360
caagaagacc tcatgagaga ggtgggaagg actttaactc ctgtttttct ggtgggtttcc420
ctttggttgt accttttaa                                439
```

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1252 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

004227 666296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

tggacctgcc cgacgccctg ctgcccgaact tgcccgcgct ggtggggcccc aagcagctga 60
tcgtgctggg aaacaaagtg gacctcctgc cccaggatgc tectggctac cggcagagggc 120
tgcgggagcg actgtgggag gactgtgccc gcgcggggct cctgctggcc cctggcacca 180
agggccacag cgccccgtca aggacgagcc acaggacggg gagaatccga atccgccgaa 240
ctggtcccgc acagtgggtca gggacgtgcg gctgatcagc gccaaagaccg gctatggagt 300
ggaagagttg atctctgccc ttcagcgctc ctggcgctac cgtggggagc tctacttagt 360
gggcgccacc aacgccggca aatccactct cttaacaacg ctctggagt ccgattactg 420
cactgccaaag ggctccgagg ccacgcagag agccaccatc tccccttggc cagggtactac 480
attaaacctt ctgaagtttc ctatttgcaa cccaactcct tacagaatgt ttaaaaggca 540
tcaaagactt aaaaaagatt caactcaagc tgaagaagat cttagtgagc aagaacaaaa 600
tcagcttaat gtcctcaaaa agcatgggta tgcgttagga agagtggaa ggacattctt 660
gtattcagaa gaacagaagg ataacattcc ctttgagttt gatgctgatt cacttgcctt 720
tgacatggaa aatgaccctg ttatgggtac acacaaatcc accaaacaag tagaattgac 780
tgcacaagat gtgaaagatg cccactgggt ttatgacacc cctggaatta caaaagaaaa 840
ttgtatttta aatcttctaa cagaaaaaga agtaaatatt gttttgcaa cacagtccat 900
tgttccaaga acttttgtgc ttaaaccagg aatggttctg tttttgggtg ctataggccg 960
catagatttc ctgcagggaa atcagtcagc ttggtttaca gtcgtggctt ccaacatcct 1020
ccctgtgcat atcacctcct tggacagggc agacgctctg tatcagaagc atgcaggtca 1080
tacgttactc cagattccaa tgggtggaaa agaacgaatg ggcaggattt cctcctcttg 1140
ttgctgaaga cattaatggt taaaagaaa gactgggggc aacctggaag cagtgggccg 1200
acatcaaagt ttcctctgca ggtaatttta tgccaagcac tttttaaaaa gt 1252

```

## (2) INFORMATION ON SEQ ID NO. 74:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 695 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227 9602250

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

tggttcattgc ctccctgagcg tagtccagtt acttttcaggc tcgggggagtg aaggcctcgt 60
tgagagaagg totcattcgg tgttttggga agagagtcgt gtggggcccag gtatcgtagc120
ggcgacacga gagagacggg cgggtgtgaca gccttccact acctgcacga gtgtattggt180
ctgtctgcta tcagctatgc cgtgcccgt tgcgctgcag acccgcttg ccaagagagg240
catcctcaaaa catctggagc ctgaaccaga ggaagagatc attgccgagg actatgacga300
tgatcctgtg gactacgagg ccaccagggt ggaggggccta ccaccaagct ggtacaagg360
gttcgacct tctgcggggc tcccttacta ctggaatgca gacacagacc ttgtatcctg420
gctctcccca catgacccca actccgtggg taccaaatcg gccaaagaagc tcagaagcag480
taatgcagat gctgaagaaa agttggaccg gagccatgac aagtcggaca gggggccatga540
caagtcggac cgcagccatg agaaactaga caggggccac gacaagtcag accggggcca600
cgacaagtct gacagggatc gagagcgtgg ctatgacaag tccaggaacg ggattcggga660
ccgcgggtat gaccaagcag accgggaaga gggcc 695

```

## (2) INFORMATION ON SEQ ID NO. 75:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2514 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004221 565660

cggcgacggc	gcggggggcag	ctgggaatcc	ggaatgctgc	cggatggccc	tgggtcctcg	60
ctgtggggga	atccgggctt	gcagacgagt	tttagaaaga	gcgttttcgc	tacgtaaagc	120
acattcgata	aaggcatatg	aaaatacttt	gcagctgggtg	agaaatatca	tacctcctct	180
gtcttccaca	aagcacaaaag	ggcaagatgg	agaatatggc	gtagttaggag	gctgtcagga	240
gtacactgga	gccccatatt	ttgcagcaat	ctcagctctc	aaagtgtgac	agccccaatg	300
ctgttcatga	ggtggagaag	tggctgcccc	ggctgcatgc	tcttgctgta	ggacctggct	360
tgggtagaga	tgatgcgctt	ctcagaaatg	tccaggggcat	tttggaaagt	tcaaaggcca	420
gggacatccc	tgttgtcatc	gacgcggtga	gttgacttct	ctcctcctgg	ctcggactcc	480
cggaaaggcct	gtgcagtgag	cacggctcct	tgttctgtgc	aggatggcct	gtggtaggtc	540
gctcagcagc	cggccctcat	ccatggctac	cggaaaggctg	tgtctactcc	caaccacgtg	600
gagttcagca	gactgtatga	cgctgtgctc	agagggcccta	tggacagcga	tgacagccat	660
ggatctgtgc	taagacttcag	ccaagccctg	ggcaacgtga	cgggtggtcca	gaaaggagag	720
cgcgacatcc	tctccaacgg	ccagcagggtg	cttgtgtgca	gccaggaagg	cagcagccgc	780
agggtgtggag	ggcaaggggga	cctcctgtcg	ggctccctgg	gcgtcctggg	acactgggcg	840
ctccttgctg	gaccacagaa	aacaaatggg	tccagccctc	tcctgggtggc	cgcgtttggc	900
gcctgtcttc	tcaccaggca	gtgcaaccac	caagccttcc	agaagcacgg	tcgctccacc	960
accacctccg	acatgatcgc	cgagggtggg	gccgccttca	gcaagctctt	tgaaacctgal	1020
gcccgcgcag	accagaagta	aacaggcacc	ttggacgggg	gagagcgtgt	gtgtgatggg	1080
aaaatccgga	cccacgcgtg	tgctgaaggc	gtacgggtgct	tgccagattt	tcaacttagl	1140
cataaattgg	ttgccattga	gaatttaaga	atctggaata	tttcagcttt	tggttaaact	1200
taatgcatgg	ttagagatgt	tatggcgaca	ctaaacaaag	tattcctgaa	ctttccttag	1260
ctccttggtg	gtaactggga	agacagaaat	gaagaaaatc	acatgagaat	gaagaattct	1320
ttagcagctc	aacagagttt	ctcggcctgc	tcccagatcg	gcgaagtttc	tacttgttac	1380
tctctctgcc	ggcgcccttc	gttctctctc	tgttccctt	ccctagtctt	tcctccggca	1440
gggagctggg	caggggtccc	cgggtgtctc	cctgagtcct	gactgcactg	actgggtcca	1500
tcagagggct	gcttcgttct	ccagctcatc	ttcttttaaa	gtggtgacta	gcttgggtgg	1560
atctggctgc	tgggtgttgg	cttattgaca	tactccaggg	taatcaatga	tgactttgtt	1620
tggaaaacct	tttggaggca	ccatgggaac	agaaggaaac	atgagtga	ctgacctgtg	1680
agtgtgtggg	tggggagctc	tgagacgcct	ctgtgccac	gctctccggt	gtccgtgtct	1740
acacaggggt	ccccatgata	cccaccggcc	cagcaggggc	agaccggacc	ggggacgggc	1800
acggtgaagg	gctgcagcct	ggggcttgac	gtggccctta	gtgctgtctc	aggagaaggc	1860
tctggaggac	ttgaggcatg	ctgggcctgg	tgcagtgatg	gcgctaagga	gaccggggga	1920
aagacagtat	cgtgggtcag	tatgcttagg	aagcagcaca	gccgtgtcct	tagggatgtt	1980
cgcgtccagt	aaagacactg	gtaactgcgg	tttcagccaa	cactcttcat	ggcagtgctg	2040
acctcggggt	agcttctgtt	gtotttgtgg	atggttttcc	tggagcggcc	tgacgttgac	2100
gtgttctctg	gtcccatgtc	ttagcggggc	atggtacggg	ttcgtgcctg	acgcgtgcat	2160
taggggtgtt	tcttataact	tcagtagcat	ctttccacag	caagggccaa	acctctctgg	2220
ttcccttcag	agtctttttg	gcoctgatgat	gactcttgag	tgataccctg	tgcgtcagac	2280
atgcccccaga	tggattctac	ttcttttaaa	actatgggact	ttcaagatta	aaaaaaagat	2340
tgctactact	aatttgacgc	ctaacttcag	aagcttctact	gtctacatgt	gaacttttcc	2400
agaaaaactg	tggcatggac	atttttcctc	tggggaatta	acatctaaat	tctggtaact	2460
attaaaaagac	agatctgggt	aatttaaaaa	aaaaaaaaaa	aaaaaaaaata	aaaa	2514

## (2) INFORMATION ON SEQ ID NO. 76:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 274 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
cagagatctg ctgtgattat tccttttcac aaaccacaat gactctggaa aacctggctg 60
taaacaccag cactgccacc agctaaggat ctgtgatcag gactgccatc tcacggtaac120
aggcagaaga caaaagtga accgggctga tgcgaatcac tgggaaactg gctttggcac180
ctccagagaa tgaactgttt catagcctag ctgaccatcc atgaaaatgg ctgcctggag240
aggcagtgat cagcccatc cctgcaaggt gaag 274
```

## (2) INFORMATION ON SEQ ID NO. 77:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 449 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227 5666360

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

cgggttttagc ggcagctctt cgggattggt tccattgcc aacctaacgt gctggcctat 60  
 gaacggtaca ttgcggtggt ccatgccaga gtgatcaatt tttcctgggc ctggagggcc120  
 attacctaca tctggcteta ctcaactggcg tgggcaggag cacctctcct gggatggaac180  
 aggtacatcc tggacgtaca cggactaggc tgcactgtgg actggaaatc caaggatgcc240  
 aacgattoct cctttgtgct tttottatct cttggctgcc tgggtggtgcc cctgggtgtc300  
 atagccatt gctatggcca tattctatat ttccattcga atgcttcgtt ggtgtggaag360  
 atcttcagac aattcaagt atcaagatt taaaatatga aaagaaactg gccaaaatgt420  
 gcttttaatg atattcacct tcttggtcg 449

## (2) INFORMATION ON SEQ ID NO. 78:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 346 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

atataacatc tgaattggga gatagctcat tgtggcctgg gtgctggact tttcatatta 60  
 agtcctgtct tagccaaggg agaagaatgt aaggataaga ccaccaatat cacaggggct120  
 gtctgagcct ttacctgtga ttttgtagca ctctgtggcc ttctggagca atggacaacc180  
 aagtcagcta tgcagttcat aaaagtggac ctggttatat gtcattccaac agcatatggt240  
 ccctgcaagc ctgttttggg agccaatatt ctataacctc caggaatcca cttgaatctg300  
 atgtcttttg aagcaatata ttttccagg gttccaatgg actacg 346

## (2) INFORMATION ON SEQ ID NO. 79:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

00221 366360

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

cccccatca gttcgaattt ctgcagtga agcatotggg gttattgtga ccaactgaaa 60
gtctcagaga gtacccacgt gctccagccc ttctcccca gcattcctga tggcttaatt 120
cacctagcag ccagtttcag ctccagaggtc ctcaacctgg tgatggagac cctgtgcata 180
gtttgtacag tagaccocga attcacagca agcatggaaa gcaaaatctg ccccttcacc 240
atcgccattt tcttaaagta cagtaatgat cccgtcgtcg cctcactggc tcaggacata 300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaagag gctgattccc 360
actctggcca gcataatgca ggccccagca gacaagattc ctgcagggtt ttgtgcgaca 420
ccattgatat cctgacaaca gtagtacgaa atacaaagcc tcccctttcc cagcttctca 480
tctgccaagc ttccctgtgt gtggcacagt gtacccttca cacagatgac aatgccatca 540
gtgcagaatg gcgagagtg cttgcgggcc tatgtgtcag tgaccctgga acaagtagcc 600
cagtggcatg atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag 660
ctcctggacc cccgcacctc agagtctact gcggcctttg tgggcccgcct tgtttccacc 720
ctcatctcca aggcaggcg ggaactcggg gagaatctag accagattct tcgtgccata 780
ctcagtaaga tgcagcaggc agagacgctc agtgatcatg agtccctgat catggtgttc 840
gctcatctgg tgcacactca gctagaacct ctcttgaggt tctgtgttag cctcccagga 900
cctactggca aacctgctct agagtgtgtg atggctgagt ggacaagccg acagcacctg 960
ttctatggac agtatgaagg caaagtcagc tctgtggcac tctgtaagct gctccagcat1020
ggcatcaatg cagatgacaa acggctacag gatatacgtg tgaagggaga ggagatctac1080
agcatggatg agggcatccg caccgcctct aagtcagcca aaaaccaga acgctggaca1140
aacattcctt tgctggtcaa gatcctaaag ctgatcatca acgagctctc caacgtcatg1200
ggaggctaata ggcgtccgc caggccactc ctgcagagtg ggagtcaaag gtgcacgaag1260
gccccttact tcccaggaag acttttagcc tgggcagatc aagttacaaa ttgtcaaatt1320
atccaggaa                                     1329

```

(2) INFORMATION ON SEQ ID NO. 80:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 805 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:



accagggtcaa	gctcacccca	aactattacc	ttcgatgcat	gtgttggtcat	accctgtgga	60
gatctccaaa	gtcaaaagca	actgtcagac	tcagagaagt	atctgtgcc	ctttaagata	120
aaaggctccc	cctatcaaga	cccttggtcc	ttaacgaatg	caggaaaaca	ggtctgccat	180
agctggaatg	aggtgggtgtg	gacaactgaa	tatcaaggct	ggacctcgtc	aaccgggtggt	240
tgtatgtcct	taaaaccata	cattcacttc	actaaagaaa	gtacccccca	taattgccag	300
cctataccaat	gtaatccagt	gcaaatcttc	attctcattc	caactctcac	tgaccctaaa	360
tctaacttta	gttgccggtat	atggcatggg	agccgaaata	gcaggggcac	atcttattgg	420

## (2) INFORMATION ON SEQ ID NO. 82:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00221 3662960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

cggcgcgcct tttttttttt ttttttaagt tgaacagaac atttttatttc tcagcaattc 60  
tatgcgtaca aattaaacat gagatgaata gagactttat tgagaaaagca agagaaaatt 120  
cctatcaacc ccaaggagga ctcaaagtga ggctggaaga ggacttagaa gagtatgaaa 180  
gtactctaag attttatcta agttgccttt tctgggtggg aaagtttaac cttagtgact 240  
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 300  
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 360  
ggtgccagcg caccagctag atgctctgta acttctaggc ccatttttcc cctctgaaaa 420  
taagagggtt ggatcaaacg atctctgggg ccttagcatc tcaaatcctg tggatcctcc 480  
tacttaccoc tttagagagcc ttactgggaa gtcagtcatt aatgatgtgg ccagttattt 540  
gcaagtggta agagcctatt taccataaat aataactaaga accaactcaa gtcaaactt 600  
aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca cattaacttg 660  
attttaaaat cagttttgtg agtcattttac cacaagctaa atgtgtacac tatgataaaa 720  
acaaccattg tattcctgtt tttctaaaca gtcctaattt ctaacactgt atatatcctt 780  
cgacatcaat gaactttgtt ttcttttact ccagtaataa agtaggcaca gatctgtcca 840  
caacaaactt gccctctcat gccttgccctc tcaccatgct ctgctccagg tcagccccc 900  
tttgccctgt ttgttttgtc aaaaacctaa tctgcttctt gcttttcttg gtaatatata 960  
tttagggaag atgttgcttt gcccacacac gaagcaaaag aaataaaagac caaaaatgtt 1020  
caaattctaa gccacttaat agcgttttgt acattaaaaa tgacaagggt tattatacaal 1080  
gtagcctttt aaaaaattct cacacagaac agctttgtat ttagacttaa agctgttgct 1140  
actttgctag tgacgtttgt gttaacagtc agtgctctag gccattgatt gattgattgt 1200  
cagaatcaga agtgactaca caagagcatt agccagactt ttcagtgaga acaggtaacal 1260  
ggctggcacc agcacttggt acagcacgtg gacaggacga cggaaccocag agttctctgt 1320  
ctctccttca cagcagatgg actcttctat aggtggctgt taatttacac aaagttatat 1380  
tccagaatca ggaagccccg tgtcgccaac acttgaagga gaactatgtt ccagttttgg 1440  
tggtgaactt ctacagaaat acctactacc aaaaattgtg acaccttatt agacacttcc 1500  
aaagtacccc ccaaaaagctg tttaaaagac cattccattt tttcctacac aaagtgcatal 1560  
ctaaaatttc acaataatca tcttcagatg tacattttat ttagtacatt tcacagtttt 1620  
cagtattcag tccctcatga acattttata gtcactctct cggccctgtt gtgaaatatg 1680  
tgattccagt tcaattcaga gtgtatgatt ccgcttttca cgctgatcaa gtaaatattat 1740  
ggtgtctctt ttctgatctt caacattaaa aacatctatg tttctgtcat tccctgccag 1800  
ggctgcttgc ttgtctgtct cagattctgc ttcattttca tccatgttgt agtcatcttc 1860  
tcctctcagt ttctgctggg ttctcccttc ccggcagctt tctgctcct cctcctgtcc 1920  
gtcggggatg acaagctggg ctcgctcagg gccctccatc tctggatttt cctggctcac 1980  
tgacagggca gctgcacct gtgggtctg gccagttct cggctcccc cgaagcctct 2040  
tccacctaca ggtctgtctt caacacctgc tcccgccctg gctcctgcgg cagcctgtcc 2100  
ctctgaggct ccgatcaaca ctgatctcat ggttcccttc cca 2143

## (2) INFORMATION ON SEQ ID NO. 83:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 450 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

tttttttaaa gccagctttt cttcagattt ttttggtggg caggctcgtga aagacagggtg 60
aggaagtaga tcttgggctc agcatgcctc taaaagtata atttcttttt tttaatgtgg120
aaagaaatgc ataactctgt ttctgttctt gtcccccctct ctgcctctgt ggtgcctgag180
atactgggga tcccacagct ggggccactc agaggctacc aggaacgctt ccagtttgca240
tctggctggt agtgccagga ccagaaaacc acagacctct tcacagacct cctgaccgtg300
atgtccctga agcctggaag gtgtccacac aatgaagcag aattgagtga tgggggtgtt360
tgtggaaccg agtgaaactg tgtaaacaca gtggaactgt gtttaatttg agtggaagtt420
caagttccgt ggagttcatt gggcccgttt 450

```

## (2) INFORMATION ON SEQ ID NO. 84:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 408 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

0967395 12700

(A) LIBRARY: cDNA library

tgcgaactgtg	cacccagctt	gccagatttt	tccccattac	acccccagtg	tggcatatcc	60
ttggtcccca	gaggcacacc	ccttgatctg	tggacctcca	ggcctggaca	agaggctgct	120
accagaaacc	ccaggccctt	gttactcaa	ttcacagcca	gtgtggttgt	gcctgactcc	180
tcgccagccc	ctggaaccac	atccacctgg	ggagggggct	tctgaatgga	gtctgacac	240
cgcagagggg	aggccatgcc	cttatccgca	ctgcacgggt	ctgtcggccc	agcctggctc	300
agaggaggaa	ctcgagagc	tgtgtgaaca	ggctgtgtga	gatgttcagg	gctagttcca	360
accaagagtg	tgctccagat	gtgttggggc	cctaacttgg	cacagagt		408

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN  
(C) ORGAN:

(A) LIBRARY: cDNA library

tacagttttt	atcagtgatc	acatttttagt	gtaatacatg	aaactgaggc	ttgatagaaa	60
acaggagaga	aggcatgagt	gcatggggta	catagggaga	tgagggcaag	catcaccaag	120
gagcggcagt	gagatagacg	ctctcatgga	ctgctgcttt	acaacctccc	tggagagcaa	180
tttaaaaaa	tgaatcaaga	tccttttgat	ccactaatca	tccagaaatc	tacacagaaa	240
tatgcacaaa	aatatgtggg	catccattga	ctttccaacc	tcttctcttt	ccagggggaa	300
tattccttaa	a					311

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 487 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```
gtcttttgaa atctgtttcc actacagcta tggcgaagtc tatcagccgg tgctaccagg 60
agtcactgcc agggctgccg ttctcctgaa cccagtgcc cagaatcata agccctgaccl20
ccatccctag aaagatgagg tcccagcaat ggccagagca tttctcacca gttctgtgag180
atagcacata aaaatagagt tctttgggca aaacttttgg gaagcaatgc atcctacatg240
ggctgatatt cagcctgagc tgttctcaag aggagagtgg tactggcagt ttatggctga300
aatccattct gattggttgg agtctatgct ataccagttg ttaaaccattt tgagtatcac360
tcttgcatat tggttactatt atatttcctc tatatataga cagaaaggcc atttttagga420
tattaaaggc tctgaaaatt tctgcagtag acccaactga aggttctatt aaggcagggt480
tcctaaa
```

(2) INFORMATION ON SEQ ID NO. 87:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1902 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```
gaggaaaaag aacaatgaac agcaacgata ttgactgtgc aactcagaca ttcctgcaga 60
aaagacatat gttgctttac aagaaggcca aagaactatg gggccttccc agcatttgac 120
tggttcattgc atagaatgaa ttaaataatcc agttacttga atgggtataa cgcataaatg 180
```

00221 5552950

```

tgtgatttta ttaggggcat ctgccaattc tctcactgtg gttccttctc tgactttgcc 240
tgttcatcat ctaaggaggc tagatccttc gctgacttca ccattcctca aacctgtaag 300
tttctcactt cttccaaatt ggctttggct ctttcttcaa cctttccatt caagagcaat 360
ctttgctaag gagtaagtga atgtgaagag taccaactac aacaattcta cagataatta 420
gtggattgtg ttgtttgttg agagtgaagg tttcttggca tctggtgcct gattaaggct 480
tgagtattaa gttctcagca tatctctcta ttgtcttgac ttgagtttgc tgcattttct 540
atgtgctgtt cgtgacttgg agaacttaaa gtaatcgagc tatgccaact tggggtggtg 600
acagagtact tcccaccaca gtgttgaaag ggagagcaaa gtcttatgga taaacctctc 660
tttcttttgg ggacacatgg ctctcacttg agaagctcac ctgtgctgaa tgtccacatg 720
gtcactaaac atgttatcct taaaccccc gtatgcctga gttgaaaggg ctctctctta 780
ttaggttttc atgggaacat gaggcagcaa atctattgct aagactttac caggctcaaa 840
tcatctgagg ctgatagata tttgacttgg taagacttaa gtaaggctct ggctcccagg 900
ggcataagca acagtttctt gaatgtgcca tctgagaagg gagaccagg ttgtgagttt 960
tcctttgaac acattggtct tttctcaaag ttctgcctt gctagactgt tagctctttg 1020
aggacaggga ctatgtctta tcaatcacta ttattttcct gttacctagc atgggacaag 1080
tacacaacac atatttgtgt agtcttctaa aagactcctc tgattgggag accatatcta 1140
taattgggat gtgaatcatt tcttcagtgg aataagagca caacggcaca accttcaagg 1200
acatattatc tactatgaac attttactgt gagactcttt attttgcctt ctacttgcgc 1260
tgaaatgaaa ccaaaacagg ccgttgggtt ccacaagtca atatatgttg gatgaggatt 1320
ctgttgctt attgggaact gtgagactta tctggtatga gaagccagta ataaacctt 1380
gacctgtttt aaccaatgaa gattatgaat atgttaatat gatgtaaatt gctatttaag 1440
tgtaaaagcag ttctaagttt tagtatttgg gggattgggt tttattattt ttttccctt 1500
tgaaaaatac tgaggggatct tttgataaag ttagtaatgc atgttagatt ttagttttgc 1560
aagcatgttg tttttcaaat atatcaagta tagaaaaagg taaaacagtt aagaaggaag 1620
gcaattatat tattcttctg tagttaagca aacacttggt gagtgcctgc tatgtgcacg 1680
gcatgggccc atatgtgtga ggagcttgtc taattatgta ggaagcaata gatctcggt 1740
gttacgtatt gggcagatac ttactgtatg aatgaaagaa catcacagta atcacaatat 1800
cagagctgag ttatccccag tgtagcttgc ttggggatcc cagtttctgg gaacgagagt 1860
tagggccatt ttatttataaa gaaactcccg gttgagaccg gt 1902

```

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1048 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

ctcaccgctcg tctacaccgt gttctacgcg ctgctcttcg tgttcaccta cgtgcagctc 60  
 tggctggtgc tgcgttaccg ccacaagcgg ctcagctacc agagcgtctt cctctttctc 120

tgcctcttct gggcctcccg gcggaaccgt ctcttctcct tctacttcaa agacttcgtg 180  
 gcggccaatt cgctcagccc cttegtcttc tggtgctct actgcttccc tgtgtgctg 240  
 cagtttttca ccctcacgct gatgaacttg tacttcacgc aggtgatttt caaagccaag 300  
 tcaaaatatt ctccagaatt actcaaatac cggttgcccc tctacctggc ctccctcttc 360  
 atcagccttg ttttctgtt ggtgaattta acctgtgctg tgctggtaaa gacgggaaat 420  
 tgggagagga aggttatcgt ctctgtgcga gtggccatta atgacacgct cttcgtgctg 480  
 tgtgccgtct ctctctccat ctgtctctac aaaatctcta agatgtcctt agccaacatt 540  
 tacttgagat ccaagggctc ctccgtgtgt caagtgaact ccacggtgta caccgtgata 600  
 ctgctttaca cctctcgggc ctgctacaac ctgttcatcc tgtcattttc tcagaacaag 660  
 agcgtccatt cctttgatta tgactggtag aatgtatcag accaggcaga tttgaagaat 720  
 cagctgggag atgctggata cgtattatct ggagtgggtg tatttgtttg ggaactctta 780  
 cctaccacct tagtcgttta tttcttcgga gttagaaatc ctacaaagga ccttaccac 840  
 cctggaatgg tccccagcca tggattcagt cccagatct tatttctttg acaaccctcg 900  
 aagatatgac agtgatgatg accttgctg gaacattgcc cctcaggac ttcagggaag 960  
 gttttgctcc agattactat gagttgggga caacaaacta acagcttcct ggcagaagca 1020  
 gggacttttg aaagcctcaa agtttgga 1048

## (2) INFORMATION ON SEQ ID NO. 89:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 804 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227-866296



```

gcccccatca gttcgaattt ctgcagtgg agcatctggg gttattgtga ccaactgaaa 60
gtctcagaga gtacccacgt gctccagccc ttctctccca gcatccttga tggcttaatt120
cacctagcag ccaggttcag ctccagaggtc ctcaacctgg tgatggagac cctgtgcatc180
gtttgtacag tagaccccg attcacagca agcatggaaa gcaaaatctg ccccttcacc240
atcgccattt tctaaagta cagtaatgat cccgtcgtcg cctcactggc tcaggacatc300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaatgag gctgattccc360
actctgggta gcataatgca ggccccagca gacaagattc ctgcagggct ttgtgcgaca420
gccattgata tcttgacaac agtagtacga aatacaaagc ctcccccttc ccagcttctc480
atctgccaa g ctttccctgc tgtggcacag tgtacccttc acacagatga caatgccacc540
atgcagaatg gcggagagtg cttgcggggc tatgtgtcag tgacctgga acaagtagcc600
cagtgccgat atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag660
ctcctggacc cccgcacctc agagttcact gggcgctttg tgggcgcctt tgtttccacc720
ctcatctcca aggcaggggc ggaactcggg gagaatctag accagatttc ttcgtgccat780
ccttcagtta agatggcagg aggt
804

```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 581 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

tctttgatca	gatttagtgt	cttaggtaat	taaatcagaa	agtctatttta	gctatttctag	60
aagtgtatgt	gtagggtattg	ggtgggtggg	gttctttgag	cgaacttgtc	agaaactcca	120
ttcttaacat	cagaatcagg	gcaggattga	aaacattgtg	gctggatctt	gaaattgcta	180
taacatctat	tgcagaaaat	gataggtcag	atggatagca	ataataatta	tatatcagat	240
cttagtaaca	aaattaccaa	gctttatcta	gtggatatat	gtaaaagaat	attttttaaat	300
gtccagcatt	gatgtatttt	ctttaagaat	tattacagta	tataagcatt	ctttgggaat	360
acagtataaa	aacataaaatt	ttttcgtatt	tttaattttt	tttatttttt	tgggtcaagga	420
tgaatcctcc	cctgtaaaaa	attgattttc	gcctaaattt	cgggggtttcc	ctggcacata	480
atagcatctg	ccccaaacttc	ggagatggcg	gatgcgggta	aaaagccaaa	aggatggatg	540
gggataccga	aatacgtggt	ggaatggaag	cgaatccaat	a		581

## (2) INFORMATION ON SEQ ID NO. 91:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

tggagatatt agtcagtttc tttagtgata tttgtttcct tgatgtgcct ttttgttttt 60
ctttgggggt tttggaatcc ggatgctgtt gaagggcaat agcagactcc tccagctaag 120
agacaggaca tgttcttgag ccactgtagc tgttgaagct ggacaccaga cgctccctat 180
aacccccccg ccaggccata gcgtgtatgc atgtgcactt ccaccacacag aggagggtgt 240
gaagccttga gaacctcaag aaagggtctg attctgccat acctttgggt ctaccttggg 300
actgctggtt gccaacgtgt caaccagcct gtgttccttg ccaccacgc acttgctgag 360
gtgtggctga ggcagaatca tgtgaatggg tgcattcaag gagttcaggg ccctgcttgg 420
agaagaaata ctttagcatc atgaaaggga aagaacgtgc accccttttt tgtttcttta 480
gtgaatgcaa gatttaataa aagtgaataa tgagcttccc ctttgggagt ggagcccagt 540
gcagctcact gacaggggtg acatcagtat gatgtgttgg actgaaactg tatgtctgta 600
ggtaggtgtg tgccttttag ggcagaccac ggtggccacc ccatttctcc aagtggtgtt 660
acctagcttg tgtatattag acattgccac cctcacctct ggccaaaaat tcttgattta 720
aaaagaaaaa tctattttgt taacgacagg ctctgttgta tgtgttacta tcccaagcct 780
ggattatttt atttatttaa aagtatttta atttccatat tggctttatt ctaatcccat 840
ccatccctgt ggagctgcag agcatcttca tgtgagtaga cggatggaca taaatagatt 900
catgctcatt taggaagctg ggagtctcgt gaagctgagg gtgagttcct gtgattcttg 960
ttcgttcaa caaaaagtgg gagaccaagt ttttatagca aaagaccaa ttagctgtag 1020
agtcttgaat gcagaaaaaa attaccctag ctttcttagc acttaggggt ttgtgaggat 1080
tcagtgttta gcacagtgtc tggcacatag taagccctag taaatgttaa atattgttat 1140
tagtgtttctg taaaacttga gaaatagagc tgagctcatt cccttctgtg tgattcaaaa 1200
ataataccta catgaaaaca tgattccaag ttgattgaat gttgtaggaa ttactgggtt 1260
agagtagccc agttctcggc ctaccctgct ggttgggata ttactgtatt cttgaatgca 1320
ctgggttgaa aatatgccag acttcagccc ccaaggaaac aaggctgcaa gaatttatga 1380
actccagctg gaaaaggtaa aggtgacctt tggctagcca catactggac cttacccac 1440
tgacgtcttt cagaacattc caagggtttt cctcaaggaa catttttgag ctagaaatta 1500
aaatgggttc tctggcagac tgcacccctt gagtcaaagt taacagtatt cctttgaatg 1560
caataataga ggcttttctg cgttaaggga gaaggaatga ccaattgaac ttacacattc 1620
cccaggcagg tcccttttgc ggccctaca ggctgggggt gccctcctg tcctcaggga 1680
tcagactccc agactggtta gttctgcatt tttccatcaa attaaagggt attccctggc 1740
cgctccttg agaaaaccaa cccaccctg ccagctgggg gcaatggggc agggattt 1800
gcctctcaga acagctccta gaggctgctc atgactgaat gttttcccaa atcacctaa 1860
tatcggtttg ctttttgttt tgggggagag gatttagcct cttacttccc tgatggattc 1920
aaagttttat ctatctcctt atctcctgcc ctgtcttggc acaactctgg atagattgca 1980
ggtgtggaat ttgctggagt ttggtggctc cccaaattcc ttgatctgtc cgcaaagaga 2040
ag

```

2042

002227 5624960

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 430 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

gttaaaaaacc tagtattcat tttttttttt cctgtaccaa aacaatcatc ttcctttatt 60
tttcttgagg cggaagagg agagtggaga agaaggaag aatgcaaagt gtcactttga120
acttctcggt caccacacac gtgggagtc actcatgtca gcagcctccg tgcacaggcc180
ccaggtgaaa gaaagaatga ggtctagttg gaccagctaa cactgcctgc cttgtgttta240
cgaaaggcag ctgcctctgt ggtgtgattt caggggagcc agacagggcc ggggccacga300
acctgcatcc tgcattccta gcacctattt gccatgcggt gaggcttaac ttgggaaact360
tcaatttgct tggggtgcag attagctttc caaactattg tgatgctcat gcttgacttc420
ccaaggactt
430

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 592 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

aattaaaaata aatagaaaca tacggagatt cttttatgtt ggatttatta taccctccac 60
catttttggtc cctgaaaagg gaaaagatac acggtcgagt agtacaggta tgtgtttccc120
actacacatt atggctataa tggagttgaa ttgcaaacag taaaattttg ttttggattgl180
gtttcccttg atccccccag acaggagctt cctctcccac cctacctgcc tgcccttaag240
ttgtgtctta ttaaaactga cacaaatctc accggctttt agtctaataa ttgaatcata300
gctacacacg gtgacaccag aatagctact tgttttttta tgttaccagt gagtaacttg360
tttatccttg tatgtagaaa ctaatttcac catgatcaca gatctgtgta acatctctag420
tttgaatttc cacacaattt taaaatgtct actaggaaaa cttacacctt tttgttccaa480
gggtgctctt catctattaa aaccgtgggg gcatacttcc agtggtgctt ctgagggccca540
aattttgtgg gtcgtggggg acaattttgt attaacatac gttattttgt aa 592

```

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 674 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

aaggccgcgc aagtgcactt gcgtgtcacc gttaccgtag cgactgggct tctggactgt 60
atatcctagc tgccttgta acatcttcga gcatcgagc ctccggaggc cggggtaact120
ggcagcaggt aggaaactat gtgaaagaat ctctgatgt cataatttcc ggggtgtcaccl180
ggaacatttg atcatcattc ctttggcaat tccagccttc tgtggaaagg ccagtagaaa240
gcattgattt attcacctct acaggaatca gactcagcct cttttggtt tcagtgaagt300
atgccttttc aatttggaac ccagccaagg aggtttccag tggaaggagg agattcttca360
attgagctgg aacctgggct gagctccagt gctgcctgta atgggaagga gatgtcacca420
accaggcaac tccggagggt ccctggaagt cattgcctga caataactga tgttcccgta480
actgtttatg caacaacgag aaagccacct gcacaaagca gcaaggaaat gcatactaaa540
tagcaccatt aagtcttttg tcaaggcttg actaggtaa gggtaatgga ccagtatcat600
ctggtgatct ggtaaacaaa taaaagtggt ggcaccttta gatgatgaaa aaaaaaaaaa660
aaaaaaaaaa aaaa

```

004227 5662950

## (2) INFORMATION ON SEQ ID NO. 95:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 324 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
gttccttttca ttccatcact ttaggtgatg ggtaagattt ttgaaagcct tatatTTTTT 60
gattttgttg tctagtttaa tcctacctt aatagtttg tttggtaaaa ttcccacttg120
aatgtgacac tgataataat tatgctgatt tttagcatct cttataggaa tcaaagtTt180
ttaaagttac atagaggatt gaaaaatgta tatcactcaa tttttatcta aggagggata240
gggtataaag ggaggtacct aaatagctca aataatggat ataatcctt tttccataac300
catttgggat gctttaaggc aatt                                     324
```

## (2) INFORMATION ON SEQ ID NO. 96:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 709 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002221 566660

ggatgcgcca	ctataacatc	cccgtcagag	tgtgtgagga	gaccagtcta	tgagagacgc	60
atgtcctga	cagcctggcg	acgtggcgaa	gatgcacagg	tggctcctgg	gcttgggctg	120
caggtttggg	ggtctctaag	aacaatctct	gagaagaacc	cttggggccc	tgggagccaa	180
gttggacagg	atgtcctgaa	gactagcttt	tgataagaga	aattaaccaa	gtctttcccc	240
tcatctatga	tgcaatatat	ttcagtgggg	gccttcagag	cacacctgtt	ggacggtgca	300
aaccataatc	tctccagaag	gcaaataact	ttgtatcaga	ggaaactcag	ttttggagag	360
gaatatgttc	tttatatctc	aaatcaaaac	tctctcta	ggtaaactgg	cttctaattt	420
ttttaagtac	agtatttttt	tttccccttt	agtagtaacg	ggtttctata	gatcttctca	480
tacagtctgc	tttaactcag	gaccttgaga	ttatgagact	gacgtgctgc	ccactgcact	540
gagggggctt	ctaaccagct	gctttaagtg	gtataattct	gggatagatc	tgttactggc	600
atagtcatga	caacctctgg	taatcttacc	ttctcctttt	tatgaaggga	agagcaatgg	660
tttgacttta	catctaaatt	aaggctat	taagcagatt	gttttgcaa		709

(i) SEQUENCE CHARACTERISTIC:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 562 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```
gtccagatgg aatgactccc atcctctcct catctcccct ttgacgagcc tcaaactgct 60
cagctcatca aagagccatt gccaaacttc gtatgtggtt ctgggtccca gggagccttg120
gaacctggca ccctgggggtg gtttaatttc ggcacgagag cattcctgct tctcaaggga180
cacagtggcc tgcattggcc agcatggacc ctgggctgat catgtgcatt cctgcttctc240
tggggacaca gtggggccac atggggcagc atggaccctg ggctagagca agcacatctc300
catctcttcc acctcaggca gtgtggctcc agatgtcagg agggactgac ctcaggacct360
tccaggttcc tctgtgccag gaatgagagg ccaggcccgga tcctaccacc tcgccttgac420
cctgaagtca gagcaggcca gccaaagcagg aagcacactg ttttaattttt tgcattggaaa480
gtaaatgtgt actttgatag ggttaaaaata tgggtcttttt taagttgctc aaccccataa540
tttgagccat tgccttgctt aa
562
```

## (2) INFORMATION ON SEQ ID NO. 98:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1948 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

gatcaccaag acacacaaaag tagaccttgg gctcccagag aagaaaaaga agaagaaagt 60  
 ggtcaaaagaa ccagagactc gatactcagt tttaaacaat gatgattact ttgctgatgt 120  
 ttctccttta agagctacat cccctctaa gagtgtggcc catgggcagg cacctgagat 180  
 gcctctagtg aagaaaaaga agaagaaaaa gaaggggtgtc agcacccttt gcgaggagca 240  
 tgtagaacct gagaccacgc tgcttctag acggacagag aagtcaccca gcctcaggaa 300  
 gcaggtgttt ggccacttgg agttcctcag tggggaaaaa aaaaataaga agtcacctct 360  
 agccatgtcc catgcctctg ggggtgaaaac ctcccagac cctagacagg gtgaggagga 420  
 aaccagagtt ggcaagaagc tcaaaaaaca caagaaggaa aaaaaggggg cccaggaccc 480  
 cacagccttc tcggtccagg acccttgggt ctgtgaggcc agggaggcca gggatgttgg 540  
 ggacacttgc tcagtggga agaaggatga ggaacaggca gccttggggc agaaacggaa 600  
 gcggaagagc cccagagaac acaatgggaa ggtgaagaag aaaaaaaaaa tccaccagga 660  
 gggagatgcc ctcccaggcc actccaagcc ctccagggtc atggagagca gccctaggaa 720  
 aggaagtaaa aagaagccag tcaaagtga ggctccggaa tacatccca taagtgatga 780  
 ccctaaggcc tccgcaaaga aaaagatgaa gtccaaaaag aaggtagagc agccagtcac 840  
 cgaggagcca gctctgaaaa ggaagaaaaa gaaggagaga gagagtgggg tagcaggaga 900  
 cccttggaag gaggaacacag acacggactt agaggtgggt ttggaaaaaa aaggcaacat 960  
 ggatgaggcg cacatagacc aggtgaggcg aaaggccttg caagaagaga tcgatcgca 1020  
 gtcaggcaaa acggaagctt ctgaaaccag gaagtggacg ggaaccagc ttggccagtg 1080  
 ggatactgct ggttttgaga acgaggacca aaaactgaaa tttctcagac ttatgggtgg 1140  
 cttcaaaaaa ctgtccctt cgttcagccg ccccgccagc acgattgcaa ggcccaacat 1200  
 ggccctcggc aagaaggcgg ctgacagcct gcagcagaat ctgcagcggg actacgaccg 1260  
 ggccatgagc tggaagtaca gccggggagc cggcctcggc ttctccaccg ccccaacaal 1320  
 gatcttttac attgacagga acgcttccaa gtcagtcaag ctggaagatt aaactctaga 1380  
 gttttgtccc cccaaaactg ccacaattgc tttgattatt ccatttatgc tggagattac 1440  
 aaattttttt tgtgaaaaaa tcagatcttg gtgaggacct cgagcagtaa gatataaata 1500  
 actcccataa gcttagcgtt ccagtaatgg aacactaggc ataatgggt tattcagttg 1560  
 tgcaaatgaa agccatctga cagttggctc acattgaaca cctgtggaga ttaaggacga 1620  
 ggacaactat attgatggc ttggatgaac tggggcaggg cagctcatat ttccggagcc 1680  
 aggagaacga gtgagtgcta aaacctctg ttttctgtgt taaacattcc gtccctgttt 1740  
 gagacatcag tatgtacagt taacttttgt tgagtgttta gcaggtacta gggacatact 1800  
 agtgttttcc ttaatgtatt taatcttcat aattatgaaa tgggtgctat tattagcccc 1860  
 atcttataga tgaggcaact gaggttcagg gataaagtaa taaaattgcc tggggtcacc 1920  
 cagccactaa aaaaaaaaaa aaaaaaaa 1948

00226 3662950

## (2) INFORMATION ON SEQ ID NO. 99:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 483 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

aatttatggg gtctatcttt gaccacgtga taccacttac ctgattctat gtactgatta 60
atgtatctaa cagttttata gtgaaagtac tttttaaaaa agtatttgaa tggtcatttc120
tatttttccc cttttgctgt acaagttaat ttttactcat cttttgctgt acaaattaac180
tttcatcaat acaaataaga ggctagtttt aagtcaattt atttgcatg agcccaggaa240
caattaaatt ctataaagta atgtattaaa atagtacact ttaaaaatta ttttccttct300
ttttttctct ttaaatttta agaccatcat aataaattat cattacaaag tcaaacatac360
tatatactac tatcagtcaa tggggaaaaa ataagtccat atgttttatg ggtaaaatgc420
tgtaatagat tgggattgtc caatttgcct tgaaaaaaat cacagcagtt tttaggtttc480
cct

```

## (2) INFORMATION ON SEQ ID NO. 100:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 437 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

002221 55555555



## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

cccgcttgag gcgtaggggg tggcgctctc cgttcggcgg cgctcccatg gcgcacatta 60
ccattaacca gtacctgcag caggtgtacg aagccatcga cagcagagat ggagcatctt120
gtgcagagtt ggtgtctttt aaacatcctc atgttgcaaa cccacgactt caaatggcct180
ctccagagga gaagtgtcaa caagtcttgg aacccccctta tgatgaaatg tttgcagctc240
atttaagggtg cacttatgca gtggggaatc atgacttcat agaggcatac aagtgccaga300
ccgtgatagt ccaatcatto ttgcgagcat tccaggccca caaagaagaa aactgggctc360
tgctgtcatg tatgcagtag cgcttgacct ttcgagtgtt tgccaataat gcagttcaac420
cagttggtta aggaagg                                     437

```

## (2) INFORMATION ON SEQ ID NO. 101:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 359 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

cagatctagg ggcttcagct gtgtgcagac cccatgccac ttcagggaag tgacacaggc 60
ctgtgtcatc tcgcttttggc agcaggtggg tggccttcct caggggagga ggtggcctga120
gatgtgtttc aggtctttga cccatcactc cctacacaca cgacgtgaac accactcctg180
gagcattctc agaatggaga tttgaattcc atgtggcagc ttctcacaca caaacctgcc240
atcattcccc acacacccac tcacgacatt caacagccat gagccaaaag aagttccttg300
tttcagattt gaaggtttta tgaatccact tcttcggat gtagctcttt aatgatttt 359

```

## (2) INFORMATION ON SEQ ID NO. 102:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 501 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```
tcggcgctcac atcctgagtc ggcctctctgc cgaggcggag cggacatgca ggctccccgc 60
ggcaccctag tcttcgcctt ggtgatcgcg ctctgtcccg tcggccggga accttctagc120
caaggatctc agagtgtctt acagacatat gagctgggaa gtgaaaacgt gaaagtccct180
atTTTTgagg aagatacacc ctctgttatg gaaattgaaa tggaagagct tgataaatgg240
atgaacagca tgaatagaaa tgccgacttt gaatgtttac ctaccttgaa ggaagagaag300
gaatcaaadc acaaccacaag tgacagttaa tcctaaacct gaatggcgct catgttttcc360
aagagaagca gcccttgagg gagtctgctg aggctgcca cagaggatga agaggataca420
aatttaatta atttcaaatc aacatagaca caagaacctt ttgctgtttc ttccaacgcc480
cactcttcct aatgatggca t                                     501
```

(2) INFORMATION ON SEQ ID NO. 103:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1102 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00422T 5622960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

cgggatctcc cgaaggaatt tacggggatt cctcggacca ttatcctcag gcaagaaaca 60
aaaccaaact tggactctcg tgcagaaaat gtagccatt accacatgta gccttggaga 120
cccaggcaag gacaagtaca cgtgtactca cagagggaga gaaagatgtg tacaaaggat 180
atgtataaat attctattta gtcacactga tatgaggagc cagtgttgca tgatgaaaag 240
atggtatgat tctacatatg taccattgtt cttgctgttt ttgtactttc ttttcaggtc 300
atttacaatt gggagatttc agaaacattc ctttcaccat catttagaaa tggtttgcc 360
taatggagac aatagcagat cctgtagtat ttccagtaga catggccttt taatctaagg 420
gcttaagact gattagtctt agcattttact gtagttggag gatggagatg ctatgatgga 480
agcataccga gggtagcctt tagcacagta tcagtacatc ttatttgtct gccgctttta 540
aaaaataccc attggctatg ccacttgaaa acaatttgag aagttttttt gaagtttttc 600
tactataaat atggggcaat tgtagcctt acatgttggt tagacttact ttaagtttgc 660
accottgaaa tgtgtcatat caatttctgg attcataata gcaagattag caaaggataa 720
atgccgaagt cacttcattc tggacacagt tggatcaata ctgattaagt agaaaatcca 780
agctttgctt gagaactttt gtaacgtgga gagtaaaaaa tatcggtttt attctttgct 840
gatgtccttt ctgcttgaaa taacagtcac catcacagta aaggagagga gtttctttcc 900
ttctaagtag gcagaaatgg tatcattatg ttgccgtctt ccaatctccc agagctcgt 960
ctctagagaa tcaccttctt tcgcgttttt tttttttttt gagggtagga gtctcactat 1020
gttgccccaa gactaggcct gggaactgtt ggggggcca ggggattgct cccgtcccgc 1080
aggcctcccg agtaggccg ga                                     1102

```

## (2) INFORMATION ON SEQ ID NO. 104:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 306 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

gaccaacctt ccttgccatt tatacggcat aaaaccctca atctcaccag tatggctacc 60
aaaattatag gttcacctga aacaaagtgg attgatgcaa cttctggaat ttacaactca 120
gaaaaatctt caaatctatc tgtaacaact gatttctcgg aaagccttca gagttcta 180
attgaatcca aagaaatcaa tggaattcat gatgaaagca atgcttttga atcaaaagca 240
tcttgaatcc attttttttg aaaaacctta aaaagggcga tcacaatttt tttgaacaag 300
ggtcat

```

00221-5552960

## (2) INFORMATION ON SEQ ID NO. 105:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

tggagatatt agtcagtttc tttagtata tttgtttcct tgatgtgcct ttttgttttt 60
ctttgggggt tttggaatcc ggatgctgtt gaagggcaat agcagactcc tccagctaag 120
agacaggaca tgttcttgag ccactgtagc tgttgaagct ggacaccaga cgctccctat 180
aacccccccg ccaggccata gcgtgtatgc atgtgcactt ccaccacag aggaggggtg 240
gaagccttga gaacctcaag aaagggctgg attctgccat acctttgggt ctaccttggg 300
actgctgggt gccaacgtgt caaccagcct gtgttcctct ccaccacgc acttgctgag 360
gtgtggctga ggcagaatca tgtgaatggg tgcattcaag gagttcaggg ccctgcttgg 420
agaagaaata cttttagcat atgaaaggga aagaacgtgc accccttttt tgtttcttta 480
gtgaatgcaa gatttaataa aagtgaataa tgagcttccc ctttgggagt ggagcccagt 540
gcagctcact gacagggttg acatcagtat gatgtgttgg actgaaactg tatgtctgta 600
ggtaggtgtg tgccttttag ggcagaccac ggtggccacc ccatttctcc aagggtggtt 660
acctagcttg tgtatattag acattgccac cctcacctct ggccaaaaat tcttgattta 720
aaaagaaaaa tctattttgt taacgacagg ctctgttgta tgtgttacta tcccaagcct 780
ggattatttt atttatttaa aagtatttta atttccatat tggctttatt ctaatcccat 840
ccatccctgt ggagctgcag agcatcttca tgtgagtaga cggatggaca taaatagatt 900
catgctcatt taggaagctg ggagtttctg gaagctgagg gtgagttcct gtgattcttg 960
ttcgcttcaa caaaaagtgg gagaccaagt ttttatagca aaagaccaaa ttagctgtag1020
agtcttgaat gcagaaaaaa attaccctag ctttcttagc atttaagggt ttgtgaggat1080
tcagtgttta gcacagtgtc tggcacatag taagccc . . . . . ttaa atattgttat1140
tagtgtttcg taaaacttga gaaatagagc tgagctca . . . . . ctgt tgattcaaaa1200
ataataccta catgaaaaca tgattccaag ttgattgaat gtttcaggaa ttactggttt1260
agagtagccc agttctcggc ctaccctgct ggttgggac ttactgtatt cttgaatgca1320
ctggtttgaa aatatgccag acttcagccc ccaaggaaac aaggctgcaa gaatttatga1380
actccagctg gaaaaggtaa aggtgacctt tggctagcca catactggac cttacccac1440
tgacgtcttt cagaacattc caagggtttt cctcaaggaa catttttgag ctagaaattal500
aaatgggttc tctggcagac tgcacccctt gagtcaaagt taacagtatt cctttgaatg1560
caataataga ggcttttctg cgttaaggga gaaggaatga ccaattgaac ttacacattc1620
cccaggcagg tccctttgcc ggccctaca ggctgggggt gccctcctg tccctcaggga1680
tcagactccc agactggtta gttctgcatg tttccatcaa attaaagggt attccctggc1740
cgctcctcgt agaaaaccaa cccacccctg ccagctgggg gcaatggggc agggattttg1800
gcctctcaga acagctccta gaggtgctc atgactgaat gttttcccaa atcacctaaa1860
tatcggtttg cttttgtttg tgggggagag gatttagcct cttacttccc tgatggattc1920
aaagttttat ctatctcctt atctcctgcc ctgtcttggc acaactctgg atagattgca1980
ggtgtggaat ttgctggagt ttggtggctc cccaaattcc ttgatctgtc cgcaaagaga2040
ag

```

2042

002227 5662360

(2) INFORMATION ON SEQ ID NO. 106:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 320 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

aatcttttta	ccatgaaatt	tcttccagaa	ttttccccc	ttgacacaaa	ttccatgcat	60
gtttcaacct	tcgagactca	gccaaatgtc	atctctgtaa	aatcttccct	gagtcttcca	120
agcagtaatt	tgccctctoc	tagagtttac	ctgccatttt	gtgcacattt	gagttacagt	180
agcatgttat	tttacaattg	tgactctcct	gggagttctg	gagccatata	aagtgggtcaa	240
tagtgatttc	tgcccttgaga	gttgaatgac	atcttctctc	tgtttttgga	ttactgtaga	300
tttcgatcat	tcttttggtta					320

(2) INFORMATION ON SEQ ID NO. 107:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 506 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

gtcgaacagc aaagccaaga cttgttaaaa aggtttgaag aggaaggacc ataacaattg 60
aaaggggggaa attataagat acagtaaatt cctcttcaaa gatttagcct gttgacttcc120
ttattctttg ttctcaaaact cgacttcctt gttgtccatg cctccttgtc cctagttact180
gtgaacaacc ttcccaccag ttctaataca taactcacat ctgctccctt ggttaccac240
tctgcaccca ttcttccac tgaaactgca cttcccacca ctgtaactca catccccctt300
cccttcctta tttggaaaag tattcacaaa tagccaatcg ggtcaactta gaatgagcgg360
tccaaccoca gccctgggg gagtgacaca gaggtaggga ctgtgttagg gataaaaacc420
tttcccttcc tttgttcagt gtgctgctgt gatcatgatt gatgcaggca gcagcctttt480
tgcagaagta aattgccttg ctgagg                                     506

```

## (2) INFORMATION ON SEQ ID NO. 108:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004221" 56E2960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

gcgcggcgccg cgcctgcggg ggcagaggggt cggggcggaag gggaagctac gtcccgagg 60  
 tgccgtgtgg ggcaccgggc ggggcgcggc gaaccgggcg cccacggagc tgctgctgtc 120  
 agaccaaccc cgggccccca tcatcactgc gcgcgcgttt caggcgccga gaactaccgt 180  
 tcccggcatg ccatgaaatt ggcctcggcg ctgaggcggg gtccggccct ccaccgctc 240  
 ccgcccgcgc cgaatcgcgg tcgcgagcca tggaggagga ggcatcgctc ccggggctgg 300  
 gctgcagcaa gccgcacctg gagaagctga ccctgggcat caccgcgcat ctagaatctt 360  
 ccccagggtg gactgagggt accatcatag aaaagcctcc tgctgaacgt catatgattt 420  
 cttcctggga acaaaagaat aactgtgtga tgctgaaga tgtgaagaac tttacctga 480  
 tgaccaatgg cttccacatg acatggagtg tgaagctgga tgagcacatc attccactgg 540  
 gaagcatggc aattaacagc atctcaaaac tgactcagct caccagctc tccatgtatt 600  
 cacttcctaa tgcacccact ctggcagacc tggaggacga tacacatgaa gccagtgatg 660  
 atcagccaga gaagcctcac tttgactctc gcagtgtgat atttgagctg gattcatgca 720  
 atggcagtgg gaaagtgttc cttgtctaca aaagtgggaa accagcatta gcagaagaca 780  
 ctgagatctg gttcctggac agagcgttat actggcattt tctcacagac acctttactg 840  
 cctattaccg cctgctcatc acccacctgg gcctgccccca gtggcaatat gccttcacca 900  
 gctatggcat tagccacag gccaaagcaat gggtcagcat gtataaacct atcacctaca 960  
 acacaaacct gctcacagaa gagaccgact cctttgtgaa taagctagat ccagcaaaag1020  
 tgtttaagag caagaacaag atcgtaatcc caaaaaagaa agggcctgtg cagcctgcag1080  
 gtggccagaa agggccctca ggaccctcg gtccctccac ttctccact tctaaatcct1140  
 cctctggctc tggggaaaacc ccaccggga agttgaggca cccttccttc caatttgct1200  
 aaccagtttc caggagtggg gtgggttttt ccgtggcaca ggttggggcc ttagggggg1260  
 ttggacgttc cttttt 1276

## (2) INFORMATION ON SEQ ID NO. 109:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 373 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

aaatacattt atgtttcttg aaatgtgtta agtggccttt gtcaaggtgt ttataataga 60  
 agagtatata aaaatgaatt tctctagaga tgcagcatal tctaaagatc catcattaga120  
 taattaaaaa tatgtaagtc atgctaactt tccatataat aaatggagaa cattaactct180  
 cctactgttt agttataaaa taccaaaattt tgtaattatc ctatctggaa ttacactata240  
 ctgcaaaaaat gccagttact tcaacttttaa atttgacaat gtatgtgatg aattataaaa300  
 tttaatagcc tacatctttt cctccttgta tccaaaattt tccggacctt aatgcttaaa360  
 ccttttggtt acc 373

004227-1200

## (2) INFORMATION ON SEQ ID NO. 110:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 492 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```
gttttttgaa atctgtttcc actacagcta tggtaagtc tatcagccgg tgctaccagg 60
agtcactgcc agggctgccg ttctcctgaa cccagtggc cagaatcata agccctgaccl20
ccatccctag aaagatgagg tcccagcaat ggccagagca tttctcacca gttctgtgag180
atagcacata aaaatagagt tctttgggca aaacttttgg gaagcaatgc atcctacatg240
ggctgatatt cagcctgagc tgttctcaag aggagagtgg tactggcagt ttatggctga300
aatccattct gattggttgg agtctatgct ataccagttg ttaaacattt tgagtatcac360
tcttgcatat tgttactatt atatttcctc tatatataga cagaaaggcc attttaggaa420
tatttaaagg gctcttgaaa attttctggc attagaccca actgaagggt ctattaaggc480
agggttccta aa                                     492
```

## (2) INFORMATION ON SEQ ID NO. 111:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1678 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

00227 3552950



(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

gcctcagcag actccttggg cggtagcagg gagatgggtgc aacggcccca gcctgcacag 60
gaaccgagca ggccctggatc tgccaacccat agacacggga tatgattccc agccccagga 120
tgtcctgggc atcaggcagc tggaaaggcc cctgcccctc acctcogtgt gttacccccca 180
ggacctcccc agacctctca ggtccaggga gttccctcag tttgaacctc agaggatatcc 240
agcatgtgca cagatgctgc ctcccaatct ttccccacat gctccatgga actatcatta 300
ccattgtcct ggaagtcccg atcaccagggt gccatatggc catgactacc ctcgagcagc 360
ctaccagcaa gtgatccagc cggctctgcc tgggcagccc ctgcctggag ccagtgtgag 420
aggcctgcac cctgtgcaga aggttatcct gaattatccc agcccctggg accaagaaga 480
gaggcccgca cagagagact gtcctttcc gggtctcca aggcaccagg accagccaca 540
tcaccagcca cctaatagag ctggtgctcc tggggagtcc ttggagtgcc ctgcagagct 600
gagaccacag gttccccagc ctccgtcccc agctgctgtg cctagacccc ctagcaaccc 660
tccagccaga ggaactctaa aaacaagcaa tttgccagaa gaattgcgga aagtctttat 720
cacttattcg atggacacag ctatggagggt ggtgaaattc gtgaactttt tgttggtaaa 780
tggcttccaa actgcaattg acatatttga ggatagaatc cgaggcattg atatcattaa 840
atggatggag cgctacctta gggataagac cgtgatgata atcgtagcaa tcagccccc 900
atacaaacag gacgtggaag gcgctgagtc gcagctggac gaggatgagc atggcttaca 960
tactaagtac attcatcgaa tgatgcagat tgagtgcata aaacaaggaa gcatgaattt 1020
cagattcatc cctgtgctct tcccaaatgc taagaaggag catgtgccc cctggcttca 1080
gaacactcat gtctacagct ggcccaagaa taaaaaaaaac atcctgctgc ggctgctgag 1140
agaggaagag tatgtggctc ctccacgggg gcctctgccc acccttcagg tggttccctt 1200
gtgacaccgt tcatccccag atcactgagg ccaggccatg tttggggcct tgttctgaca 1260
gcattctggc tgaggctggg cggtagcact cctggctggg ttttttctgt tctccccga 1320
gaagccctct ggccccaggg aaacctgttg tgcagagctc ttccccggag acctccacac 1380
accctggctt tgaagtggag tctgtgactg ctctgcattc tctgctttta aaaaaaccat 1440
tgcagggtgcc agtgtcccat atgttcctcc tgacagtttg atgtgtccat tctgggcctc 1500
tcagtgttta gcaagtagat aatgtaaggg atgtggcagc aaatggaaat gactacaaac 1560
actctcctat caatcacttc aggctacttt tatgagttag ccagatgctt gtgtatcctc 1620
agaccaaact gattcatgta caaataataa aatgtttact cttttgtaaa aaaaaaaaa 1678

```

095395-1200

## (2) INFORMATION ON SEQ ID NO. 112:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

gtcgccatga ctgccaagga ctgctccatc atgattgcac tgtctcooctg tctgcaggat 60
gccagctctg atcaaaggcc tgtggtccct tcatcgaggt ccagggtttgc cttttccgtg120
tctgtgctgg accttgacct caagccctac gagagcattc cccatcagta taaactggac180
ggcaagatcg tcaactatta ttcaaagact gtacgtgcc aagacaacgc cgtgatgtcg240
actcggttca aggaaagcga agattgcaca ttagttctcc acaagggtcta actctttccc300
tgcagtgtct ttgaaacttg aacataatgt gaaggctgaa tgatagagat attttctgtt360
gtgttgggtg accttttggt gtgaatgttt ttgcttttaa ccccttttga ggtgggattg420
cctcttgagg acatggaatt gaagagcact agaaacaact tccctggacaa ggaatgtagg480
aagtgaagtgc tgtgtcccag gaagctgctc acactcttaa aatggaagtg tccgttaagc540
cctgggaaga cgttctggat agttcttctt tcccaaccag ggctcatgtc tgattctcta600
atgcgaaaag ccttattcta agacccaagg tttggatctg ctaccaaccag actcctaaca660
tagaaaactt gaattgtcac atacatttta cagtttggac ttttaagaaa acatggatac720
tactgggaac ttcccccagc tgagttacat gggcactttt tcagtgcagg ccacatatca780
acacagggtt ttaaggtggg tgccctggctg cacacgtgaa ccccggtggc cccagatgc840
cgattctgag ccagtgtaga cccagg          866

```

## (2) INFORMATION ON SEQ ID NO. 113:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

gcgcggccgg cgcctgcggg gcgagagggt cggggcgaag gggaagctac gtcccggagg 60  
 tgcggtgtgg ggcaccgggc ggggcccggc gaaccggcgc cccacggagc tgctgctgtc 120  
 agaccaaccc cgggccccca tcatcactgc gccgcgcttt caggcgccga gaactaccgt 180  
 tcccggcatg ccatgaaatt gccctcggcg ctgaggcggg gtccggccct ccaccgctc 240  
 ccgcgcgcgc cgaatcgcgg tcgcgagcca tggaggagga ggcatcgctc ccggggctgg 300  
 gctgcagcaa gccgcacctg gagaagctga ccttgggcat caccgcgcat ctagaatctt 360  
 cccaggtgt gactgaggtg accatcatag aaaagcctcc tgctgaacgt catatgattt 420  
 cttcctggga acaaaaagaat aactgtgtga tgctgaaga tgtgaagaac ttttacctga 480  
 tgaccaatgg cttccacatg acatggagtg tgaagctgga tgagcacatc attccactgg 540  
 gaagcatggc aattaacagc atctcaaaac tgactcagct caccagctc tccatgtatt 600  
 cacttcctaa tgcaccact ctggcagacc tggaggacga tacacatgaa gccagtgatg 660  
 atcagccaga gaagcctcac tttgactctc gcagtgtgat atttgagctg gattcatgca 720  
 atggcagtgg gaaagtgtgc cttgtctaca aaagtgggaa accagcatta gcagaagaca 780  
 ctgagatctg gttcctggac agagcgttat actggcattt tctcacagac acctttactg 840  
 cctattaccg cctgctcatc accacctgg gcctgcccc gtggcaatat gccttcacca 900  
 gctatggcat tagccacag gccaaagcaat gggtcagcat gtataaacct atcacctaca 960  
 acacaaacct gctcacagaa gagaccgact cctttgtgaa taagctagat cccagcaaag1020  
 tgtttaagag caagaacaag atcgtaatcc caaaaaagaa agggcctgtg cagcctgcag1080  
 gtggccagaa agggccctca ggacctccg gtccctccac ttcctccact tctaaatcct1140  
 cctctggctc tggaaacccc acccggaagt gagcaccct cctccaact cctaccagc1200  
 tccagagtgg tggtttccat gcacagatgg ccctaggggt gacctccagt tttgcgtgtg1260  
 gaccgtaggc ctctttctag ttgaatgacc aaaattgtaa ggcttttagt cccaccgacal320  
 ttagccaggc tcgtagttag gcctccagag caggttgtgc tgtcccctgc ctctggaagc1380  
 aatggggaat gtggaatcaa gacaatgcc aaaaaatttt taatgcagct ggtc 1434

(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 914 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

00227-5662360

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

ttggcagcgg ggagagggaa agaggaggaa atgggggtttg aggaccatgg cttacctttc 60
ctgcctttga cccatcacac cccatttcct cctctttccc tctccccgct gccaaaaaaa120
aaaaaaaaag aaacgtttat catgaatcaa cagggtttca gtccttatca aagagagatg180
tggaagagc taaagaaacc accctttgtt cccaactcca ctttaccat attttatgca240
acacaaacac tgtcctttt gggtccctttc ttacagatgg acctcttgag aagaattatc300
gtattccacg tttttagccc tcagggttacc aagataaata tatgtatata taacctttat360
tattgctata tctttgtgga taatacatc aggtggtgct ggggtgattta ttataatctg420
aacctaggta tctcttttg tcttcacag tcatgttgag gtgggctccc tggatatgta480
aaaagccagg tataatgtaa cttcacccca gcctttgtac taagctcttg atagtggata540
tactctttta agtttagccc caatataggg taatggaaat ttcctgacct ctgggttccc600
catttttact attaagaaga ccagtataa ttaataatg ccaccaactc tggcttagtt660
aagtgagagt gtgaactgtg tggcaagaga gcctcacacc tcaactagggt cagagagccc720
aggccttatg ttaaaatcat gcacttgaaa agcaaaccctt aatctgcaaa gacagcagca780
agcattatac ggtcatcttg aatgatccct ttgaaatttt ttttttggtt ggtttggttt840
aaaatcaagc ctgaggctgg gtggaacag gtagcctaca caccaccaat tgggggtggt900
cccgggggaa tggtt

```

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 685 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00221 5664960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

gaaaatccag ggggtgaagaa tagatctgtg gtggcagggg tgggaaaggg ggggaggatt 60
tgcctactga ggggcagcac aagagaattt tgcggggcga tggatctgtc tgtatcttga120
ccatagtgat gatacatgac tgtgcatttg tcagaactca caggactgaa tgaaaagaga180
agtgaatttt actgcatgtg aattgttaaa ataaatgcta gacagtattt taaaaatcaa240
gccagatcc tgcaagacat tatggctccc caccagaagg ggagagacgg ggaaagagaa300
gtgtccccaa agttaacca cgttccctgg gacccacctc cctccccact gccacttccc360
accagcctca cgcacgggcc aggcccttc ctttgcagct cacagcccag cagatgttag420
gtcagaatgc gtcccctcac ttgactaaag gtttacagcc agcagggtgg gaaatgaacc480

agatattaac accccctcct ccatgccctg cccaccttct gggccagtag cagtgaaggc540
aggaagccac ttctcccacc ccaggtgtg tcccaaagcc ctggaagaac ccaaggaaag600
gcaggagcca agttgggagt tgaccttgat gaccaggggc cagttggccc agtttccctt660
gtttagttgg ggggagggaa ccctt                                     685

```

## (2) INFORMATION ON SEQ ID NO. 116:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2646 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004221 5555555555

ttaattttaat	agcttttcattg	tgattaaaaaa	tagctaacta	gactcaagga	ttcacaatat	60
ttaggtgtat	tttcaatacc	tccagaaaag	aaacctcagt	taatcagagg	aaatagtttc	120
agtcttcatt	tgagcatgtc	tttccatctc	aaaaaaatac	tcttagtagg	ttggagtga	180
gatagcaagg	ttttgaagca	tattttgtcct	aatccacagt	gacacttttt	atcttccagg	240
agcactccta	ggaggttccg	tgccataatca	atgttgactg	ctttgcagat	ctcaagggaa	300
taaaatgaca	aaagcagggg	aagttaacaga	ttcaaacagc	attttaactc	atgttgatct	360
ggataatcaa	tctttttctaa	agatgtgtag	tttcttggaa	aacagtgata	tcacatgatt	420
aaaattacat	ttttatcaac	ataattgtct	ggaaaagata	agccctcaa	ttttctacca	480
gttgactttt	attcattaga	tacagaaggt	gcagttattac	acatcaccag	ctgcctttgt	540
gaatggctca	ctacacagcc	attgggggtac	aactgtgtgc	atgggcagaa	acagcaagtg	600
ccctcattgt	ggtcattggg	tggggagtgc	cttttgtcaa	ggagtctgca	ggaattggct	660
tatttctgta	tgccaaaagt	atcaacacac	caaagtctct	gccataaaga	atgtggcttc	720
cttgcatcct	ccatccctgt	actctgggcc	cagtaatttg	atgtaactgt	ctgattgtac	780
tagagacagg	agtataccca	gcttattcat	aatcaagtaa	agagactcag	attagatttg	840
attttttagc	ctcctctaga	gccaatcagg	cagttaagag	taataaaagga	aaagggtttg	900
gtcacaaaac	ctaccattat	ctggagatta	cttcctgtct	cactcctgtc	ttgcctatga	960
cgtcttgccc	cctcactttt	ctgcagccta	gcagcttact	tcaacttatt	gccttgtaaag	1020
tgtcaggcct	cctgggcgct	ctggaaaaga	cagggagcca	ggccctctca	cccctactgg	1080
taacagggtca	ttgctgggtg	cacaagaggg	aggtgatttg	catcatggtc	atgctgcatg	1140
ggcttcactg	ggatgctgtt	aaacaccaga	ggagccaacc	tatcagaatc	ccagcagcaal	1200
aggaaaactc	agatttttaga	ggctttttac	aataaagtag	cgtaaactcta	ggtcatgatt	1260
gatttcaaat	gcctgccatg	aatgattttg	aagtaattat	gtaggatcca	tcaaagcagt	1320
attgtaggct	tttgaaattg	cccagtggat	ccgggaccct	atttcactgt	ctctcttgat	1380
cgtgtaaatg	atgcaatcag	agttcaagac	aggccccatc	aagtctgact	gcactgggat	1440
ggagaaatga	atttcttccc	actgaaggaa	actctttctc	attcgcagcc	aagacgggag	1500
tggccactgt	cctctcttca	ctcctgagat	actgcttctg	gaagcgggtg	tcacttctct	1560
tctagtacct	cttctcttct	ctgaagtgtg	tgactatctc	ctagtgttca	aatttggcag	1620
ttactcgcca	tgtatgtcag	catagaaaag	gaaatgtttt	taccttatct	cctgtatgtal	1680
tgatagaact	taaaagaaat	gtgcattttgt	tttcatagcc	ccagcagaga	aaatcctctt	1740
catagattaa	atgtgctgct	gtggacagga	gggaaaaaaa	aacctctac	atattgaaag	1800
gcaccaaagt	taatattctga	cactgttaag	atgccaaaaa	gagcaaagtt	gtagtggaga	1860
tgcagggtca	tttcccatatg	ccatccacag	tgtttgttag	tgagtccacg	gctgacttgc	1920
agtgataaag	aaaagcatgg	agctgtgtct	gcagacaatg	gtggctgcat	ctgtaagtg	1980
cttcagaggc	agcagccctg	gggaaattga	tgggtgtggc	agtggacctg	tgaagaggga	2040
gaactagacc	ttcagcctgt	ccagtgttaa	ccactagaga	aactgagctt	tatatctttt	2100
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attaaacatc	cctcagataa	tttagctata	tatcattaga	aagggaagc	tatcattttt	2220
atttttaaac	taaaacaaggc	catcttataa	actgtcacca	aagtcttccc	ttttttattg	2280
catgtgtgcc	ttgaatttca	taaaacatta	attcacaatg	ggggtcagaa	tgtactcttg	2340
ttgaaacact	tcttgtagca	ttttatgttc	atattatgtt	tgagagggtg	aaaatgtatg	2400
agcagcttaa	ctgaagttaga	actattcatg	atgcttttca	cacattgtgg	cataagatgt	2460
aaagtttgta	attaatgtta	atttctgtgc	attttaatat	tctttttata	ttattaatgt	2520
taatttctgt	gcatttttaat	attccttttat	aattatgagc	attttaataa	attcattttt	2580
acaaacata	aaaaaaaaaa	aaaaaaagga	ggaagggaaa	aggaagaagg	aggggggaag	2640
aqgaag						2646

## (2) INFORMATION ON SEQ ID NO. 117:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2667 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

ttatcttggga agtctgtgta tcaaaatgaa gaattcagat ggtaggaggt tctatagtcc 60
ttttaaaagct gactcttgag tgtcagttga atatccatta aattggattt ggaaataacc 120
tgaggaaaagt attatgaatt cgatctgcac agatgcctct tagctgatag gtggcaggcc 180
tgtgggtttg ggttctccct cttttctctg gaacatatga caattccaga ttaaagaaaa 240
atgtttttta ataaataccc ttggtcttct ttctagtcac ctttgaggta gatattgtga 300
ttttctggag tatagtatat cagtgtctct gtgtcttagg tttactagat gcaataatac 360
ttctctttga catttgtagt gaagtgtatt gatattaagt aaaacagtta atgtttgaat 420
ataggcatat ttatagggtt ttcccgctcc cccccaaccc acccttttta aaaaatctat 480
acaaagccct tgtttgagtc tcatcatgca catcaaatca tggagttagg tcttctctga 540
gtcaggggga acacaagtgc acagagagag atgtcttgag ggtcactacc aaagaattac 600
cctcattgtc cctcactcag gccatgtgta catgcgatgc tgctgagtgt gctgggggtg 660
gtggtggcca cgtggctccc ccagagcact tccaaactgg caagctggga gaccattac 720
tggtgaactt tgtggaaatt agaactgta cttttacata atcttggcat attacatttc 780
ataataaaaa catacattta gttgcatgct acatcactat tgattttata attaatctct 840

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002227 56E2960

```

taagcttcaa ccatgtttta taccttattt cgttacatca tatatttgta atgtgtaata 900
tgaaaacctt tgctttaaat tcttttttta aaatgtagaa tgttctaaac ttgaaaggca 960
attgaatgta gtatgatgaa aatgtgaatg ttttgctgct ttcattgacca aagatacagg1020
gctagtggac atttagaata ataattaaag ctatagctct gtatgtcttt tctttgaagg1080
agttctaacc ttgtaaattg agaattgactt cagagaattt tgattaagaa aacattaaaa1140
tcttaaccgg cacaacactt ccaatttttt tctactgtgaa gccgcaagca attttttttc1200
tttttctttc aaaagcctgc cttctgaatt tatttcttgt ttactcattt cagagaggg1260
agtaaagaag atctatttct ggtagtcata tgccttgaaa ggtattggta aatgtgttt1320
cagtcgtgac catgtggaaa gtgaacagt ttggcaaaca ttaccgagaa aatcatgctt1380
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aattgtgaat tccatttctt atttcagttt ctgctgcagt aatgggttcc caccactat1500
aattcccagc atttatgttc tgttgtattc tccccttagc ccagtaacat ttttatctaa1560
taccocatct cccaagtttt gagacagatt gacccctac tcattatgtg gctctagttg1620
aattttaaaa tgtggaatat tgggcttgca ggcagtagga gctgcaaatc tggtagagt1680
ggagtgtgga gttaatggtg agtatgttaa taaagggaaa ctgtctctga cagaatctca1740
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agtaacctca ttacaaatac tgttactaga agggcatgtg ctgtctgtca ccttcagtaa1920
tatttgtgcc atctcttgat gactgatgac ctggatcgag tatttctatg aagggtcttc1980
ttaggcccct tacatacgca agaggggtgc tctagtacca tagctgtagt tcacaggaag2040
gacaccagga gaagtatac ctagggtac tgagcagctc atcatccctg tttctgcaca2100
gtttcctgaa actggccatc agggcctctg aggcactcaa atcagtttac ttttagcatg2160
cccccatcag ggtgggtctc actgttagtg aggatacggg tctqggttga tgtttttcta2220
ggcaaaatgc ttaagtgttc tggttatgcc attcattcat acgatgtgtg aaatttgctt2280
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ttaattttat tgtaaaaata aggaaaaata tgtgaatatg tgaatttttt aagcctgaga2400
gatgatagaa tgttcccata ttttcttgt aaagaaaata atattttaac ttacacatcc2460
tgtagaaaat accacctttt ccccttgat tacagtacaa tgtttacatt actatactgt2520
caagctgaaa gtataaaaaa tgtacatata cattttgagt tatgtatcct ttttttaaaa2580
aaaggtgcgg ggctgtggca ctgggctgga catgactaaa gttgacagag gctatgctag2640
atttataatc actagtctct ggacttg

```

2667

## (2) INFORMATION ON SEQ ID NO. 118:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 544 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:



(A) LIBRARY: cDNA library

catctgtgca	tggatgagtg	gccgactttg	gagcccaggc	tgttacttcc	tggctcgggtg	60
gtgaatcctc	catagtctga	gagtaagatc	cttgatactg	gctcagcatg	gaacatctgg	120
cacacagtat	gcactgagga	aatacttggt	ggaataatca	gtgaatcata	gatgaaaact	180
taaccttgga	attaattatg	agactgctca	gaggaagaga	atgggagaca	aaggacctgg	240
tgattagacc	cccaagacac	tgggctgtct	gcttgtgtct	cgggtggaac	aggcccagcg	300
agagtcttta	gggccagaac	tcaaggaatt	tattgagcca	tggcaaacag	gcagtaaaaca	360
gccattcttg	gctgctgtat	tgagaaagaga	atgtggtgga	cagatataga	agcatggaaa	420
cctgtatagg	ctattgcaat	cactcagaaa	agaggcgatg	gcagcttgga	cctgttgaa	480
cagtagagtg	ctttccaggg	aggagaaaagg	acctgaaggt	taatttgatc	accatggggc	540
atga						544

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1340 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

gtttgatact ttcctgcact taggtttgtc ctattcttca tttattcaga ctaggataga 60  
 aaatTTTtGga atcagaaaaat agatccagtG tttagctaca tacaatctag tacaagtGaa 120  
 tttttattct taaacatagg tgtgttgGct ctttttttaa aagatgcGct ctacctGaaa 180  
 agGaaattGg attttagaac tggatgtGgt gcagtgaagt attttaggcc cagggtctgtG 240  
 tacacatttt atagaagaaa tgaagtactc tgaagtattt tggttgcctt ttcatttcaa 300  
 ctgtgttttg aatttgtcag atcacacata tattgtgtta ttggggcGctg tggtatcttt 360  
 tataaaacct cttgcttGtg tgcaaaagtT cctaaaagga aacacaagta atgcctatcc 420  
 attactagca tgctatGctg catgctttac tgccattGct gtatgcttta ctgtctttgt 480  
 aaaaatcccc ctctcccttT ttctggtaac tggaaaagca tgctaaaaat agtcttataT 540  
 tttcacccca taagtgcaga atcagtaatt ccttgGctta aagctcttat ataatcaata 600  
 ttattggtGg taaataccaa gtttggtatc tcatagctat ctttttttaa agaaattaag 660  
 ttcttgaaaa tttagccaaa tcccgtttta tgggaatGct ctttagaatt cattttgttc 720  
 agcccttttg ttctatggtt gagaaatctg aggccttacg aagggttaaga gaactttccc 780  
 cgtgtctcac aggtaggtag aggcagagct ggaactagat atctggtctg ttgactctag 840  
 ctcaGtgctc tctggttaact gttgaaaatt gtcttagttt gagagatggc tgaaataatg 900  
 aacataaaat gctattttata ataacaagta tatgtgaaat ttcttattgt aagactacta 960  
 ccggcttact gttgaatagt ttggttatag tgtttaggct agaaatgcct ccacattgg1020  
 taataaacat tacaaaaatac aatgtatttt taggtaggca ttttataaaa tgcattatgc1080  
 catggttgct tttgagatag attgtagctc gggtagcatc tttaaaatgt atgtgggctt1140  
 aactgttggt catatcagga gatgctctga ttgtataggt gagactctgt ttctgttatt1200  
 tttattgct gtatgaaatg tgatcagatt attttactac caacagttat agtttgaaag1260  
 tccaactgta ttaattgact gataatatga taatatagag attaaattgt ttgtcttcat1320  
 tccttaaaaa aaaaaaaaaa 1340

## (2) INFORMATION ON SEQ ID NO. 120:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2376 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ggatatgaat aaattgttaa tataaagtcc tacagaaatt aatttatgaa atttctctaa 60  
 atcacacaaa acttaaatat agatgactac taccctgaga ctgaaaaata tgttctaatt 120  
 tatagtgtta tttttgggca gttttggtgt cagaatacct atcaacacat tcttttttta 180  
 ttaggaaaaa aaggatgtct acataacaat ttgtaaagtgt ataaaaatcca ttagtttttta 240  
 agtcttctga tagcattggc tattataaga aacaagtatt tgctctcggt tttaacggga 300  
 taataatgct atgtctacat aaaatgattt ctaccacctt aaatagctca ctgtagaaat 360  
 tcatgtataa atggaaccat atagtacata catatcatat tcttaggtct ggcaaataatt 420  
 tgaggttcat ccataatttta tttcactcca tcagtagttg taaacacatt cttaaagtag 480  
 ctttttcaga tatgaataag cagggatgaa ataagtatta gggtaaggga aatgggtgag 540  
 gctttcctaa gtgaagtgtt aaaaccacag ctttcttttt aatgggatgt ctaatatgca 600  
 tttatctgtt caagcatttt aagatttcca tgaaaatgtc ctgaaaaatc aagattcttc 660  
 attgaggggtg aggatctccc aatgggagac tgctctgaaa agagcatgtg ctttttgaat 720  
 tagataacct actataatca tggatgttct tgaatactta gcaaacatac cagcatccca 780  
 aagtcaccaa gataaacctt cctactccaa catcacatga tcttctaatt ctacctgtaa 840  
 aaataagcat aacaattaat tagaatataa ttacgttata tacattactc cacctagaaa 900  
 aaaaaatagt tcattatgta gagaaatgct ttttttagta catagagaaa taaaaaatat 960  
 agatactcac tagtgaacaa aaaatgtcca aagccagcca caacagatcc taatgaacca1020  
 tacaatattg aatgocgggc gcagggagta ttttcaacat ctaaaaatcc taggagctta1080  
 agggactaga atgaaaaaaa agaacctaga ttgagtaaga aagtatttca ttttgggggt1140  
 ctttggcaaa aatgacaata caccatttct tttctttagt ttgaggggtt aaactagagt1200  
 atgtgccacg tgacaacctt aatcagcttg cgttgtcttt gtccaccttt ggtatgcagt1260  
 ctgaatcttt aaatccgaaa accttacaaa ttggaccgga aaacctttaa gcagtaggggt1320  
 aacttgagc tgtatcttaa tttgctaata aactgacttg gaaataggat aattcatttt1380  
 atgagctctt taaatgagtt ttttgggaa tatgcctatc attggaattg aaagcagcat1440  
 agcttgcttc agtaactcca ataatttggg aagcagaaat ggaaaaagta atttgagtca1500  
 tgtttgctta tgtagtgcg tttaaaattc ccttagtaac tacctttcat attttattaal1560  
 ctaggttaac atcaactgtg gttgtaagag taaatgtttc accttaagat aaacatgggc1620  
 aatatattaa actctagtct gttttcttgc ctgtgaagtg aggctgcact tgattatatt1680  
 tgattctttg ttcgtaatac atgggaacga cagctaagtg tggtgaaaaa cgcggggatc1740  
  
 caaagagctg gatttttctc tcagatctgc cgctaacttt tgtatctat aggctacttt1800  
 ttttctatg gtctcaatct ataacatgaa tgggttgggt taaatgactg aagttccttc1860  
 aagtgtctaa attctttttc tacagtcttc attggattta tgtatttctt attcctaata1920  
 tgtttaactg ggatgtctgt cactctaggg cggcaagaca gacattttaa agtaacagtc1980  
 acactgctga actggcattt ctgttaacac aaaagttagt aaaaactcac gtaactgtta2040  
 cttgatthaa gtgtatataa aattttcagt aaggctgctt ttaaaaggaa ccactgtcca2100  
 tttaaagggt tcatagttat cttcaatggg tttagtattg ttggggcagg acattaaact2160  
 agaagggtt ctataggatg aggtgatacc tagaaggtaa tatattgtaa ggcaaaagag2220  
 attagaagaa atggggggaa aggatagtaa aaggcaagtc agattaaagg gttgaaacat2280  
 gaagatatcc ccattgtatt cggcccccgt gtttgcctt tttggctcca gcatcgtgtt2340  
 tggaaagggc caatgtgcc cgggtcccta ataaag 2376

## (2) INFORMATION ON SEQ ID NO. 121:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 225 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```
cagttgtgaa gttttgtaaa atggtcaccc aacttaaaac taggaaatta cgaagaagag 60
aaaattgccc ggtatctgtt aaggtctgcc tgtagatctg ctgtagggct tgtcaccatt120
ggaagcaagg tcctacttca gtggcagatc ttgtggcctt tgagtggctg aagaccacca180
ccctgcacag ggctggggcc atgcacaggc atccttccct acctt                225
```

## (2) INFORMATION ON SEQ ID NO. 122:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1967 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

0022256250

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

acgggaggcg cccgcgctcg caggccaactc tctgctgtcg cccgtccgcg cgcctcctcc 60
gacccgctcc gctccgctcc gctcggcccc gcgcgcgcgc tcaacatgat ccgctgcggc 120
ctggcctgcg agcgcgctcg ctggatcctg cccctgctcc tactcagcgc catcgcttc 180
gacatcatcg cgcgagcccg cgcgagcctg ttgcagtcta gcgaccacgg ccagacgtcc 240
tcgctgtggt ggaaatgctc ccaagagggg ggcgccagcg ggtccctacg ggagggctgt 300
cagagcctca tggagtacgc gtggggtaga gcagcggctg ccatgctctt ctgtggcttc 360
atcatcctgg tgatctgttt catcctctcc ttcttcgccc tctg-gyacc ccagatgctt 420
gtcttcctga gagtgtattg aggtctcctt gccttggtcg ctgtgttcca gatcatctcc 480
ctggtaattt accccgtgaa gtacacccag accttcaccc ttcattgcaa ccgtgctgtc 540
acttacatct ataactgggc ctacggcttt ggggtggcag ccacgattat cctgatcggc 600
tgtgccttct tcttctgctg cctccccaac tacgaagatg accttctggg caatgccaa 660
cccaggctact tctacacatc tgccctaactt gggaatgaat gtgggagaaa atcgctgctg 720
ctgagatgga ctccagaaga agaaactgtt tctccaggcg accttgaacc ctttttttgg 780
cagtgttcat attattaaac tagtcaaaaa tgctaaaata atttgggaga aaatatTTTT 840
taagttagtg tatagtttca tgtttatctt ttattatgtt ttgtgaagtt gtgtcttttc 900
actaattacc tatactatgc caatatctcc ttatatctat ccataacatt tatactacat 960
ttgtaagaga atatgcacgt gaaacttaac actttataag gtaaaaatga ggtttccaag1020
atttaataat ctgatcaagt tcttgttatt tccaaataga atggactcgg tctgttaagg1080
gctaaggaga agaggaagat aagggttaaaa gttgttaatg accaaacatt ctaaaagaaa1140
tgcaaaaaaa aagtttattt tcaagccttc gaactattta aggaaagcaa aatcatttcc1200
taaattgcata tcatttgtga gaatttctca ttaatatcct gaatcattca ttttagctaal1260
ggcttcatgt tgactcgata tgtcatctag gaaagtacta tttcatggtc caaacctgtt1320
gccatagttg gtaaggcttt cctttaagtg tgaaatatatt agatgaaatt ttctctttta1380
aagttcttta taggggttagg gtgtgggaaa atgctatatatt aataaatctg tagtgttttg1440
tgtttatatg ttcagaacca gagtagactg gattgaaaga tggactgggt ctaatttatc1500
atgactgata gatctgggta agttgtgtag taaagcatta ggagggtcat tcttgtcaca1560
aaagtgccac taaaacagcc tcaggagaat aaatgacttg cttttctaaa tctcagggtt1620
atctgggctc tatcatatag acaggcttct gatagtgtgc aactgtaagc agaaaacctac1680
atatagttaa aatcctggtc tttcttggtt aacagatttt aaatgtctga tataaaacat1740
gccacaggag aattcgggga tttgagtttc tctgaatagc atatatatga tgcacggat1800
aggtcattat gatTTTTTtac catttcgact tacataatga aaaccaattc attttaaata1860
tcagattatt attttgtaag tcttggaaaa agctaattgt agttttcatt atgaagtttt1920
cccaataaac caggtattct aaacttgaaa aaaaaaaaag tcgacgc 1967

```

00227.36E2360

## (2) INFORMATION ON SEQ ID NO. 123:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 612 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

cctagctgtc cccctgagat gaagaaagag ctccctgttg acagctgect gccccgctca 60
ctcgagcttc accctcagaa gatggatccc aagagacagc acattcagct cctgagcagc120
ctgactgagt gcctgacggt ggacccccctc agtgccagcg tctggaggca gctgtaccct180
aagcacctgt cacagtccag ccttctgctg gagcacttgc tcagctcctg ggagcagatt240
ccaagaagg tacagaagtc tttgcaagaa accattcagt ccctcaagct taccaaccag300
gagctgctga ggaagggtag cagtaacaac caggatgtcg tcacctgtga catggcctgc360
aagggcctgt tgcagcaggt tcagggctct cggctgccct ggacgcggct cctcctgttg420
ctgctggtct tcgctgtagg ctctctgtgc catgacctcc ggtcacacag ctcttccag480
gcctccctta ctggccggtt gcttcgatca tctggcttct tacctgctag ccaacaagcg540
tgttccaagt ttactcctac agtctgcaag gttacagggt ggttggggga gaaatgccgt600
tttgggggttc ca                                     612

```

## (2) INFORMATION ON SEQ ID NO. 124:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

004227 5622960

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

tttcggcaca	gcatgaatgg	ctgcgagaag	gacagctcgt	ccacagattc	tgctaacgaa	60
aaaccagccc	ttatccctcg	tgagaaaaag	atctcgatac	ttgaggaacc	ttcaaaggca	120
cttcgtgggg	tcacaggccc	aaatattgag	aaatcagtga	aggatttgca	acgctgcacc	180
gtttctctaa	ctagatatcg	cgtcatgatt	aaggagaag	tggatagttc	cgtgaagaag	240
atcaaagctg	cccttgctga	attacacaac	tgcatcattg	acaaagaagt	ttcattaatg	300
gcagaaatgg	ataaagttaa	agaagaagcc	atggaaatcc	tgactgctcg	tcagaagaaa	360
gcagaagaac	taaagagact	cactgacctt	gccagtca	tggcagagat	gcagctggcc	420
gaactcaggg	cagaaattaa	gcactttgtc	agcgagcgta	aatatgacga	ggagctcggg	480
aaagctgccc	ggttttcctg	tgacatcgaa	cagctgaagg	cccaaatacat	gctctgcgga	540
gaaattcacac	atccaaagaa	caactattcc	tcaagaactc	cctgcagctc	cctgtctgctt	600
ctgctgaatg	cgcacgcagc	aacctctggg	aaacagagta	acttttcccg	aaaatacatcc	660
actcacaata	agccctctga	aggcaaagcg	gcaaacccca	aaatgggtgag	cagttotcccc	720
agcaccgccc	acccctctca	ccagaccatg	ccggccaaca	agcagaatgg	atctttctaac	780
caaagacgga	gatttaaatcc	acagtatcat	aacaacaggc	taaatgggcc	tgccaagtcg	840
cagggcagtg	ggaatgaagc	cgagccactg	ggaaagggca	acagccgccca	cgaacacaga	900
agacagccgc	acaacggctt	ccggcccaaa	aacaaaggcg	gtgccaaaaa	tcaagagggt	960
tccttgggga	tgaagacccc	cgaggccccc	gccatttctg	aaaagccccc	gcgaaggcag	1020
gcacgttcga	ggacacctcg	ggaggcccg	gggccttttc	ggggttagtt	ttcggttagg	1080
ggtttctaca	gttgcatttt	tttgcccca	cggagatta	ggaagttttt	ccacagatgg	1140
caaggcatttt	ttttgaagttc	cccqgttttt	gacgttttgq	ttg		1183

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 891 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

cggaggcagc ggaaagccga gccaggcgcc tgcgcgctgg gaagagtagg ttcagagtgc 60  
 attccggaac cggggcgcg gcgcactgcg caggcgccg gactccgctc agtttcgggt120  
 gcggcgaaca ccaaagtcg ggaacttaag cttttcggt ttctagggtt gttacgaagc180  
 tgcaggagcg agatggaggt ggacgcaccg ggtgttgatg gtcgagatgg tctccgggag240  
 cggcgaggct ttagcgaggg agggaggcag aacttcgatg tgaggcctca gtctggggca300  
 aatgggcttc ccaaactc ctactgggtg gacctctggc ttttcacct tttcgatgtg360  
 gtgggtgttc tctttgtgta ttttttgcca tgacttggtc gctgatatct aaattaagaa420  
 gttggttctt gagtgaattc tgaataatggc tacaaaactt ttgaataaag aagacaggac480  
 totcaataga agaatttcac atctccaagg gaccttctct ttcattttac actttgttac540  
 taatttgcag aactctatta attgggtagg atttcaccca ttcctagcta agttcttaaa600  
 attaaaccct ttgggtcgtg tttaaaaact ttcaaaccat tgatggcttt acaggggctg660  
 aatataaaag cttttgtact taaaggtctt gtgtattcat taagaaatat agtaatgtct720  
 tttaatgttt taagagttga tcaggggttt actatggatt gcaagtaata gggatgatta780  
 ataaggggaa ggtttttatg gaatttcaaa agtcaattta tttcaaaagc gggggaaagg840

gttttgagag gaggggggccc caaggtgttc ctgggggtttg ccgagggagg c

891

## (2) INFORMATION ON SEQ ID NO. 126:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 482 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

tctctaaata gtaccttttc agtcttgccc cagaagttcc ctcaatttca gcagcaccga 60  
 gcggtttata attcattcag ttttccaggc caggcagccc gctatccttg gatggccttt120  
 ccacgcaata gcatcatgca cttgaaccac acagcaaacc ccacctcaaa tagtaatttc180  
 ttggacttga atctcccgcc acagcacacc acaggtctgg gagggatccc tgtagcaggg240  
 gaagaagagg tgaaggtttc gacctgcca ctgtcaacct cttcccatte attacaacaa300  
 ggacagcagc ctacaagtct ccacactact gtggcctgac aacagaactg agaggagagg360  
 attagactct ggggtgcttg catgggcaac tggatttttg catgattcct ttatgatttt420  
 gcttttaatg tatacaccga gaagagccaa tataaacgtt cctcatgcct aaaaaaaaaa480  
 aa

482

004227 5622960



## (2) INFORMATION ON SEQ ID NO. 127:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 610 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```
ctcgagccgt gggcagtggc cgcgaatgcg cggagacact gaccttcagc gcctcggctc 60
cagcgccatg gcgcccctcca ggaagtctct cgttggggga aactggaaga tgaacgggcg120
gaagcagagt ctggggggagc tcacgggcac tctgaacgcg gccaaagggtgc cggccgacac180
cgaggtggtt tgtgtcccc ctactgccta tatcgacttc gcccggcaga agctagatcc240
caagattgct gtggctgcbc agaactgcta caaagtgact aatggggctt ttactgggga300
gatcagccct ggcattgatca aagactgcbg agccacgtgg gtggtcctgg ggcactcaga360
gagaaggcat gtctttgggg agtcagatga gctgattggg cagaaagtgg cccatgctct420
ggcagaggga ctcgagtaga tcgcctgcat tggggagaag cttagatgaa aggggaagctg480
gcatcactga gaaggttggt ttcgagcaga cagagggtca tcgcagataa cgtgaaggac540
tgtggcaagg tcgtcctggc ctatgagcct ttttttgggc catttggtgc ctggcaaggc600
cttcaaacag                                     610
```

## (2) INFORMATION ON SEQ ID NO. 128:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

002227 3552360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

ttcaaaagtca	gcatgatcca	cagactgcga	ttcacaacog	acgtacagct	aggatatctct	720
ggagacaaaag	tagagataga	ccctgttacg	aatcagaaaag	ccagcactaa	gttttggatt	780
aagcagaaaac	ccatctcaat	cgattccgac	ctgctctgtg	cctgtgacct	tgctgaagag	840
aaaagcccca	gtcacgcaat	atttaaactc	acgtatctaa	gcaatcacga	ctataaacac	900
ctctactttg	aatcggacgc	tgctaccgtc	aatgaaattg	tgctcaagggt	taactacatc	960
ctggaatcgc	gagctagcac	tgcccgggct	gactactttg	ctcaaaaaaca	aagaaaactg	1020
aacagacgtc	cgagcttcag	ctccacgaag	gagaaagaaat	ccgggcagca	gtgacactgg	1080
cctccagcct	caatctgttc	cgtagctcag	agcctgcctg	ccagggccaa	gtgccctaga	1140
gccaccccg	tgtcctgaag	tcctcgggg	gaggccagcc	cctggctcac	tgccacaggg	1200
caggtgggct	ctcggggaag	gtgtcgggg	ccccctagga	gggagcgctg	gggacattgc	1260
catgggacgg	aagtctgctt	ggcagtggt	ttgataagcg	atgcttgggg	gtcagaccac	1320
cccctagagg	agccacgtgc	cgcccagcca	ccttcaatgc	ctgccacct	gcccagggat	1380
gtacagagcc	gtgcccacac	atttcccttc	aacttgatca	aatttcttaa	agcaaacac	1440
aaaaatgtac	atttctgttt	ttccttttaa	taaacagggt	tactctttat	catggttggt	1500
atgatgtacc	attctttggg	gccgaggatt	gattatgita	ctctcttttaa	aatctgtttcc	1560
catattgaac	aggcagattg	gaaaagctat	ggttcgattt	ctcagaagaa	atgtttagggt	1620
cttagtcaat	agtttttaact	atgccatttg	tttaaagttag	tgcatattgct	tcgagggttag	1680
tgtcttacta	aaagtttagga	acagagacct	agtgggtgtg	ccaaggccgt	gtcactttcc	1740
ccttcagcac	accccagctt	ctgacctcag	agcccaggag	ctgcgtggac	agtgtggggg	1800
gccaggagga	ggggcggtgg	ctggtcctca	ggcacgctgc	actcccagcc	agacatgggt	1860
tttccgtttc	ttaagttagca	agtgtaggtt	tcagctggca	gttccacctg	catgttctct	1920
gcttcgctgc	cttggaaagg	gccacattcc	ccattcctct	tctccttaca	gcgcctgctt	1980
cctttttaag	caggcggaag	ctgtctgttt	ctcacgtttc	aggagagagg	gtgaccagga	2040
gactgtgtcg	tgcgctcggtc	ctgggtggac	ag			2072

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN  
(C) ORGAN:

(A) LIBRARY: cDNA library

tttatggagt	tagagcaggg	gaacttaaaa	acaaaagtgt	atttaataac	ttcatgagac	60
tgtgataacc	agtttatatt	tgaaatatat	acagcacttt	gggagactga	gggttgaccc	120
tgatagtcct	ttgcacagt	atcttcagat	cttaaaagaa	aaagaaggca	tagaatatat	180
tttgcttaac	ttctctttta	aggataactt	tccatttgat	cctccatttg	ttcgagtgg	240
gttacctgtt	ctctcaggag	ggtagtgatt	gggtggagga	gcattatgta	tggaacttct	300
cacaaaacag	ggctggagca	gtgcctactc	aatagaatcg	gtcatcatgc	aaataaatgc	360
caccttagtc	aaaggcaaa	ccagagtgc	gtttggagca	aataagaatc	aatataatct	420
agcaagagcc	caacaatcct	ataattccat	tgtacagata	catgagaaaa	atggctggta	480
cacccctcca	aaggaagatg	gctaaatatg	ttgactgttg	tatgtttgga	ctaagtgtgc	540
tttaaagaaa	atctttccaa	catgcagaca	aaagctttga	gtgcccttat	tacagcagta	600
ccgaagatgt	tagttaatat	atatttttagt	ggataaatctg	tcacttgaca	tccagtataa	660
gttacagcct	tcgcattttg	ctcatttttag	atatcttgga	ctgagcagt	gggcctttac	720
tgtatttttc	ctgataaata	cacatactgg	ccactcctta	tctctttttc	ttgaaaagt	780
aactttttta	aggcagccaa	gtcaacatca	gggctactga	agttggagg	cttttagggg	840
aacttttcta	tattgagccc	atgggggttac	aaggggttgg	caatatattg	ttccctttta	900
cagccaatac	agggtttta	cggatgtttc	aatattgggt	ttaggggatt	ttaagggccc	960
tccttaagtca	taatagccct					980

## (2) INFORMATION ON SEQ ID NO. 130:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 792 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

ctgttttgga gggcgggggcg cctcggaag atggtggcg gcgcgcggtg tggctcccgt 60
cgtctggcca agtctcagcg cagcaaccg gccggcgctt cgttggcctg gagcccacac120
ccaccgggtc cctgaccccg cccccccgc gcccggttcc cggcatgcct cgcgcccgtal80
agggaacac gctccggaag ggtggtcagc gccgtggagg aggtgcccg agcagtggccc240
aagctgactc gggttccagt gacgatgagg cagccagtga ggcccgagc accgccagt300
aatgccccag ccttctcagc accactgcag aggacagcct tgggggggat gtcgtggatg360
agcaagggcc agcaggaaga ccttgaggaa aagctgaagg agtatgtgga ctgtctcaca420
gacaagagtg ccaagacccg gcaggtgcct cttgagagcc tgcgcctggc cctagcgtcc480
cgctactcc ccgacttctt gctggagcgc cgctcagc tagccgatgc cctggaaaag540
tgcctcaaga aagggaagg cgaggaacaa gccctggctg ctgctgtgct aggcctgctc600
tgctgcagc tggggccctg acctaagggt gaggagctgt ttcacagcct gcagcctctg660
ctggtctctg tgctcagtga cagcacagct agccctgctg ccggtccca cgtgagttgc720
ctgtgcccc tgaaccctt cctgcaactt atccctcagc agagtgggtg gttcccccta780
tcttcagcct cc                                     792

```

## (2) INFORMATION ON SEQ ID NO. 131:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

004221"5622960

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

gtgggtcccc ccggttccgg cgcggttgag gccttcggtg gtgaacgagt ctccagcacc 60
atgtctggtt tgtctggccc accagcccgg cgcggccott ttcogttagc gttgctgctt 120
ttgttcctgc tcggccccag attggtcctt gccatctcct tccatctgcc cattaactct 180
cgcaagtgcc tccgtgagga gattcacaag gacctgctag tgactggcgc gtacgagatc 240
tccgaccagt ctgggggcgc tggcggcctg cgcagcacct caagatcaca gattctgctg 300
gccatattct ctactccaaa gaggatgcaa ccaaggggaa atttgocctt accactgaag 360
attatgacat gtttgaagtg tgttttgaga gcaagggaac agggcgata cctgaccaac 420
tcgtgatcct agacatgaag catggagtgg aggcgaaaaa ttacgaagag attgcaaaag 480
ttgagaagct caaaccatta gaggtagagc tgcgacgcct agaagacctt tcagaatcta 540
ttgttaatga ttttgcctac atgaagaaga gagaagagga gatgcgtgat accaacgagt 600
caacaaacac tcgggtccta tacttcagca tcttttcaat gttctgtctc attggactag 660
ctacctggca ggtcttctac ctgcgacgct tcttcaaggc caagaaattg attgagtaat 720
gaatgaggca tattctcctc ccaccttgta cctcagccag cagaacatcg ctgggacgtg 780
cctggcctaa ggcctcctac caacagcacc atcaaggcac gttggagctt tcttgccaga 840
actgatctct tttggtgtgg gaggacatgg ggtaccacct acaccaaca agtcaatgag 900
ggacttcttt ttaatttggt aggatttga ctggttttgc aacaataggt ctattattag 960
agtcacctat gacaaaaaat agggggttac ctagataatg ccaaagtcag catttgtccc1020
gggtcccttt gtgggagctg tgggacgatg ttttcttttc tgcccctttt cgggagcgtg1080
gggggccaaa ta 1092

```

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1523 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673995.12200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

ctcatgtctcta	aagaaattcc	tttttgtgtg	aaaaagacta	agagcatcct	caacagtgcc	60
atgcaagaga	tggaggttta	ctgtggagaac	atccgcagaa	gtttgggggt	tttaattact	120
ctccatttag	gacaccctac	acacccaaca	gccagtatca	aatgctgctc	gatcccacca	180
accccagcgc	cggcactgcc	aagatagaca	agcaggagaa	ggtcaagctc	aacttttgaca	240
tgacggcatc	ccccaaagatc	ctgatgagca	agcctgtgct	gagtgggggc	acaggccgcc	300
ggatttcctt	gtcggatatg	ccgcgctccc	ccatgagcac	aaactcttct	gtgcacacgg	360
gctccgacgt	ggagcaggat	gctgagaaga	aggccacgtc	gagccacttc	agtgcgagcg	420
aggagtccat	ggacttccag	ggataagagc	acagcttcac	cagccatcca	ccaagacggg	480
acaagcaggg	agtttatccg	gcagcccaaa	gcccttctct	cctcaactgt	cagctcctat	540
cacgacgaaa	acggacaaaa	cctccaccac	cggcagcatc	ctgaaatcta	acctggatcg	600
aagcaaagct	gagatggatt	tgaaggagct	gagcgagtgc	gtccagcaac	agtcaccccc	660
tgttcctctc	atctctccca	agcgccagat	tcgtagcagg	ttccagctga	atcttgacaa	720
gaccatagat	agttgcaaag	cacaattagg	cataaatgaa	atctcggaag	atgtctatac	780
ggccgtagag	cacagcgatt	cggaggattc	tgagaagtca	gatagtagcg	atagttagta	840
tatcagtgat	gatgagcaga	agtctaagaa	cgagccagaa	gacacagagg	acaaagaagg	900
ttgtcagatg	gacaaagagc	catctgctgt	taaaaaaaag	ccaagccta	caaaccctagt	960
ggagattaaa	gaggagctga	aaagcacgtc	accagccagc	gagaaggcag	accctggagc	1020
agtcaaggac	aaggccagcc	ctgagcctga	gaaggacttt	tccgaaaagg	caaaaccttc	1080
acctcacccc	ataaaggata	aactgaaggg	aaaagatgag	acggattccc	caacagtcct	1140
tttgggcctg	gactctgatt	cagagagcga	acttgtcata	gatttaggag	aagaccattc	1200
tggggggggag	ggtcgaaaaa	ataagaagga	acccaaagaa	ccatctccca	aacaggatgt	1260
-tgtaggtaaa	actccaccat	ccacgacggt	gggcagccat	tctcccccg	aaacacgggt	1320
gctcacccgc	tcttccgcgc	aaacttccgc	ggctggcgcc	acagccacca	ccagcacgtc	1380
ctccacggtc	acogtcacgg	ccccggcccc	cgccgccaca	ggaagcccag	tgaaaaagca	1440
gagggcgctt	ttaccgaagg	aggactgccc	cggccgtgca	gcgggtccgt	gtggaactca	1500
tcaagtaaa	tttcaaactg	cct				1523

(2) INFORMATION ON SEQ ID NO. 133:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2241 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

cgccgcccac gcgccagaag ccgagctggg aaaagggagg cagaggaggc ggaggcagag 60
gcagaggcag agcccgggtgc cgagaccaag cgacagaccg gcggggctgg gcctcgcaaa 120
gccggctcgg cgagctctcc cgacaccgga gccggggagg aaaagcagcg actcctcgct 180
cgcatccccg ggagccgcac tccagactgg ccgggtagtc aggggctcag gagcagatcc 240
cgaggcaggc tttgctcagc ctccgacgag ggctggccct ttggaaggcg ctttcaacag 300
ccggaccaga caggccacca tgaccgagaa ttccacgtcc gccctgcgg ccaagcccaa 360
gcgggccaag gcctccaaga agtccacaga ccaccccaag tattcagaca tgatcgtggc 420
tgccatccag gccgagaaga accgcgctgg ctccctcgcg cagtccattc agaagtatat 480
caagagccac tacaaggtgg gtgagaacgc tgactcgag atcaagttgt ccatcaagcg 540
cctggtcacc accggtgtcc tcaagcagac caaaggggtg ggggcctcgg ggtccttccg 600
gctagccaag agcgacgaac ccaagaagtc agtggccttc aagaagacca agaaggaaat 660
caagaaggta gccacgccaa agaaggcatc caagcccaag aaggctgcct ccaaagcccc 720
aaccaagaaa cccaaagcca ccccggtcaa gaagggccaag aagaagctgg ctgccacgcc 780
caagaaagcc aaaaaaccca agactgtcaa agccaagccg gtcaaggcat ccaagcccaa 840
aaaggccaaa ccagtgaaac ccaaagcaaa gtccagtgcc aagagggccg gcaagaagaa 900
gtgacaatga agtcttttct tgcggacact ccctcctgtc tctattttt tgtaaataat 960
tttctccttt tttctctctt gatgtcacc accacctttt gcccccttct gttctgactt 1020
tataagagac aggtatttggg ttcttcagaa attacagaat aattcatttt tcttaacca 1080
gttgtgcaag gacagcaaca accaatctaa tgatgagaat gtacttatat tttgttttgc 1140
tattaacctt cttacggggt tagggatttg cgggggggct tgtgtgtttt gttggcttgt 1200
ttgccatgaa ggtagatgtg ggtggggaga agacacaagg cagtttgttc tggctagatg 1260
agaggggaacc caggaattgt gaggttagca ggaatatctt tagggtgagt gagtttccct 1320
tgagttgggc acccgttggt agagttagca aacctttggc cagcaggaga gaggtggtag 1380
ggagcagcca gccggcaaa gaaggaggtg gaaaaaaacc gccaccgggc tgacttccac 1440
ctcccagtg tgagcagtg gggcccaaac ccagtttct tctcattttt gttagtttgc 1500
cctttcggcc tccctatttt cttaggaag gggagtggg tccaagtgc agctggatgg 1560
gagaagccat agtttctccc agtcagctag gatgtagcca ttgggggatc tttgtggctt 1620
cagcaaatct tcttggttaa ccggagtga aacttcagg gaaggggtgg gagtcagcca 1680
agtgcctcag tgtgcctgt tgaaacttag gtttttccac gcaatcgatg gattgtgtcc 1740
taggaagact tttcttttcc tctggatttt tgttccctct gtacaagagg tgtctttgct 1800
tggtttggtg gggctgcggc cacttaaaac ctccgatct ctttttgagt cttttattat 1860
aagtagttgt agctgcggga gggggagggg gagtgggagg gcagtggata gtaagactta 1920
ctgcagtcga tttgggattt gctaagtagt ttacagagc tagatctgtg tgcatgtgtg 1980
tgtttgtgta tatatacata tctagggcta gtacttagtt tcacaccgg gagctgggag 2040
aaaaaacctg tacagttgtc tttctcttat ttttaataaa atagaaaaat cgcgcacttg 2100
cgcgctcccc cccaccccc ttttttaaa aagtgttact tgtgccggga aaattttgct 2160
gtctttgtaa ttttaaaact ttaaaataaa ttggaaaagg gagaaactga aaaaaaaaaa 2220
aaaaaaaaaa a

```

004227 "36E" 950

## (2) INFORMATION ON SEQ ID NO. 134:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 631 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

tgacaatggc ttctttaaaa tactcagagg acaggatcac ggtggaatcg aatcagaagt 60
ggtggctgga attccacgca ccgatcagta ctgggaaaag atctaactcg ccgtgggcct120
gtcgtgccag tcttgggggc gagatggggg tagaaatgca tgtgatgogt taagtccacg180
taagatacaa gtttcagaca gggtcgggaag gactggattg gccaaacatc agactctgtct240
tccaaggaga ccaagtcctg gctacatccc agcctgtggt tacagtgcag acaggccatg300
tgagccaccg ctgccagcac agagcgtcct tccccctcog tgatccatcc atctccaggg360
agcaagacag agacgcagga atggaaagcg gagttcctaa caggatgaaa gttcccccat420
cagttcccc agtacctcca agcaagtagc tttccacatt tgtcacagaa atcagaggag480
agatggtgtt gggagccctt tggagaacgc cagtctccca ggccccctgc atctatcgag540
tttgcaatgt caaacctctc tgatcttggt tcagatgatt cttaatagga gtttattttt600
cgggcagctg cgaatcaggg gggttaaccag g

```

## (2) INFORMATION ON SEQ ID NO. 135:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 980 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

09673395.12700



## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ggggccggga gggacttag ggccggggct ggcccaggct acggcggctg cagggtctcg 60  
gcaaccgctc cggcaacgcc aaccgctccg ctgcgcgcag gctgggctgc aggctctcgg120  
ctgcagcgtc ggggtggatct aggatccggc ttccaacatg tggcagctct gggcctccct180  
ctgctgcctg ctgggtgttg ccaatgcccg gagcaggccc tctttccatc cctgtcggga240  
tgagctggtc aactatgtca acaaacggaa taccacgtgg caggccgggc acaacttcta300  
caacgtggac atgagctact tgaagaggct atgtggtacc ttcctgggtg ggcccaagcc360

accccagaga gttatgttta ccgaggacct gaagctgcc gcaagcttcg atgcacggga420  
acaatggcca cagtgtccca ccatcaaaga gatcagagac cagggtcctc gtggctcctg480  
ctgggccttc ggggctgttg aagccatctc tgaccggatc tgcattccca ccaatgcgca540  
cgtcagcgtg gaggtgtcgg cggaggacct gctcacctgc tgtggcagca tgtgtgggga600  
cggctgtaat ggtggctatc ctgctgaagc ttggaacttc tggacaagaa aaggcctggt660  
ttctggtggc ctctatgaat cccatgtagg gtgcagaccg taotccatcc ctccctgtga720  
gcaccacgtc aacggctccc ggccccatg cacgggggag ggagataccc ccaagtgtag780  
caagatctgt gagcctgggt acagcccgac ctacaaacag gacaagcact acggatacaa840  
ttctacagcg tctccaatag cgagaaggac atcatggccg agatctacaa aaacggcccc900  
gtggagggag gttctctgtg tattcggact tctgcctaga gtcagggggt acaaaagtcc960  
cggaatttg gggggccgcc 980

## (2) INFORMATION ON SEQ ID NO. 136:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2238 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227 3662960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

cacatgttctg gggaccgagt ggggtcaatc ttctgtgtgt gctctctccag gtctctttcca 60  
ggccgggtcat agacgtactc cctctgaggc cgaccgatgg ttagaagagg tgtctaagag 120  
cgtccgggct cagcagcccc aggcctcagc tgctcctctg cagccagttc tccagcctcc 180  
tccaccact gccatctccc agccagcatc acctttccaa gggaatgcat tctcacctc 240  
tcagcctgtg ccagtgggtg tggccccagc cctgcaacca gcctttgtcc ctgccagtc 300  
ctatcctgtg gccaatggaa tgccctatcc agccccta atgtgcctgtgg tgggcatcac 360  
tccctcccag atggtggcca acgtatttgg cactgcaggc caccctcagg ctgcccatcc 420  
ccatcagtca cccagcctgg tcaggcagca gacattccct cactacgagg caagcagtgc 480  
taccaccagt ccttctctta agcctcctgc tcagcacctc aacggttctg cagctttcaa 540  
tgggtgtagat gatggcagg tggcctcagc agacaggcat acagagggtc ctacaggcac 600  
ctgccagtg gatccttttg aagcccagtg ggctgcatta gaaaataagt ccaagcagcg 660  
tactaatccc tccctacca accctttctc cagtgcctta cagaagacgt ttgaaattga 720  
actttaagca atcattatgg ctatgtatct tgtccatacc agacaggagg cagggggtag 780  
cgggtcaaagg agcaaaacag actttgtctc ctgattagta ctcttttcac taatcccaaa 840  
gggtcccaagg aacaagtcca ggcccagagt actgtgaggg gtgattttga aagacatggg 900  
aaaaagcatt cctagagaaa agctgccttg caattaggct aaagaagtca aggaaatgtt 960  
gctttctgta ctccctcttc ccttaccctc ttacaaatct ctggcaacag agaggcaaag 1020  
tatctgaaca agaattctata ttccaagcac atttactgaa atgtaaaaca caacaggaag 1080  
caaagcaatc tccctttgtt ttccaggcca ttcacctgcc tctgtcagt agtggcctgt 1140  
attagagatc aagaagagtg gtttgtgtc aggctgggga acagagaggc acgctatgct 1200  
  
gccagaattc ccaggagggc atatcagcaa ctgccagca gagctatatt ttgggggaga 1260  
agttgagctt ccattttgag taacagaata aatattatat atatcaaaag ccaaaatctt 1320  
tatttttatg catttagaat attttaaata gttctcagat attaagaagt tgtatgagtt 1380  
gtaagtaatc ttgccaaagg taaaggggct agttgtaaga aattgtacat aagattgatt 1440  
tatcattgat gctactgaa ataaaaagag gaaaggctgg aagctgcaga caggatccct 1500  
agcttgtttt ctgtcagtc ttcattgtaa gtagcacatt gcaacaacaa tcatgcttat 1560  
gaccaatata gtcactaggt tgtagttttt tttaaataaa ggaaaagcag tattgtcctg 1620  
gttttaaaacc tatgatggaa ttctaattgtc attattttta tggaatcaat cgaaatatgc 1680  
tctatagaga atatatcttt tatatatattg tgcagtttcc ttatgttaat cctttaacac 1740  
taaggtaaca tgacataatc ataccataga agggaacaca ggttaccata ttggtttgtat 1800  
atatgggtct tgggtgggtt tgttttatcc tttaaatttt gttcccatga gttttgtggg 1860  
gatggggatt ctgggttttat tagctttgtg tgtgtcctct tccccaaac ccccttttgg 1920  
tgagaacatc ccttgacag ttgcagcctc ttgacctcgg ataacaataa gagagctcat 1980  
ctcattttta cttttgaacg ttggccttac aatcaaattg aagttatata tatttgtact 2040  
gatgaaaatt tataatctgc tttaacaaaa ataaatgttc atggtagaaa aatttgccca 2100  
tgaagggtctg ttctttcccc ttctctttat tagtaaatga atttattttt cgttcttttg 2160  
gtcttactct ccattctact gctgctgtaa atccctagtt tagtgactag aaaaataccc 2220  
ttaagattca tattttca 2238

## (2) INFORMATION ON SEQ ID NO. 137:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 398 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```
tgcagattgg ttggggcagc cgggggaggc tggctccgac acacgactga gtgtgcctac 60
actggtccca caggttttca gctgtggagt ttgggatctg agcttggagc ccatttggtt120
ctggcagttc cgctcatatt ttccacttga agacatcgcc tccgttcctt ccaagctggg180
agaccagaag tcaacaacag gaggttggag aggccgggtc tcacaatccg cttggctggg240
gagtccactg aggttcttgc atcctgaagc aaaccatgga gagctggtgg ggacttccct300
gttttgcggt cctgtgtttt ctaatgcacg cccgaggtca aagagacttt gattttggca360
gatgccttg atgacctga aaccaccaa gaagccaa 398
```

## (2) INFORMATION ON SEQ ID NO. 138:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1084 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

ggcgggtggcg gaagtgggag cgggcctgga gtcttggcca taaagcctga ggcggcggca 60
cggcgaggatt ggcggccttg agagctcggg agagtccctt ggaaccagaa cttggacctt 120
ctcgcttctg tctccggtt agtctcctcc tcggcgggag cctcgcgacg gcccgggccg 180
gagccccag cgcaggcccc cgtttgaagg atgacctcta ggaagaaagt gttgctgaag 240
gttatcatcc tgggagattc tggagtcggg aagacatcac tcatgaacca gtatgtgaat 300
aagaaattca gcaatcagta caaagccaca ataggagctg actttctgac caaggagggtg 360
atgggtggatg acaggctagt cacaatgcag atatgggaca cagcaggaca ggaacggttc 420
cagtcctctcg gtgtggcctt ctacagaggt gcagactgct gcgttctggt atttgatgtg 480
actgccccca acacattcaa aaccctagat agctggagag atgagtttct catccaggcc 540
agtccccgag atcctgaaaa ctccccattt gttgtgttg gaaacaagat tgacctcgaa 600
aacagacaag tggccacaaa gcgggcacag gcctggtgct acagcaaaaa caacattccc 660
tactttgaga ccagtgccta ggaggccatc aacgtggagc aggcgttcca gacgattgca 720
cggaatgcac ttaagcagga aacggagggt gagctgtaca acgaatttcc tgaacctatc 780
aaactggaca agaatgaccg ggccaaggcc tcggcagaaa gctgcagttg ctgagggggc 840
agtgagagtt gagcacagag tccttcacaa accaagaaca cacgtaggcc ttcaacacaa 900
ttccccctct ctcttcacaa caaacatac attgatctct cacatccagc tgccaaaaga 960
aaacccccatc aaacacagtt acaccccaca tattctctca cacacacaca cacacggcac 1020
acacacacac acaggttttg acgttattca gattgcggcc tttgccgtgt tgggttcgtg 1080
gggg
  
```

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1259 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

0042155496

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

taaaatacag aagaagagtc cacacactgt ttcacgagaa ggagtgtatc atgatttgta 60
gtaatcgaag aacatgttta tgggaacagg gtgactcagc tctcctgggg aggatggatg 120
aggagttagc aggaagagag ggtaccaagt gaggggaaag cagcaggggt ggtctggggc 180
atggacagga agcagaggct gggaaaagct acatctttta ttcagtcttt ttcacaggag 240
ctgaagtggg aatcagtaca tcgagaatcc acggccgggg accagtagga cttgagggac 300
tgcttactac taagtggctg ctgcgaggga aggaccacgt ggtctcagat ttctcagagc 360
atggaagtgt aaaatatctt catgagaacc tccctattcc tcagagaaac accaactgaa 420
aagagccagg aaaaccggg aattttccaa aaggtcttca cgttaaaact gtcttatctc 480
aggagagagc ccgctcttgt ctcccagttc ctggtagggt ctgcctgttg gaaagtgtac 540
ctggatgctt ctgggctccg tttggcaata gcaatcttgg ctgatgtgca cagtctggct 600
cccagctcac cctttttttt taaaagtaag aaaatagttg ctaccgatag ggacttgcg 660
aagtccaatt atcttctagg attgaaaggt gcattttccc cataaaaaag gcgaggaa 720
cccatggctg ctttgtgtca cctcagtgc ttacagtccc ccttggcatt tagttggtag 780
tagagccagt catccttaac aaatcttttc acattttatt tctttcacat gtagtcatct 840
tcaaaaagga aagatttgga attttagaaa aggggcaact cttcttttta gcatttctcat 900
cagaaagtca caaaaatcga tggaatcatt tccactggga agattgacct tttgtattta 960
tttgtggggt aaattaataa gcattccaga tgcttcagc ttcctgcac caggagatgc 1020
tgtgttcccc gtgatgcagc tggaacccaa gctgcagcag gagatgcaag tttcaggatg 1080
ttccccactg agctggagga atatctacag cagtgatgct tgaaattttt gtatgaattt 1140
tttgtcgtc ctaccctttt cctccaaaac aaaaattaga ggattatttt aatactttgg 1200
attcttcccc cttttttgag aaataaagtt ttttatgaaa agccaaaaaa aaaaaaaaaa 1259

```

## (2) INFORMATION ON SEQ ID NO. 140:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1938 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

ccaagatggc ggcacgatgc ctgcccggct gttgggggtgg cggtgacgac aggcagcaaa 60
agaccagctg gtcccagatt cgctgctgga gtgctggatg gagcccttct ctgccctctg 120
tgacatttcc aatttttagat aatgcctcac atctctgtcc ccccgggacc cctggagcc 180
cccatgatcc ctaagaagac agcttgaacc tagatctcac cccaggatg ttgoggaggc 240
tgctggagcg gccttgacag ctggccctgc ttgtgggctc ccagctggct gtcgatgtgt 300
acctgtcact ggggggcttc cgaagtctca gtgccctatt tggccgagat cagggaccga 360
catttgacta ttctcaccct cgtgatgtct acagtaacct cagtcacctg cctggggccc 420
caggggggtcc tccagctcct caaggtctgc cctactgtcc agaacgatct cctctcttag 480
tgggtcctgt gtcggtgtcc tttagcccag tgccatcact ggcagagatt gtggagcgga 540
atccccgggt agaaccaggg ggccggtacc gccctgcagg ttgtgagccc cgtccccgaa 600
cagccatcat tgtgcctcat cgtgcccggg agcaccacct gcgcctgctg ctctaccacc 660
tgcacccctt cttgcagcgc cagcagcttg cttatggcat ctatgtcatc caccaggctg 720
gaaatggaac atttaacagg gcaaaactgt tgaacgttgg ggtgcgagag gccctgcgtg 780
atgaagagtg ggactgcctg ttcttgacag atgtggacct cttgccagaa aatgaccaca 840
atctgtatgt gtgtgacccc cggggacccc gccatgttgc cgttgctatg aacaagtttg 900
gatacagcct cccgtacccc cagtacttcg gaggagtctc agcacttact cctgaccagt 960
acctgaagat gaatggcttc cccaatgaat actggggctg ggggtggtgag gatgacgaca 1020
ttgctaccag ggtgcgcctg gctgggatga agatctctcg gccccccaca tctgtaggac 1080
actataagat ggtgaagcac cgaggagata agggcaatga ggaaaatccc cacagatttg 1140
acctcctggt ccgtacccag aattcctgga cgcaagatgg gatgaactca ctgacatacc 1200
agttgctggc tcgagagctg gggcctcttt ataccaacat cacagcagac attgggactg 1260
accctcgggg tctcgggct ccttctgggc cacgttaccc acctggttcc tcccagcct 1320
tccgtcaaga gatgctgcaa cgccggcccc cagccaggcc tgggcctcta tctactgcca 1380
accacacagc cctccgaggt tcacactgac tctccttcc tgtctacott aatcatgaaa 1440
ccgaattcat ggggttgat tctcccacc ctgagctcct cactgttctc agagggatgt 1500
gagggaaactg aactctggtg ccgtgctagg gggtaggggc ctctccctca ctgctggact 1560
ggagctgggc tctgtagac ctgaggggtc cctctctcta gggctctctg tagggcttat 1620
gactgtgaat ccttgatgtc atgattttat gtgacgatc ctaggagtc ctgcccctag 1680
agtaggagca gggctggacc ccaagcccct ccctcttcca tggagagaag agtgatctgg 1740
cttctcctcg gacctctgtg aatattttatt ctattttatg ttcccgggaa gttgtttgg 1800
gaaggaagcc cctccctggg cattttctgc ctatgctgga atagctccct cttctgggtc 1860
tggctcaggg ggctgggatt ttgatatttt ttctaataaa ggactttgtc tcgcaaaaaa 1920
aaaaaaaaa aaaaaaaa

```

## (2) INFORMATION ON SEQ ID NO. 141:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1874 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

caaaaaaacc tcttaatat ctggagtcatt cttcccttc gacagcattt tcctctgctt 60
tgaagcccc agaatcagt gttggccatg atgacaacta cagaaaaacc agaggcagct 120
tctttgcaa gacctttcaa agccatttta ggctgttagg ggcagtgagg gtagaatgac 180
tccttgggta ttagagtttc aaccatgaag tctctaaca tgatattttc tcacctctgc 240
tactcaagta gcattttactg tgtctttggg ttgtgctagg cccccgggtg tgaagcacag 300
accccttcca ggggtttaca gtctatttga gactcctcag ttcttgccac tttttttttt 360
aatctccacc agtcattttt cagacctttt aactcctcaa ttccaacact gatttcccct 420
tttgcatctt cctccttcc cttccttgta gccttttgac ttccattgga aattaggatg 480
taaactctgt caggagacct ggaggagcag aggataatta gcctctcagg ttaagtgtga 540
gtaactctgag aaacaatgac taattcttgc atattttgta acttccatgt gaggttttc 600
agcattgata tttgtgcatt ttctaaacag agatgagggtg gtatcttcac gtagaacatt 660
ggtattcgct tgagaaaaaa agaatagttg aacctatttc tctttcttta caagatgggt 720
ccaggattcc tcttttctct gccataaatg attaatataa tagcttttgt gtcttacatt 780
ggtagccagc cagccaaggc tctgtttatg cttttggggg gcataatatt ggttccattc 840
tcacctatcc acacaacata tccgtatata tccctctac tcttacttcc cccaaattta 900
aagaagtatg ggaaatgaga ggcatttccc ccacccctt tctctctca cacacagact 960
catattactg gtaggaactt gagaacttta ttccaagtt gttcaaacat ttaccaatca 1020
tattaatata atgatgctat ttgcaattcc tgctcctagg ggaggggaga taagaaaccc 1080
tcactctcta caggttttggg tacaagtggc aacctgcttc catggccgtg tagaagcatg 1140
gtgccctggc ttctctgagg aagctggggg tcatgacaat ggcagatgta aagtattctt 1200
tgaagtcaga ttgaggctgg gagacagccg tagtagatgt tctactttgt tctgctgttc 1260
tctagaaaga atatttggtt ttctgtata ggaatgagat taattccttt ccagggtatt 1320
tataattctg ggaagcaaaa ccatgcctc cccctagcca tttttactgt tatcctattt 1380
agatggccat gaagaggatg ctgtgaaatt cccaacaaac attgatgctg acagtcatgc 1440
agtctgggag tggggaagtg atcttttggt cccatcctct tcttttagca gtaaaatagc 1500
tgagggaaaa gggagggaag aggaagtat gggaatacct gtggtggttg tgatccctag 1560
gtcttgggag ctcttggagg tgtctgtatc agtggatttc ccatccctg tgggaaatta 1620
gtaggctcat ttactgtttt aggtctagcc tatgtggatt ttttcctaac atacctaagc 1680
aaacccagtg tcaggatggg aattcttatt ctttcgttca gttaagtttt tcccttcatt 1740
tgggcactga agggatatgt gaaacaatgt taacattttt ggtagtcttc aaccagggat 1800
tgtttctgtt taacttctta taggaaagct tgagtaaaat aaatattgtc tttttgtatg 1860
tcaaaaaaaa aaat

```

1874

002227 0602960

## (2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 198 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

RDIWTMNLQR YWGEIPISSS QTNRSSFDLL PREFRLVEVH DPPLHQPSAN KPKPPTMLDI 60  
 PSEPCSLTIH TIQLIQHNRR LRNLIATAQA QNQQQTEGVK TEESEPLPSC PGSPPLPDDL120  
 LPLDCKNPNA PFQIRHSDPE SDFYRGKGEP VTELSWHSCR QLLYQSGTN PGQRRAFDCA180  
 NESVLEDPNL MLAHEYWP 198

## (2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

IVWMVRLHGS EGMSSIVGGF GLLAEGWCRG GSWTSTRNS RGSKSKELLL VWLDDIGISP60  
 QYLCRFIVHM SLQVQQTFIK CQAFCVGQRL IM 92

## (2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

DPCPERSTKN RHGAQGMFKS LQGFPFRSA GAGANHRVLR SPDVQGSRTK GRSGPEPRQG60  
GTTLFTAASQ SGLGGCLDLE RPEARIASDP ESWFVD 96

(2) INFORMATION ON SEQ ID NO. 145:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 52 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

EGRVQQGSFV NVQQGPQEPF IEFHQLTQA IKSTHGTSTI PRVSRITLKD KP

52

(2) INFORMATION ON SEQ ID NO. 146:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 47 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

PSRTSHSGTL PIPRLKICFK KRGNMNKDPT TLLAQVLFTL NFLNLDN

47

004221 3662960

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 66 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

LSKFKKLRVN NTCASSVVGS LFIFPLFLKH IFKRGMGNVPL LWLVLEGYTR YPWNGRCSMC60  
ALNCLG 66

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 187 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

```

REGEGRPEGN  GDIRGGLRSG  CDLSLLAPLL  PSSSESWEK  CYPWKIKLGL  QELSVWEESM 60
AQHSACVPFC  SGSLSPPFSQ  PQRLSPSPSS  SPEDSSDGRA  GPPEPTGSSG  CTGSWCSLSP120
VHFHSHGMEC  PCILCCRSPH  LHLRGLGSPS  SPQCPQSLSQ  TVGWNMRLEA  ERGSEHHSPC180
TWVASC

```

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 147 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

REDWNRGKGE VAPCFVQPGS WQPWCWGLDP TTPAHLAEHL VPIEDCLPLL LHLQLPPLL 60  
TFHTLQDCVC SGSPGECSSC CHRASILILL LIVQLLSVCI RLSDQRVHQH QEGHVEQQGT120  
HHGOVDDNDD LDGGGLRSSY LHSRSRQ 147

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 142 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

FFFFFWREIK QFNDGFLDLH TTLRQEDKIF SPCTGTTKFR DKRQPKYRGC GVQIHAQPRV 60
SCSNRPSGSV TVDTGERRDC PDPSSAGEGT GSRVCMGTPC PSARSAQGTA NTSFQCTLKT120
QWAQGAQLSH QSCPQGSWSG WG                                     142

```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 464 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
RQQTVLGSCS SSILPCQLLK HQGSSKTEMT KNWLIQTKRR YFSSPKQMSM THWPRTAWLT 60
GCSVTLFLEFP SQYVDVASLG LVPQLTGGTL YKYNFQMHM DRQQFLNDLR NDIEKKIGFD120
AIMRVRTSTG FRATDFFGGI LMNNTTDVEM AAIDCDKAVT VEFKHDDKLS EDGALIQCA180
VLYTTISGQR RLRIHNGLN CSSQLADLYK SCETDALINF FAKSAFKAVL HQPLKVIREI240
LVNQTAHMLA CYRKNCASPS AASQLILPDS MKVLPVYMNC LLKNCVLLSR PEISTDERAY300
QRQLVMTMGV ADSQLFFYPQ LLPIHTLDVK STMLPAAVRC SESRLSEEGI FLLANGLHMF360
LWLGVSSPPE LIQGIFNVPS FAHINTDRTL LPEVGNPYSQ QLRMIMGIIQ QKRPYSMKLT420
IVKQREQPEM VFRQFLVEDK GLYGGSSYVD FLCCVHKEIC QLLN 464
```

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 172 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
TMLEKIPKEE QEETSAIRVG FITYNKVLHF FNVKSNLAQP QMMGVTDVGE VFPVLLDGFL 60
VNYQESQSVI HNLLDQIPDM FADSNENETV FAPVIQAGME ALKAADCPGK LFIFHSSLPT120
AEAPGKLNK DDKKLVNTDK EKILFQPQTN VYDSLAKDCV AHRLLCDTLP LS 172
```

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 141 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GSTVFTEFVI VLELHGHC LV TIDGSHFYIG GVVHQDSTKE ISGSETCAGT NPHNSIKAYF 60  
-LFNIISEVVQ KLLSIQVHLE IVVFVKGSSS ELRNQPQRGH VHILTRKEEE CHRAAGEPRS120  
PWPMShRLHF GAGKVSSLCL Y 141

(2) INFORMATION ON SEQ ID NO. 154:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 504 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

LDRCGLYPVS SLLQVEGSLW RAAGVFQPPP GLAHANDWRF TARVHGGALG EHKMVAAT 60  
GSEILLWALQ AEGGGSEIGV FHLGVPVEAL FVGNQLIAT SHTGRIGVWN AVTKHWQVQE120  
VQPITSYDAA GSFLLGCGNN GSIYYVDVQK FPLRMKDNDL LVSELYRDP A EDGVTALSVY180  
LTPKTSDSGN WIEIAYGTSS GGV RVIVQHP ETVGSGPQLF QTFTVHRSPV TKIMLSEKHL240  
ISVCADNNHV RTWSVTRFRG MISTQPGSTP LASFKILALE SADGHGGCSA GNDIGPYGER300  
DDQQVFIQKV VPSASQLFVR LSSTGQRVCS VRSVDGSPTT AFTVLECEGS RRLGSRPRRY360  
  
LLTGQANGSL AMWDLTTAMD GLGQAPAGGL TEQELMEQLE HCELAPPAPS APSWGCLPSP420  
SPRISLTSLH SASSNTSLSG HRGSPSPPPQA EARRRGGSF VERCQELVRS GPDLRPPPTP480  
APWPSSGLGT PLTPPKMKLN ETSE 504

(2) INFORMATION ON SEQ ID NO. 155:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 289 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

002227 5624960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

(2) INFORMATION ON SEQ ID NO. 156:

(vi) ORIGIN  
(A) ORGANISM: HUMAN

```

VPQDQGI PRH HGSCVVQKEV SLSFILGGVR GVPRPLEGHG AGVGGRRRSG PLRTSSWQRS 60
TKLPPRRRRR SACGGGLGLPR WPDKEVLLEA EWRLVREMRG EGLGRQPHEG AEGAGGASSQ120
CSSCSISSCS VRPPAGAWPR PSMVVVRSHM AKLPLAWPVS R 161

```

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

QLWGFAAGSD SRPAMGCDGG TIPKRHELVK GPKKVEKVOK DAELVAQWNY CTLSQEILRR 60  
 PIVACELGRL YNKDAVIEFL LDKSAEKALG KAASHIKSIK NVTELKLSN PAWEGDKGNT120  
 KGDKHDDLQR ARFICPVVGL EMNGRHRFCF LRCCGCVFSE RALKEIKAEV CHTCGAAFQE180  
 DDVIVLNGTK EDVDVLKTRM EERRLRANWK RKQRNPRQQS LFQNMVSVKK PQGHQKLRQG240  
 SLKKPALILE RRPPTWLPKA QQ 262

(2) INFORMATION ON SEQ ID NO. 158:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 138 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

CHRAQWHQGG CGRAEDKDDG EKAESELEKK TKKPAAESV SKPDVSEEAP GPSKVKTGKP 60  
 EEASLDSREK KTNLAPKSTA MNESSSGKAG KPCCGATKRS IADSESEAY KSLFTTHSSA120  
 KRSKEESAHW VTHTSYCF 138

(2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 168 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

HLVLKQTLLEP WVSLSFSPIR SQPSLLHPCL QHVHILLGAI EHDDIILLEG SPTRVANFRF 60  
 YLFQGSRLRKH TAAAPKEAEP VSAVHLQAHN GADETRPLEV IVLVTFVSF IPFPGRIRK120  
 LQLCHILNAF NVRCCLPKSL FCRFVQEKFN DGIFVIKSAK FTGNYWSS 168

(2) INFORMATION ON SEQ ID NO. 160:

004221 562960

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 238 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

HQWHITAMGS QHSAAARPSS CRRKQEDDRD GLLAEREQEE AIAQFPYVEF TGRDSITCLT 60  
 CQGTGYIPTE QVNELVALIP HSDQRLRPQR TKQYVLLSIL LCLLASGLVW FFLFPHSVLV120  
 DDDGIKVVKV TFNKQDSLVI LTIMATLKIR NSNFYTVAVT SLSSQIQYMN TVVNFTGKAE180  
 MGGPFSYVYF FCTVPEILVH NIVIFMRTSV KISYIGLMTQ SSLETHHYVD CGGNSTAI 238

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

SSHEDHYVVH QDLRYRAEEV HIGKRSSH LG LPGKIHHC VH VLNLAGQAGH CHRVEVGVPD60  
 FQGGHDGENY KGVLLIKCDF HHFDAVIIHK D 91

004227 9622960



## (2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

MRKQEEHQHT RCQETKQDGQ EDILLSSLRA QSLITVWDQS HQLIYLLCWN VACPLARETG 60  
DAISPGEFHI WELSNQFFLL SFSQQTVPVI FLLSPAGGGA SSSGMLRPHG RDMPLVSCPA120  
SSVGGAARTQ RAG 133

## (2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AAGAAGPHRR RHPLHPSLLR EHHSQAQAP E GVRPGQSTLS RIEAVQPQLP RPSGLPSLWG60  
WLPWLLGTRP QRHPEIPPET QCASTAVRRS A 91

## (2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004221 8822950

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

LDNPTQRNKD QLIRAAVKFL DTDTCYRVE EPETLVELQR NEWDPPIEWA EKRYGVEISS 60  
 STSIMGPSIP AKTREVLVSH LASYNTWALQ GIEFVAAQLK SMVLTGLID LRLTVEQAVL120  
 LSRLEEEYQI QKWGNIEWAH DYELQELRAR TAAGTLFIHL CSESTTVKHK LLKE 174

(2) INFORMATION ON SEQ ID NO. 165:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 66 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CLGLLHPVAD GVGVOQLHGC PDQLILVSLG WVVQSRVAQC GQVHGVLVDG ILLGIPLSTL60  
 CTCQGL 66

(2) INFORMATION ON SEQ ID NO. 166:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 132 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SWRETEIKEQ LTHELCTIIQ QNELRKAKKL EELMQQLDVE ADEETLELEV EVERLLHEQE 60  
 VESRRPVVRL ERPFQPAES VTLEFAKENR KCQEQAVSPK VDDQCGNSSS IPFLSPNCPN120  
 QEGNDISAAL AT 132

002221 35522950

## (2) INFORMATION ON SEQ ID NO. 167:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

QILMSHSPPQ AEMASLNEPL VSLILLVLRV AISRPPQAP KSLHRLHLV VASTPPTSWP60  
FGAHFAV 67

## (2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

NGLSKRTTGL LDSTSCSCSN LSTSTSSSKV SSSASTSSCC INSSNFLAFR SSFCCMIVQR60  
CSVSCSFISV SRHE 74

## (2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

004221 9922950

```
GRGGLGCRSW RCAGSSRPYS EVFSVALLER GSSCILRIFC ISAPFSSRCH RMPQIGPVPS60
VNOTSETASL OGQSPSTDEL ERDSEMORP                                     89
```

(2) INFORMATION ON SEQ ID NO. 170:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 74 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

GPLHFRIP LK LICTWTLTLK RGGFRSLIHR GDRTYLGHPM AARREGSRNA KYSQDAGGTP60  
LKERHGENFR VRAR 74

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

AVAFQNPSQA HLYLDSDEA RRFKSDSPR GQDLFGASDG SEKRREPCKC IFSRCRRNPS60  
QGAPRRKLQS TGAMIQHNR TCSPAHLSP 89

## (2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

PSPAVLGDQP PSASGAVHRK LSLEVCCCQE RAQMGPVMAA TSTSCGRARL LARSAQWLTT 60  
 MLSSAAVWLG SRRLTTCGEN PSYALVAFLC LSRESPSAKP 100

## (2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 495 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

SRTNTPVETW KGSKGKQSYT YIIIEENTTS FTWAFQRTTF HEASRKYTND VAKIYSINVT 60  
 NVMNGVASYC RPCALEASDV GSSCTSCPAG YYIDRDSGTC HSCPPNTILK AHQPYGVQAC120  
 VPCGPGTKNN KIHSLCYNDC TFSRNTPTRT FNYNFSALAN TVTLAGGPSF TSKGLKYFHH180  
 FTLSLCGNQG RKMSVCTDNV TDLRIPEGES GFSKSITAYV CQAVIIPPEV TGYKAGVSSQ240  
 PVSLADRLIG VTTDMTLDGI TSPAELFHLE SLGIPDVIFF YRSNDVTQSC SSGRSTTIRV300  
 RCSPQKTVPG SLLLPGTCSG GTCDGCNHFH LWESAAACPL CSVADYHAIV SSCVAGIQKT360  
 TYVWREPKLC SGGISLPEQR VTICKTIDFW LKVGISAGTC TAILLTVLTC YFWKKNQKLE420  
 YKYSKLVNNA TLKDCDLPAA DSCAIMEGED VEDDLIFTSK KSLFGKIKSF TSKRTPDGF480  
 SVPLKTSSGG PDMDL 495

## (2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:



SAVKRGWDLN MAAVVAATAL KGRGARNARV LRGILAGATA NKASHNRTRA LQSHSSPEGK 60  
EEPEPLSPPEL EYIPRKRGKN PMKAVGLAWA IGFP CGILLF ILTKREVDKD RVKQMKARQN120  
MRLSNTGEYE SQRFRASSQS APSPDVGSQV QT 152

(2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 114 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

EGRSAPQVCT PDPTSGDGAL WEEALNLWLS YSPVLDNRMF CRAFICFTRS LSTSRLVRMK 60  
RRIPQGKPKMA QASPTAFMGF LPLFLGMYSS SGDRGSGSSL PSSELWLCRA RVLL 114

(2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GLATAWASCA LWWTSEARTG IWAKPEDLTV NSLGGSQRSS GLHPRPNIRG RGTLLGGSPEP 60  
LALILARVGQ PHVLPSLHLL HTVLVHFPLG EDEEEDTTRE ADGPGQSHSF HGV LAPLSGN120  
VFOLRG 126

(2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes





TVKFLRRLKV RGTKAGEISL SPEEGEADGS QQPALFLRVI FKFANCITGG PTFCFYQEFF60  
FCSKTLVMGI F 71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

YLNLOIVLOE GLLSVFIKSF SFVQRHWLWE YFERVRNAGI KRCCRLILKV LTEPV 55

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

KQGRLLTSIC FSLLRKANKL PCFGSPHFQP SQEFHCS

37

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 37 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

SPLLWFPALS AFSGISLFII YFHDLSAKLL IFCRKKV

37

(2) INFORMATION ON SEQ ID NO. 188:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 100 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

MPDFKIARRK QTLRIKKAGH LLNPWLHHKA LGLGFLYLIE VFSVALGAVC LSPTPKDARK 60

TSTISHVATF TSMPhKCLSE SPNSAFPQNK PNAIQKKKK

100

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 256 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual

004321 3664960

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

RSQAGPEAGQ PLPGSGKRSS CCHCSSGACS MGPLPRTVEL FYDVLSPYSW LGFEILCRYQ 60  
 NIWNINLQLR PSLITGIMKD SGNKPPGLLP RKGLYMANDL KLLRHHLQIP IHFPKDFLSV120  
 MLEKGSLSAM RFLTAVNLEH PEMLEKASRE LWMRVWSRNE DITEPQSILA AA EKAGMSAE180  
 QAQGLLEKIA TPKVKNQLKE TTEAACRYGA FGLPITVAHV DGQTHMLFGS DRMELLAHLL240  
 GEKWMGPIPP AVNARL 256

(2) INFORMATION ON SEQ ID NO. 190:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 196 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

SLAFTAGGIG PIHFSPSRCA SSSIRSEPNN MWVWPSTWAT VMGSPKAPYL QAASVVSLSW 60  
 FFTFGVAIFS RSPWACSADI PAFSAAARML CGSVMSSFLD QTRIHSSRDA FSSISGCSEF120  
 TAVRKRMA DK LPFSSITDKK SLGKWMGIWR WCLRSEKSF A MYSPLRGSRP GGLFPLSFM180  
 PVMRLGRNCR LMFQIF 196

(2) INFORMATION ON SEQ ID NO. 191:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 116 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00221 55554950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

EQRASAMRSS RAFRTVCSSW ATHGQLPAGL DDKTNIKTVC TYWEDFHSCT VTALTDCEG 60  
 AKDMWDKLRK ESKNLNIQGS LFELCGSGNG AAGSLLPAFP VLLVSLSAAL ATWLSF 116

## (2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 182 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

KRESGFPTIL YECFQHHRES QRPQRTNGSS SRFPQAWSEC GWARGGSWPH AQKESQVAKA 60  
 AERDTRSTGN AGSRDPAAPL PLPQSSNKLP WMLRFLDSFL SLSHISFAPS WQSVRAVTVQ120  
 LWKSSQYVHT VLMFVLSSRP AGSWPCVAQL EQTVRKALED RIALARCSHG LHQIRYLHRE180  
 DQ 182

## (2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 105 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

HLANKTQEIK RNKKENQDFP QSYMSVFSIT ENHNVPKELM DLPLDFREHG VSVGGRAGGA 60  
 GPTLRRKARS LKLPRETPGA PGTPGAGTPP PRCRCRRVRI SCLGC 105

## (2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:



(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

LILIIHPHGN TTTFFKVMYQ VCHLLGSVTW CVGYLYFSRP RNNKISCSVL IPISMTTYDD60  
RFYPSHTKPG DIFADNGFSE DRATQNISYG AIW 93

(2) INFORMATION ON SEQ ID NO. 197:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 410 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TDQPNIQSVK IHSPLLRNPN KGCECPRRD GFGFIKCVDR DVRMFFHFSE ILDGNQLHIA 60  
DEVEFTVVPD MLSAQRNHAI RIKKLPGTV SFHSHSDHRE LGTVEKEATF SNPKTTSPNK120  
GKEKEAEDGI IAYDDCGVKL TIAFQAKDVE GSTSPQIGDK VEFSSISDKQR PGQQVATCVR180  
LLGRNSNSKR LLGYVATLKD NFGFIETANH DKEIFFHYSE FSGDVSLEL GDMVEYSLSK240  
GKGNKVSARK VNKTHSVNGI TEEADPTIYS GKVRPLRSV DPTQTEYQGM IEIVEEGDMK300  
GEVYPPGIVG MANKGDCLQK GESVKFQLCV LGQNAQTMAV NITPLRRATV ECVKDDQFGFI360  
NYEVGDSKKL FFHVKEVQDG IELQAGDEVE FSVIPKSSGG LAGSGACRCF 410

(2) INFORMATION ON SEQ ID NO. 198:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 126 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

LNAILNFFHM EKELLAISYF IVNEAKLIFH TFHCGPAQGC DVVSHSLCIL AQDTQLELDA 60  
LPFLQAIPFV GHPNDAKWID LTFHIALLN LNHSVLVSLC WINTPQGANY FARVNGGISF120  
LSNAIH 126

004221 0602960

## (2) INFORMATION ON SEQ ID NO. 199:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 85 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

KSHTSCNLLS RPLFVTNTKF NLISYLRRSR SFHILGLKSN SQFHPTVIIS NNAILSLLLF60  
AFIWASGFRI GKSGFFFYRA QKTVI 85

## (2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 79 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

ATMRLSVCLL MVSLALCCYQ AHALVCPAVA SEITVFLFLS DAAVNLQVAK LNPPPEALAA60  
KLEVKHCTDQ ISFKKRLLI 79

## (2) INFORMATION ON SEQ ID NO. 201:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 50 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004227" 56E2950



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

SVQCFTSNLA ARASGGGLSL ATWRFTAASL KNKKTWISEA TAGQTRAWAW

50

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 72 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

QVAVEKTLET QVEHFYMSHT HIFSLFPPT FSNEKPFLKR YLIGAVLHFQ LGCKSFWRWI60  
KFGNLEVYRS VT

72

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 53 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

SFSPSLTTRA MNSSASSTST CSSYTLGTRL PVGGRGPTKV TCCTSNRLTL SLD

53

004221 3622950

## (2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

ALVVRELTQR FIGDYERNAG NLYTRQVQIE GETLALQVQD TPGIQVHENS LSCSEQLNRC 60  
 IRWADAVVIV FSITDYKSYE LISQLHQHVQ QLHLGHPAAC GSWWANKSDL LHIKQVDPQL120  
 G 121

## (2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 205 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GPLPALAAGS TFPVLACSSA MAPKGSSKQQ SEEDLLLQDF SRNLSAKSSA LFFGNAFIVS 60  
 AIPIWLYWRI WHMDLIQSAV LYSVMTLVST YLVAFAKYNV KFVLKHKVAQ KREDAVSKEV120  
 TRKLSEADNR KMSRKEKDER ILWKKNEVAD YEATTFISIFY NNTLELVVVI VASFFILKNF180  
 NPTVNYILSI SASSGLIALL STGSK 205

## (2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

VLHQDSSPSC LLAPNRPCQL HPLALCLWVA CGIWKSSRVV RVGDTRCFYS LEPLKNPAEC 60  
NSVFVYWLF DRLLKLNELK GKLRVLGRLL KGKKCLAMCC NHKRRK 106

(2) INFORMATION ON SEQ ID NO. 207:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 105 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

STYGQYVVHC GVEVLQYEEG SNNDHDQEQS VVIEDGKCCS FIISNFILLP QDSFIFLLPR 60  
HLSIISFRKF SSHFFGNSIL PLLCYFVLEN KFHLVCKGY QICAY 105

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 549 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00221 566650

LYPNFLVNL	ILKQKQFEE	KRFKLDHVS	STNGHRWQIF	QDWLGTDDQN	LDLANVNLM	60
ELLVQKKKQL	EAESHAALQ	ILMEFLKVAR	RNKREQLEQI	QKELSVLEED	IKRVEEMSG	120
YSPVSEDSTV	PQFEAPSPSH	SSIIDSTEYS	QPPGFSGSSQ	TKKQPWYNST	LASRRKRLTA	180
HFEDLEQCYF	STRMSRISDD	SRTASQLDEF	QECLSKFTRY	NSVRPLATLS	YASDLYNGSS	240
IVSSIEFDRD	CDYFAIAGVT	KKIKVYEYDT	VIQDAVDIHY	PENEMTCNSK	ISCISWSSSYH	300
KNLLASSDYE	GTVILWDGFT	GQRSKVYQEH	EKRCWSVDFN	LMDPKLLASG	SDDAKVKLWS	360
TNLDNSVASI	EAKANVCCVK	FSPSSRYHLA	FGCADHCVHY	YDLRNTKQPI	MVFKGHRKAV	420
SYAKFVSGEE	IVSASTDSQL	KLWNVKGKPYC	LRSEFKGHINE	KNFVGLASNG	DYIACGSENN	480
SLYLYYKGLS	KTLLTFKFDT	TKSVLDKDRK	EDDTNEFVSA	VCWRALPDGE	SNVLIAANSQ	540
GTIKVLELV						549

## 549

(A) LENGTH: 90 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

GTVLSSSLTGE YKPLISSTLL ISSSKTLSSF WICSSCSLLF LLATLRNSIR ICSWAACDSA60  
 SSCFFECTSN SNIRLTLAKS RLSWSVPNQS 90

## 90

(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

FPSSLLFFFF FFFFCGSIN FYCFVIYFYS KEFVLSQKL DNTTKSSNVH GVTLMVESWL60  
GIPNVKVIK EGKEKKKKIF KTNPKPMMTL GRDIT 95

## (2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

KKMVRGLGFS CLLAIYSLW IVCIPYLLSI GLCVDILFLF VQHLLPHLLV TQPLFICGEP60  
 IPCGLGEHVT RGPLLSPTAS 80

## (2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

LKKGKWAKAI HNRKCKWPRN MKRCSSSLIF KEKKEILPTR LAKIFKDSGL ADYRQTGILT60  
 NDGVVNW 67

## (2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

03421" 36660

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

SPEVGQALGT AGSRASRKMT SELSSLSISA SIRVSPQTDS LHMAQIQAYM VLGSWDLHKA60  
FFPVVPAEVL LRAFLSLA 78

## (2) INFORMATION ON SEQ ID NO. 214:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

QAGKRALYKH TQTNTSGDGC VLLEQRLLKH SVCWLSVPLL ENNELGKEQL IRKCALLTVH 60  
ITTKSWQLLK EKGLCRCRSN LSVNSCQQPQ RLPPQHTLIT CVCLA 105

## (2) INFORMATION ON SEQ ID NO. 215:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 216 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes.

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LSLTSRMEEA ELVKGRLQAI TDKRKIQEEI SQKRLKIEED KLKHQHLKKK ALREKWLLDG 60  
ISSGKEQEEM KKQNQQDQHQ IQVLEQSILR LEKEIQDLEK AELQISTKEE AILKKLKSIE120  
RTTEDIIRSV KVEREERAE SIEDIYANIP DLPKSYIPSR LRKEINEEKE DDEQNRKALY180  
AMEIKVEKDL RTGESTVLSS IPLPSDDFKR SRSKSL 216

00673305-12700

## (2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

FCFFISSCSF PLLIPSRSHF SLKAFFFKCW CFSLSSSIFR RFCEISSCIF LLSVMAWSLP 60  
 FTSSASSILE VKDSQTGKQV QSYHKSRSLG GERSGGDRRE AGRNPLFAPV EK 112

## (2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 339 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

SSQLRRRLVP APAAPRPRPN HGVLGRRLRG DRWQWSHWAK WAMLFASGGF QVKLYDIEQQ 60  
 QIRNALENIR KEMKLEQAG SLKGSLSVEE QLSLISGCPN IQEAVEGAMH IQECVPEDLE120  
 LKKKIFAQLD SIIDRVILS SSTSCLMPSK LFAGLVHVQK CIVAHPVNPP YYIPLVELVP180  
 HPETAPTTVD RTHALMKKIG QCPMRVQKEV AGFVLNRLQY AIISEAWRLV EEGIVSPSDL240  
 DLVMSEGLGM RYAFIGPLET MHLNAEGMLS YCDRYSEGIK HVLQTFGPIP EFSRATAEKV300  
 NQDMCMKVPD DPEHLAARRQ WRDECLMRLA KLKSQVQPQ 339

## (2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

KDPQITQKGI TKIITKIFCP HINMKTTITG CQIILKCNQA EKEKVKISRL SAQVAGNRQP 60  
RERKCCCAAR PRAMIQSDGQ TTGLHHPTQA AHKTASLGSP WAATYVTEG 109

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 98 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

LNIPSALRCM VSRGPMNAYR MPNPSDMTRS RSLGDTIPSS TSRQASLMIA YCRRFRTKPA60  
TSFWTRMGHC PIFFIRAWVL STVVGAVSGW GTSSTSGM 98

(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 129 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TMFFTCGPNE AMVVS GFCSR PPVMVAGGRV FVLPCIQQIQ RISLNTLT LN VKSEK VYTRH 60  
GVPI SVTGIA QVKLSE PFPH SPLPHHPLSQ TLRHLLATVF STLACRE VPL LVSSFPGT PR120  
HLPPPPFFP 129

004221" 36662960





## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

GRRTLFLATF GGYPGSLGCS LSGEANISLV SFFHPLNCKL RITQAHHSYR LGLASQSTLC60  
 PACHCCKELL LCQPKQRKYG FSCIIFPGW FVF 93

## (2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 94 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

NLIYPNSSMY SDTFSEKARI IGAVLSIKGK SSDHLHYNFL CLFSAGEEIH IYSTPHWTLQ60  
 NACIFCPSAI CSLPFCLLKE LSNIVFPMF STGH 94

## (2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 92 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GHHMHILDRF CTAQLEWVPV TWTGVQYTIC VQYRKPSAV ARELYSNSLS AQANQVRKTA60  
 IWLEDFQETA VPVRGRYYLR GGRGTDIKQE GF 92

## (2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 458 amino acids  
 (B) TYPE: Protein

004227 342960

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

RGKRRRRHRLP	ALPPRLLSPS	AATMSASAVF	ILDVKGKPLI	SRNYKGDVAM	SKIEHFMPLL	60
VHGGEEGALA	PLLSHGQVHF	LWIKHSNLYL	VATTSKNANA	SLVYSFLYKT	IEVFCEYFKE	120
LEESIRDNF	VIVYELLDL	MDFGFPQTTD	SKILQEYITQ	QSNKLETGKS	RVPTVTNAV	180
SWRSEGIKYK	KNEVFIDVIE	SVNLLVNANG	SVLLSEIVGT	IKLKVFLSGM	PELRLGLNDR	240
VL FELTGRSK	NKSVELEDVK	FHQCVRLSRF	DNDRTISFIF	PDGDFELMSY	RLSTQVKPLI	300
WIESVIEKFS	HSRVEIMVKA	KQGFKKQSA	NGVEISVPVP	SOADS PRFKT	SVGSAKYVPE	360
RNVVSIWIKS	FPGGKEYLMR	AHFLGPSVEK	EEVEGRPPIG	VKFEIPYFTV	SGIQVRYMKI	420
IEKSGYOGPA	LGERYIHP EW	AITNFRYOLG	RGEEMGGF			458

(2) INFORMATION ON SEQ ID NO. 227:

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

LVTKVGNRPL WVNVAKPQGR ALVTTFLNDL HVSDLDPRDG EVGDLKLDPD GGPALHLFLF 60  
HTGEAKVGSH QVLLAPRERL NTPNHDSLR HILGAAHTGL ESGGVGIAGY RHRYLHTVGH120

(2) INFORMATION ON SEQ ID NO. 228:

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```
GISNLTPMGG RPSTSSFSTL GRPKWARIKY SLPPGKDLIL QITTFLSGTY LALPTLVNL 60
GESASLGTGT DISTPLATDC FLNCPLALTM ISTRLENFS MTDSIQISGL TWVLRDMS120
SKSPSGGMKE MVRSLSKRES RTHWWNFTSS SSTDLFLLRP VSSKSTRSLR PSRSSGIPDR180
NTLSLMVPTI SLRRTLPLAL TSRLTDSMTS MKTSFFLYLI PSERQDTALV TVGGTRDLPV240
SSLLLC 246
```

(2) INFORMATION ON SEQ ID NO. 229:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 275 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```
MNTRLQVEHP VTEMITGTDL VEWQLRIAAG EKIPLSQEEI TLQGHAFEAR IYAEDPSNNF 60
MPVAGPLVHL STPRADPSTR IETGVRQGDE VSVHYDPMIA KWVWVAADRQ AALTCLRYSL120
RQYNIVGLPT NIDFLLNLGS HPEFEAGNVH TDFIPQHHKQ LLLSRKAAAK ESLCQAALGL180
ILKEKAMTDT FTLQAHDQFS PFSSSSGRRL NISYTRNMTL KDGKNNVAIA VTYNHDGSYS240
MQIEDKTFQV LGNLYSEGDC TYLKCSVNGV ASKAK 275
```

(2) INFORMATION ON SEQ ID NO. 230:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 117 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```
SEVIILENTI YLFSKEGSIE IDIPVPKYL SVSSQETQGG PLAPMTGTIE KVFVKAGDKV 60
KAGDSLVMVI AMKMEHTIKS PKDGTVKKVF YREGAQRNH TPLVEFEEDS SDKRESE 117
```

002227 56662950

## (2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

SLRFTSNSIN RTFQVSAVSL AVKITKDLES FIFNLHAIRP IMVIRYSYGY IVFTIFKSHV 60  
 SGIRDIQSSS TARRKWRELI MCLKSESVGH GFLLDETQG CLA 103

## (2) INFORMATION ON SEQ ID NO. 232:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 234 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

ADKMFLPLP AAGRNVVRL AVRRFGSRSL STADMTKGLV LGIYSKEKED 60  
 NFDKLLAGKL RETLNISGPP LKAGKTRTFY GLHQDFPSV LVGLGKKAAG 120  
 KENIRAAVAA GCRQIQDLEL SSVEVDPCGD AQAAAEAVL GLYEYDDLKQ KKKMAVSAKL180  
 YGSGDQEAQW KGVLFASGQE LGHANLMGDA SQLRLTPTRF CRNYLRRFSK LVVS 234

## (2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein

```

QVRRAALLSS  AMEDSEALGF  EHMGLDPRLL  QAVTDLGWSR  PTLIQEKAIP  LALEGKDLLA  60
RARTGSGKTA  AYAIPMLQLL  LHRKATGPVV  EQAVRGLVLV  PTKELARQAQ  SMIQQLATYC 120
ARDVRVANVS  AAEDSVSQRA  VLMEKPDVVV  GTPSRILSHL  QQDSLKLKRD  S  LELLVDEAD 180
LLFSLWL

```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

DIGHS DIPST VGS QLL NHGL CLPC QLL GRN KNKASH CLFY HRTCLR PMEQ QLQHRNS ISG60  
RLPGARAGPS QEVLPF 76

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 112 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

TGLCNISLS ACTSSIKVAD MRKALLKSGG KVTRGRLLLEL FFKAKGKKEG QLRPPPKAPG 60  
SHEVSGCLAA SGLICEMGSL LPHLASPSAQ LSERLSLQQL RHWPLGHPEH SR 112

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 108 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(A) ORGANISM: HUMAN

```
CHARLNTDSS  RLAMKLLMVL  MLAALLLHCY  ADSGCKLLED  MVEKTINS DI  SIPEYKELLQ  60
EFIDSDAAAE  AMGKFKQCFL  NQSHRTLKNF  GLMMHTVYDS  IWCNMKSN           108
```

(A) ORGANISM: HUMAN

LVEETLLEFP HSLCSGITVY ELLKKLFVFR YRYVGIDGLF NHVLQEFAAR ICIAVQEEGR60  
QHEDHQQLHG EAAAVCVQSC VA 82

(A) ORGANISM: HUMAN

LLFILHQMLS YTVCIISPKE FRVLCDWLRK HCLNFPIASA AASLSMNS

(2) INFORMATION ON SEQ ID NO. 241:





## (2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GSSWAEDFKC DISVPKTSLL FAQSCRSMYF LLQYVPIYKF ISHTYNRAHV CTCTRTHHS60  
LSTR 64

## (2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

SGPLLPKAKNR EVAGLKTLSV TFQFLKHHCY LLKVVGLCIS FSNTSPFISL FPIHTTVHMC60  
ARAHATHTH SQLV 74

## (2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00222T 5632950

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

ARIQTPEQHS QVTLEFDYNEE MKMGGYLGIG IPSALKVSKL LTCEQHRTPL LWSSFQLRML60  
QFSKSIYYS 69

(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 236 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

QLRGGVQRHD RREGEMVCVE LVASDKTNTF QGVIFQGSIR YEALKKVYDN RVSVAARMAQ 60  
KMSFGFYKYS NMEFVRMKGK QGKGHAEMAV SRVSTGDTAP CGTEEDSSPA SPMHERVTSF120  
SRPPTPERNN RPAFFSPSK RKVPRNRIAE MKKSHSANDS EEFFREDDGG ADLHNATNLR180  
SRSLSGTGERS LVGSWLALNR ADGNFLLYAH LTYVTLP LHR ILTDILEVRQ KPILMT 236

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 161 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DEEVALGQRQ RGVLPGGRRW SRSAQCNPQA VSVPVGHRTV PGRVLAEAEQ SRWKLP SLCT 60  
LNLRHVAAAS DENRHPGSSA EAHPD DLAAC GACAEPRPGP ALGVLPSAYL STATGVCDGT120  
PVLEPQPGEA TRLPGPGPTA RTPAQTEVPL TGPAGAASAL C 161

004227 960960

## (2) INFORMATION ON SEQ ID NO. 249:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 218 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

VCIEKEVSIC SVQLQPGPDQ GPSCARQGPR PQVGCIVQIG STVVLPEELL AVVGRVRLH 60  
 LSDPVPGLHP LEGWGEGRP VVPFWGGGSA EGGHPLVHGR SWAGVLFSP TGGCVTCRHS A120  
 DRHLGVALAL GALHAHKLHV AVLVEAKRHL LCHAGGHAHP VVIHLRLV ADGALKDDPL180  
 ERVGFVTSHQ LRTDHLSP T VMSLNTSSKL SIMKKMLG 218

## (2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

YPQDPGGAS RRLDDLELC PGEKTAPVWA LSAEEEEAMH FSLAFFLHGS SVFLQITCCH 60  
 EFLCMRHISS CLYAEVFFIL SIGWWTGERG PRCPTSCASA VGGDRAPRHG GGGHLPHVWG120  
 GRRHPGTEGS LQR 133

## (2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

RLPSVPGCLR PPQTCGRCP PPCLGARSPP TALAHVGH L GPLSPVHQPI ERMKGTSAYR60  
HDEICLMHKN S

71

(2) INFORMATION ON SEQ ID NO. 252:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

RGLQHTDMMK YASCIKHDN MLFAKKQTNH AGKMPGKSAW QLPPQHSGPT QERFSPQDTA60  
PSRPEASVMP LLAGPEGIRA PLLLTVDAAT HSMQH

95

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 194 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

QKKKMSFRKV NIIILVLAVA LFLVLHNF LSLSSLLRNE VTDSGIVGPQ PIDFVPNALR 60  
HAVDGRQEEI PVVIAASEDR LGGAIAAINS IQHNTRSNVI FYIVTLNNTA DHLRSWLNSD120  
SLKSIRYKIV NFDPKLLEGK VKEDPDQGES MKPLTFARFY LPILGSQRQR KARLHGVDV180  
ICGRWDFLPF TLQQ

194

00422T 5622960

## (2) INFORMATION ON SEQ ID NO. 254:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

RFHGFPLVRI LLYFSFQKFR VKIDNFVSDA FQGITVEPGP EMVCCIVESN NVENHIGASV 60  
VLNAVYSCNG PPKPVFRCSD DHRNLLLSPI YCMSESIWDK VYRLRPYNS 109

## (2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

NLAKVKGFM D SPWSGSSFTF PSKSLGSKLT ILYLMLFRES LLSQDRRSA VLLRVTM 57

## (2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 230 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00422" 566660



## (2) INFORMATION ON SEQ ID NO. 259:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

ERSHLQPGAV GITESPILGL GSAMTTEIGW WKLTF LRKKK STPKVLYEIP DTYAQTEGDA 60  
 EPPRPDAGGP NSDFNTRLEK IVDKSTKGKH VKVSNSGRFK EKKKVRATLA ENPNLFDDHE120  
 EGRSSK 126

## (2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

YVLNTIIVGK GEEKIPHPLP RFGPCSFPLR VCDLPSAKVM AKTG TNRP NY HQSSLLQHPN 60  
 RVPGSSVPSA PEGKVPGSLL PVLGGELKFS VSASGSTETS PYHVASGKCA LLRIGPGSSH120  
 R 121

## (2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

004227 563395 122700



(vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

86

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

73

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

106

## (2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

VLRWYSSDPS IDTGRVMERD TSITTTVGMM KMIPVFPIRM QTDSFKISQE NVGSGSLSWK60  
EGAEGS 66

## (2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GCACFRPPSP AGGARTSAGR SPSSADVGSR TQSRSRRAA HSRCCVAFPS SFTPRSRRRP 60  
KRRRRRRREND PAASSLPPAH LPCSVSQSAA GARLVLRPRA CGAQAQRP 108

## (2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

004227-12200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

109

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

157

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 156 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

156

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 112 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

LGACSWWWPW ALGVSPWMRR RRSGNSHRSL PAWLRPVAVK DWFGVDSTKL PAFMYPLPEP 60  
SLGKGTDVLR TLFAETPENR WLSLLWSHSL ASDPSVQASL AAGSLPHAEA LE 112

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 130 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

SQRVCKYSPG SLLPYPRILV RSSNGFRTWV LFSCDHSSAH CMKTGLSQCF NLTRAVSWST 60  
PRSLVPYDS PHQMTLAKSR FLCGQGWLAD WWKVGWTKGG HVSSQHQFCT SSASVLVGVPI20  
VSPGPGWARA 130

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 267 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

GTSGTSHLHP RSICMIQKYN HDGEAGRLEA FSQGESVLKE PKYQEELEDR LHFYVEECDY 60
LQGFQILCDL HDGFSGVGAK AAELLQDEYS GRGIITWGLL PGPYHRGEAQ RNIYRLLNTA120
FGLVHLTAHS SLVCPLSLGG SLGLRPEPPV SFPYLHYDAT LPFHCSAILA TALDVTVPY180
RLCSSPVSMV HLADMLSFCG KKVVTAGAI I PFPLAPGQSL PDSLMQFGGA TPWTPLCACG240
EPGTRCFAQ SVVLRGYRQS MPHKPQT                                     267

```

(2) INFORMATION ON SEQ ID NO. 272:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 118 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

QVARVAGPGS HPRTRGRQES CEQSGARDQK LCLIDDRCF S GPPHDGRDQV AGPRLLFPAL 60
NIHLVAALPP SRLPQRSHRA GHTGSGSPAS SHIPERRNAA CPPALPGTWV PLGHFPLG 118

```

(2) INFORMATION ON SEQ ID NO. 273:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 133 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

LGKATCSRRL PTCTQWGPWG GSSKLHQGIR KGLAWSQGER DDCSCCHLF PTEAQHVSQM 60
NHGNWRGTQA IRNSDCVQGC SQDGTAVEGQ SGIIMQVREA DRWLGSQAQA PTQGQGADKR120
AVSSQVHETK SCV                                     133

```

002227 9662960

## (2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 124 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

PQAWRRRLCRC CSARPVAPGA RRLVPCRTPT RQPAGGTCHH PAAFRGRSRH IPVPHALGFG 60  
 ASAGRSVPLQ ALSQSPGAAD LQVFSTGAAP VIHTRLLEDP ILGATLPAGP IRCRAVGLVP120  
 RHCH 124

## (2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

GSSRRHGGGY AAVALLVLLL LGPGGWCLAE PPRDSLREEL VITPLPSGDV AATFQFRTRW 60  
 DSELQREGVS HYRLFPAKALG QLISKYSLRE LHLSFTQGFW RTRYWGPPFL QAPSGAELWV120  
 WFQDTVTDVD KSWKELSNVL SGIFCASLNF IDSTNTVTPT ASFKPLGLAN DTDHYFLRYA180

VLPREVVCTE NLTPWKKLLP CSSKAGLSVL LKADRLFHTS YHSQAVHIRP VCRNARCTSI240  
 SWELRQTLNV VFDAFITGQG KKDWSLFRMF SRTLTEPCPL ASESRYVVDI TTYNQDNETL300  
 EVHPPPTTTY QDVILGTRKT YAIYDLDLTA MINNSRNLNI QLKWKRPPEE EAPPVPFLHA360  
 QRYVSGYGLQ KGELSTLLYN THPYRAFPVL LLDTPVPWYLR LLHPLPACPG PAATPPPGDA420  
 DSAAGQ 426

## (2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

SPSILYGSCT CHSHKAFGGP DTGGHPSCR P HQVQSCGSGS KTLSLMWINL GRSSVMSSQG 60  
 SSAPLSTSSST PPTQSLPLPP SNPWVWPM TL TTTFCAMLCC RGRWSAPKTS PPRSSCPVV120  
 PRQASLCC 128

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 481 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

AQDTGGPGRQ SGHGGDLQIP ISLFLRRLNT QHWRPGSRKV MAVVPASLSG QDVGSFAYLT 60  
 IKDRIPQILT KVIDTLHRHK SEFFEKHGEE GVEAEKKAIS LLSKLRNELQ TDKPFIPLVE120  
 KEVDTDIWNQ YLEYQQSLN ESDGKSRWFY SPWLLVECYM YRRIHEAIIQ SPPIDYFDVF180  
 KESKEQNFYQ SQESIIALCT HLQQLIRTIE DLDENQLKDE FFKLLQISLW GNKCDLSLSG240  
 GESSSQNTNV LNSLEDLKPF ILLNDMEHLW SLLSNCKKTR EKASATRVYI VLDNSGFELV300  
 TDLILADFL L SSELATEVHF YGKTIPWFVS DTTIHDFNWL IEQVKHSNHK WMSKCGADWE360  
 EYIKMGKWVY HNHIFWTLPH EYCAMPQVAP DLYAELQKAH LILFKGDLNY RKLTGDRKWE420  
 FSVPFHQALN GFHPAPLCTI RTLKAEIQVG LQPGQGEQLL ASEPSWWTTG KYGIFQYDGP480  
 L 481

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

FHISVSTNFS TKGINGLSVC NSFRNLERRE IAFFSASTPS SPCFSKNSLL CRCNVSITLV 60  
KICGILSLIV RYANDPTSCP ERDAGTTAIT FRDPGRQCWV FNRRRNREIG ICKSPPCPDC120  
RPGPPVSC 128

(2) INFORMATION ON SEQ ID NO. 279:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

ELLNQVKGDH RTEIFHIFQW STSWAQRPGA VPLAQADQP EFQLLMFLWY RVVQDGSHE60  
PDEMEQKTPI FCHLSTSCNS NHP 83

(2) INFORMATION ON SEQ ID NO. 280:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 168 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

004227 5632960



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

FYDRRDCFVA VSFLRGLSLW LHFYLWWLCY GGAEMRQKRK GDLSPAELMM LTIGDVIKQL 60  
 IEAHEQGKDI DLNKVKTKTA AKYGLSAQPR LVDIIAAPP QYRKVLMPKL KAKPIRTASG120  
 IAVVAVMCKP HRCPHISFTG NICVYCPGGP DSDFEYSTQS YTGYEQPP 168

## (2) INFORMATION ON SEQ ID NO. 281:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 70 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

GGTAAMISTR RGWAERPYLE AVLVFTLFRS MSFPCSWASI SCLITSPIVS IISSAGLRSP60  
 FRFCLISAPP 70

## (2) INFORMATION ON SEQ ID NO. 282:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

IDVFPLLVG F NQLFNNISYS QHHQLSRAEI SFPLLPHFCA AVAEPPEIKM QPQTQTTEKA60  
 DSHKTIPPVV K 71

## (2) INFORMATION ON SEQ ID NO. 283:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00673395 122700

PHHTNPTCFK LFLIRCPVPV RKRVHIWHGI APHGGWLIQ CKTGWNTQNQ NQVPPRAVYT60  
YISCKTDVWT SVGFAHSHSD SNPTSSSDGF RL 92

## (2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

DLSRPGGTRF VLTIQQTFFS KVFVQDNFKN NIKINNGFDF SLKIEKKGVG GGVNHWPPFF60  
WRGPIGIVRP WSGLS 76

## (2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

RTFVLFYHRL TLQLLINTSF GDVWCKTHKH TQKSTSPLHD PSLLSGTISA ASCTLLGPPP60  
IHRGFRGTQI TAGFQFFFN TFLWSVPTAL SVLLKLE 97

## (2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

004227 566460

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ILHLEMYGVK HTNTHKKAQA RCMTRL SFLG LFLLRPAPSW AHLRTEVSG GPKSLLVFNF60  
FLTIHFCGQF QQHCPYF 77

(2) INFORMATION ON SEQ ID NO. 289:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 28 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

ILIDGVRAAF IPYREYNGAR LSRDFISA

28

(2) INFORMATION ON SEQ ID NO. 290:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 28 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

HQFHNYFNLL GFHLLIILKF HQQWGTEK

28

(2) INFORMATION ON SEQ ID NO. 291:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 29 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual

004227-5522950

33

## (2) INFORMATION ON SEQ ID NO. 294:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AINKVSSGYG PLALLGFSVS VEAAQRISLN FSQKWLLT

38

## (2) INFORMATION ON SEQ ID NO. 295:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

FTSFNLLIPR TILSTTNRNE ILIHKRKLKT FIAYVGLSNK

40

## (2) INFORMATION ON SEQ ID NO. 296:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

004227 55555555

VNLLKYGQIH LAVKQLNIHC YLIKVFVSVL PGPNIKTTSV QKINVQRAVC SLFWYVHFKK60  
 TPLSSLANOE Y 71

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 67 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

REFLYFILSR GTNSRHTFAR PSCRKTQSRK GKNKIAIKYM VLGAGRTRNP QGDQFLARSF60  
FRVYPVE 67

(2) INFORMATION ON SEQ ID NO. 298:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

KNLEFFSPST SYLLQNSSE GFIYILSYPE GPTAGIPLPG LLAERHRAVK AKIKLQ 56

(2) INFORMATION ON SEQ ID NO. 299:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 140 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

```
TPNSRAGAGRV VRGSARGVGR SCASWLPVGR RCRTSETGSG ASRRSRAIGS PPPSPCPWSA 60
NSASSARPTS SSGPKPSFIA FRFGQQLPP FISLWVQELD FFIWSIYISY ISILRDLKQE120
LLMGGQQTII SCSSLTGFAS                                     140
```

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

QSRSRPRREG	VGTGSRVAVLC	ILATCGSKMS	DIGDWFRSIP	AITRYWFAAT	VAVPLVGKLG	60
LISPAYLFLW	PEAFLYREFQI	WRPITATFYF	PVGPGTGFLY	LVNLYFLYQY	STRLETGAFD	120
GRPADYLFML	LFNYWICIVIT	GLAMDMQLLM	IPLIMSVLYV	WAQLNRDMIV	SFWFGTRFKA	180
CYLPWVILGF	NYIIGGSVIN	ELEIGNLVGHL	YFFLMFRYPM	DLGGRNFLST	PQFLYRWLPS	240
RRGGVSGFGV	PPASMRRAAD	QNGGGGRHNW	QGGFRLGDQ			279

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes



- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

IDQIKKSSSW THREIKGGSD WPPNLKAIKE GFGPEEEVGR ADEAEFADQG HGDGGGGEPIA 60  
RDRRDAPEPV SDVRHLRPTG SQDAQDRPTP RADPLTTRPA PRLIGV 106

(2) INFORMATION ON SEQ ID NO. 302:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 207 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

LEPLEPNRLE LKKGYLTLSG SGDKVAVEWD KDHGVLHSL AEKGRGMELS DLIVFNGKLY 60  
SVDDRTGVVY QIEGSKAVPW VILSDGDGTV EKGFKAEWLA VKDERLYVGG LGKEWTTTGT120  
DVVNENPEWV KVVGYKGSVD HENWVSNYNA LRAAAGIQPP GNLIHESACW SDTLQRWFFL180  
PRRASQERYE EGGRAQGRQ PAAERLP 207

(2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 153 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RWWATRAAWT TRTGCPPTTP CGLLPASSRQ VTSSMSLPAG VTRCSAGSSC RAAPARSATA 60  
RKDDERKGAN LLLSASPDFG DIAVSHVGAV VPTHGFSSFK FIPNTDDQII VALKSEEDSG120  
RVASYIMAFT LDGRFLLPET KIGSVKYEGI EFI 153

004237" 0604960

## (2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

VGTTAPTWLT AMSPKSGEAL SSRLAPLRSS SFLAVALLAG AARQEEPALQ RVTPAGRLMD 60  
 EVTWRLDAGS SPQGVVVGHP VLVVHAALVA HHLHPLRVLV HHITRSGRPL LAQAAHVQTL120  
 VLHCQPFGLA AFLHGAUAVG QNHFGHGFAA FDLVDDPRPV IHGVEFFPIEN NQVG 174

## (2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

KLVCLEADSK SSFSSEHLFS YHLISILKHH GCSCSKMGDV KENYLETFIS SPKWSFILCL60  
 S 61

## (2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00427564960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

NTMAVAAVKW VMSKRTILKH LFPVQNGALY CVCHKSTYSP LPDDYNCNVE LALTS DGRTI 60  
VCYHPSVDIP YEHTKPIPRP DPVHNNEETH DQVLKTRLEE KVEHLEEGPM IEQLSKMFFT120  
TKHRWYPHGR YHRCRKNLNP PKDR 144

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

IHQTAFSQMA NEAHFSLIPP GTSASSVFWR IQILTTSVIP SMRIPTVLSS KEHFAKLFYH 60  
RSFLKVENFF FQSGFQHLIM CFFIIMHRIW PRDFECVFIW NVHRRVVAYY CPAIRSQSKL120  
YVAIIIVW 128

(2) INFORMATION ON SEQ ID NO. 308:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 467 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

SRSKMAALRA LCGFRGVAAQ VLRPGAGVRL PIQPSRGVRQ WQPDVEWAQQ FGGAVMYP SK 60  
ETAHWKPPPW NDVDPPKDTI VKNITLNFGP QHPAAHGVLR LVMELSGEMV RKCDPHIGLL120  
HRGTEKLI EY KTYLQALPYF DRLDYVSM MC NEQAYS LA VE KLLNIRPPPR AQWIRVLFGE180  
ITRLLNHIMA VTTHALDLGA MTPFFWLFEE REKMFEFYER VSGARMHAAY IRPGGVHQDL240  
PLGLMDDIYQ FSKNFSLRLD ELEELLTNNR IWRNRTIDIG VVTAEALNY GFSGVMLRGS300  
GIQWDLRKTQ PYDVYDQVEF DVPVGSRGDC YDRYLCRVEE MRQSLRIIAQ CLNKMPPGEI360  
KVDDAKVSPP KRAEMKTSME SLIHHFKLYT EGYQVPPGAT YTAIEAPKGE FGVYLVSDGS420  
SRPYRCKIKA PGFAHLAGLD KMSKGHMLAD VVAIIGTQDI VFGEVDR 467

09673395-12200

## (2) INFORMATION ON SEQ ID NO. 309:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

QPSVHEHTHT HTHHTHTQR PISSEEQAPQ KKLIGRGDQT LLPCSPIYFS KYNILGTYDG 60  
 NDICQHVSLR HLVQTSQMGK TRSLDLASIR AAAAIRHQVH PKLSLGSLNG SICGSWRNLV120  
 ALSIQLKVMN Q 131

## (2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SQDTMRCWVL GPKVQGNVLH NCVLWRVHII PRWRLPVGCF FAWVHNSSPK LLCPFHIWLP 60  
 LPNTSAGLNR QSDSSPREQH LGRDAPEAAQ SPQRRHLTPA 100

## (2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

004227 5622960



## (2) INFORMATION ON SEQ ID NO. 314:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 162 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

SDRWTCSPPL GARSMSRFPA VAGRAPRRQE EGRSRDLQE ERLSAVCIAD REEKGCTSQE 60  
GGTTPTFPIQ KQRKKIIQAV RDNSFLIVTG NTGSGKTTQL PKYLYEAGFS QHGMIGVTQP120  
RKVAAISVAQ RVAEEMKCTL GSKVGQVRF DDCSSKETAI KY 162

## (2) INFORMATION ON SEQ ID NO. 315:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 79 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

QIGGRARLHS GPGLCPGFPPQ SRAGRQGGRR RVSGQETSRK SGSRLFASPI EKRKDARPRR60  
EELLQLFLFR NKEKRLFKL 79

## (2) INFORMATION ON SEQ ID NO. 316:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 69 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004227 66664960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

IGKVGVPVPPS WDVHPFSSLS AMQTAESRSS WRS�DRSPSS CRLGALPATA GNRDIDLAPS60  
GGEHVHRSE 69

(2) INFORMATION ON SEQ ID NO. 317:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 173 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSLFLP GAYKAQMYSD VWTNTKKKKK 60  
KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVQ TSSQAIFYQK120  
GENSCLSFLK NAFLYLSIRH YTSELYKRP G TMSLVDTFH CSVAPFLAWE ASA 173

(2) INFORMATION ON SEQ ID NO. 318:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 96 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSLFLP GAYKAQMYSD VWTNTKKHFL60  
KRKGMSFPLF DKKQPVMSKG AQERWVSHLE AFRTQL 96

004227-5622960

## (2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

## (2) INFORMATION ON SEQ ID NO. 320:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

IRKREQGRSS PAPWESVFAS VPFRGDDGIF DDNFIEERKQ GLEQFINKVA GHPLAQNERC60  
 LHMFLQDEII DKSYPSPKIR HA 82

## (2) INFORMATION ON SEQ ID NO. 321:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 159 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

004221 00000000



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

RASPCPHGGQ QRRRRRLNAE GAEGARGGGS SYSEMAETVA DTRRLITKPQ NLNDAYGPPS 60  
NFLEIDVSNP QTVGVGRGRF TTYEIRVKTN LPIFKLKEST VRRRYSDFEW LRSELERESK120  
VVVPPLPGKA FLRQFLLEEM MEYLMTILLR KENKGWSSL 159

(2) INFORMATION ON SEQ ID NO. 322:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 114 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

FTSQPFKVTV SSSNSRFFQL ENRKICLDPD FVSGEAAPAD PHRLRVAHID LEEVAGGSVG 60  
VIQVLRIGDQ PPGVSHGLRH FAVAAAAAAG SLRPLRVQPP PPPLLPVGT RARA 114

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 374 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

RRAQESPLGR QSHLPRIYQA FLMSATFNEQ VQALKELILH NPVTLKLQES QLPQPDQLQQ 60  
FQVVCETEED KFLLLYALLK LSLIRGKSL FVNTLERSYR LRLFLEQFSI PTCVLNGELP120  
LRSRCHIISQ FNQGFYDCVI ATDAEVLGAP VKGKRRGRGP KGDKASDPEA GVARGIDFHH180  
VSAVLNFDLP PTPEAYIHRA GRTARANNPG IVLTFVLPTQ QFHLGKIEEL LSGENRGPI1240  
LPYQFRMEEI EGFYRRCRDA MRSVTKQAIR EARLKEIKKE LLHSEKLKTY FEDNPRDLQL300  
LRHDLPLHPA VVKPHLGHVP DYLVFPALRG LVRPHKKRKK LSSSCRKAKR AKSQNPLRSF360  
KHKGKKFRPT AKPS 374

004221 3622950

(2) INFORMATION ON SEQ ID NO. 324:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 224 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

```

QRVRAALLSS  AMEDSEALGF  EHMGLDPRLL  QAVTDLGWSR  PTLIQEKAIP  LALEGKDLLA  60
RVRTGSGKTA  AYAIPLQLL  LHRKATGPVV  EQAVRGLVLV  PTKELARQAQ  SMIQQLATYC  120
ARDVRVANVS  AAEDSVSQRA  VLMEKPDVVV  GTPSRILSHL  QQDSLKLKRD  LELLVVDEAD  180
LLESEGFEEE  LKSLLWEGRV  TCPGFTRLFS  COLLLTRTYK  HSR$                224

```

(2) INFORMATION ON SEQ ID NO. 325:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 115 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

FFF FFF FFF FFF G AAK I FILL SR GKMPAWK CQG AKGPSTAGPR TVCSGCAVST RASPVHEGCK 60  
 PVLHNV LSSR EAQPOEGLA VGLNFFPLCL KLRSGFWDFA LLAFLQEEDS FFRFL 115

(2) INFORMATION ON SEQ ID NO. 326:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 66 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

YLQCQRSLCG AKCVTWAVET RHLSPALMT LRKEDVIQ GK FLIPKLPVHV NRTSFYSSRC60  
TGSLAP 66

(2) INFORMATION ON SEQ ID NO. 327:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 90 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

FRSCLEMLTG LLFIRQDVLV PWHLKGNPDK GKPVEPF GPI GSQDPSPV FH RYYHVFREGE60  
LEGACRTVSD VRILQSYDQ GNWCVILQKA 90

(2) INFORMATION ON SEQ ID NO. 328:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

SGLLKNHTPV SLIVVALQNS DITHSPAGTF QFSLTEH MVV TMKHRTWVLG SYGTKWLNRF60  
AFIRISLKVP GNQYILTNNK KSC 83

004227 96022960

## (2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 185 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

```
ERRSKSREER EKEREREREE RERKRRREEE EREKERARDR ERRKRSRSRS RHSSRTSDRR 60
CSRSRDHKRS RSRERRRSRS RDRRRSRSHD RSEKHRRSRS RDRRRSKSRD RKSYPKRSKS120
RDREQDRKSK EKEKRGSDDK KSSVKSGSRE KQSEDNTES KESDTKNEVN GTSEDIKSEG180
DTQSN                                     185
```

## (2) INFORMATION ON SEQ ID NO. 330:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 178 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```
YHFPSIQCLC LHS AFLDYRT SHYFFYHQIP SFLSPWIFYL VLCPDFCSCA YMTFDPGFLI 60
FFDPDFEICV FFLIDHGFCF FVDLYFCSAF FLYFVTFCGP ETCCIFCLMF GLSVYFVNDF120
SFFFLCHEPF LFLFLPLPFV FSFLFLPFLS PVLSLSLCS CFSFLRRSSR IRLFGSSP 178
```

## (2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 182 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

004221" 5622960

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

VSPSDLMSSL VPLTSFLVSL SFDSVFVSSL CFSRLPDFTL LFLSSDPLFS FSLDFLSCSL 60

SRLLLLCLYD FRSLFDLLR SRLRDLCLFS DRSWLLLLRR SLLLLRLLSL LRDLLWSRDL120  
LHLLSDVRLE CLLRERLLFL LSLSRALFS LSSSLRLFL SLSSLSLSRS FSLSSLLLLL180  
LS 182

(2) INFORMATION ON SEQ ID NO. 332:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 88 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GFGMQLVILR VTIFLPWCFA VVPVPAADHK GWDFVEGYFH QFFLTEKESP LLTQETQTQL60  
LQQFHRNGTD LLDQMHHASA TAAPLWGA 88

(2) INFORMATION ON SEQ ID NO. 333:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 61 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

PRRSRHSLPR RHKHSSCNNS IGMGQTYLTC RCMLLLQQPH CGVPDGS DNC ISPGRCCKWIK60  
H 61

00427 5622960

## (2) INFORMATION ON SEQ ID NO. 334:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 62 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

STCIFLARCS CRTHQAPHS G AAVAEACICM SSRSVPFRWN CCRSCVCVSW VRSGDSFSVR60  
KN 62

## (2) INFORMATION ON SEQ ID NO. 335:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 61 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

VCPIPMELLQ ELCLCLLGKE WRLLLGQEK L MEIALNKVPS FMVCSRGHWN GETPGQEDSN60  
S 61

## (2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 63 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

09673395.122700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

(2) INFORMATION ON SEQ ID NO. 337:

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

(2) INFORMATION ON SEQ ID NO. 338:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

SCGDUVEQKIQ FKRETASLKL LPHQPRIVEM KKGSNGYGFY LLAGSEQKGQ IIKDIDSGSP 60  
AEEAGLKNND LVVAVNGESV ETLDHDSVVE MIRKGGDQTS LLVVDKETDN MYRLAHFSPF120  
LYYQSQELPN GSVKEAPAPT PTSLEVSSPP DTTEEVDHKP KLCRLAKGEN GYGFHLNAIR180  
GLPGSFQIFV QKGGPADLAG LEDEDVIEV NGVNVLDPEY EKVVDRIQSS GKNVTLLVCG240  
KKAYDYFQA 24

## (2) INFORMATION ON SEQ ID NO. 339:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

ITGVQPEHIQ YLKNYFHLWT RQLAHYHYHYY IHGPKGNEIR TSKEVEPFNN IDIEISMFEK60  
GKVPKIV 67

## (2) INFORMATION ON SEQ ID NO. 340:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

RIFITTIFMA QKEMKYEHOQ KLNLSLIL KFLCLKKGRY LRLS

44

## (2) INFORMATION ON SEQ ID NO. 341:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 46 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

004227-5622950



(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

KVQLLMFVF HFLLGHEYSS DKYALTVVSK GGNFSSSTVC VLVVPL

46

(2) INFORMATION ON SEQ ID NO. 342:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GRWRRRLRHG RGSAAVAVGPT AMAELLQEEL SVLAAIFCRP HEWEVLSRSE TDGTVFRIHT 60  
 KAEGFMDADI PLELVFHLVP NYPSCLPGIS INSEQLTRAQ CVTVKEKLE QAESLLSEPM120  
 VHELVLWIIQ NLRHILSQPE TGSGSEKCTF STSTMDDDL WITLLHLDHM RAKTKYVKIV180  
 EKWASDLRLT GRLMFMGKII LDFTTGRQKQ PQGVLDSSN LQSRCGLKWK EMQREND 237

(2) INFORMATION ON SEQ ID NO. 343:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

YLILLQGRN NLKVYLILQK TSKVDVDSSG KKCKEKMISV LFETKVQTEH KRFLAFEVKE60  
 YSALDELQKE FETAGLKKLF SEFVLALVK 89

(2) INFORMATION ON SEQ ID NO. 344:

(i) SEQUENCE CHARACTERISTIC:

0967395-12200

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

PLPKSNAKTT KNTAILLKDS CLPFHFTRAS TNSEKSFSLSP AVSNSFCNSS NAEYSLTSNA60  
 RNLLCSVCTF VSNSTLIIFS LHFFPLESTS TLEVF 95

(2) INFORMATION ON SEQ ID NO. 345:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 72 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

RAGLFPGRRV GLEAENGPCQ HQHGDFVPCP VLSARMSQPE AEEAALVAHA VGHDCVCSGG60  
 GVLLPHHRRN NL 72

(2) INFORMATION ON SEQ ID NO. 346:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 171 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00422T 5622950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GRACFRGGAW GLRPRTALAA TNMETLYRVP FLVLECPNLK LKKPPWLHMP SAMTVYALVV 60  
 VSYFLITGGI IYDVIVEPPS VGSMTDEHGH QRPVAFLAYR VNGQYIMEGL ASSFLFTMGG120  
 LGFIILDRSN APNIPKLNRF LLLFIGFVCV LLSFFMARVF MRMKLPGYLM G 171

## (2) INFORMATION ON SEQ ID NO. 347:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

EAGCKSFHNI LSIYVGQES YWPLMPMFIS HRTDTWRFNN NIINYSSGDE EVRHHHQSIH60  
 SHGRRHVQPG RLLQLQVGTF EH 82

## (2) INFORMATION ON SEQ ID NO. 348:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 103 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

HKVIVVWNNI GEKAPDELWN SLGPHPIPVI FKQQTANRMR NRLQVFPELE TNAVLMVDDD 60  
 TLISTPDLVF AFSVWQQFPD QIVGICFLES TSFTFIQGIY SYW 103

## (2) INFORMATION ON SEQ ID NO. 349:

004427 86022350

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

ESKNKVWGAD ECVIIYHQHC IGFQFRKDLE SISHPVCCLL FEDHRDRVGP

50

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

SGNCCQTEKA KTRSGVLM SV SSSTINTALV SSSGKTWSRF LILFAVCCLK ITGIGWGPRE60  
FHNSSGAFSP ILFHTTITL

79

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

004227 362350

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GTLRHSVHV V PPKHGHKVL SSGVCSRL LG IQREGRNQEF QKHIHVATPA TSGILCSDKL60  
 HGWEVFFLAR 70

## (2) INFORMATION ON SEQ ID NO. 352:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 71 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

HLIPFMAKSS FRVGNTQTFC ACCSPKAWSS QSPEFWCVLP PPGYTERRQE SGVPEAYTCG60  
 YPSNKRHPVL R 71

## (2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

SGQCGMQLGP DQPSSEQMAV VPISTKPQRA RKNTSQPCSL SEHRMPLVAG VATCICFWNS60

## (2) INFORMATION ON SEQ ID NO. 354:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 225 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

00673395.122000

GLPARRPQCF LRAEMANSGL QLLGFSMALL GWVGLVACTA IPQWQMSSYA GDNIITAQAM 60  
YKGLWMDCVT QSTGMMSCMK YDSVLALSAA LQATRALMVV SLVLGFLAMF VATMGMKCTR120  
CGGDDKVKKA RIAMGGGIIF IVAGLAALVA CSWYGHQIVT DFYNPLIPTN IKYEFGPAIF180  
IGWAGSALVI LGGALLSCSC PGNESKAGYR APRSYPKSNS SKEYV 225

(2) INFORMATION ON SEQ ID NO. 355:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

QHHHGPGHVQ GAVDGLRHA E HGDELQNV R LGARPVRGLA GHSSPNGGLP GAGLPGHVCG 60  
HDGHEVHALW GRRQSEEGPY SHGWRHNFHR GRSCRLGSL L LVWPSDCHRL L 111

(2) INFORMATION ON SEQ ID NO. 356:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

CCHPHRSSSA TAGWRCRPPD PPSPAGPWRS PATAGPNWPF PPSENTGGAG RGDETVKQTT 60  
LGGQPHKRKL EVEFSGHPKR QKGFPGGECK SCHQTTHKST PPVKRWPRGT GSRIRREGGS120  
RONWWSPKAR RFPPGALGDP LSPPASRLLT GVGP 154

## (2) INFORMATION ON SEQ ID NO. 357:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

NLTQVTFLEFF CPPNVHASR LHFEALMNIP VLVLDVNDDF AEEVTKQEDL MREVGRTLTP60  
VFLVVSLWLY LL 72

## (2) INFORMATION ON SEQ ID NO. 358:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

SPSHLSHEVF LFGYFLSKII IDIQHQHWNV HQSLKVEPIR SVNVGTEKK KCNLSQVSHT60  
RQVLLREQI 69

## (2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

004222 004222 004222

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

KRYNQRETTR KTGVKVLPTS LMRSSCLVTS SAKSSLTSNT STGMFIRASK WSL

53

(2) INFORMATION ON SEQ ID NO. 361:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

SCWETKWTSC PRMLLATGRG CGSDCGRTVP APGSCWPLAP RATAPRQGRA TGRGESESAE 60  
LVPHSGQGRA ADQRQDRLWS GRVDLCPSAL LALPWGRLLS GRHQRRQIHS L 111

(2) INFORMATION ON SEQ ID NO. 362:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

TRNGSVFGCY RPHRFPPAGKS VSLVYSRGFQ HPPCAYHLLG QGRRSVSEAC RSYVTPDSNG 60  
WKRTNGQDFL LLLLKTLMVK RKDVGQPGSS GPTSKFPLQV ILCQALFKK 109

(2) INFORMATION ON SEQ ID NO. 363:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 381 amino acids

0937396-2270



- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GPARRPAARL ARAGGPQAAD RAGKQSGPPA PGCSWLPAEA AGATVGGGLCP RRAPAGPWHQ 60  
 GPQRPVKDEF QDGENPNPPN WSRTVVRDVR LISAKTGYGV EELISALQRS WRYRGDVYLV120  
 GATNAGKSTL FNTLLESFYC TAKGSEADR ATISFPWPGT LNLKFFICN PTPYRMFKRH180  
 QRLKKDSTQA EEDLSEQEQN QLNVLKKHGY VVGRVGRFTL YSEEQKDNIP FEFDADSLAF240  
 DMENDPVMGT HKSTKQVELT AQDVKDAHWF YDTPGITKEN CILNLLTEKE VNIVLPTQSI300  
 VPRTFVLKPG MVLFLGAIGR IDFLQGNQSA WFTVVASNIL PVHITSLDRA DALYQKHAGH360  
 TLLQIPMGKK ERMGRISSC C 381

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 182 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

QPSTTCTSVL VCLLSAMPLP VALQTRLAKR GILKHLEPEP EEEIIAEDYD DDPVDYEATR 60  
 LEGLPPSWYK VFDPSGLPY YWNADTDLVS WLSPHDPNSV VTKSAKKLRS SNADAEKLD120  
 RSHDKSDRGH DKSDRSHEKL DRGHDKSDRG HDKSDRDRER GYDKSRNGIR DRGYDQADRE180

EG

182

(2) INFORMATION ON SEQ ID NO. 365:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 149 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

RRHERDGRCD SLPLPARVYW SVCYQLCRCP LRCRPAWPRE ASSNIWSLNQ RKRSLPRTMT 60  
MILWTTTRPPG WRAYHQAGTR CSTLPAGSLT TGMQTQTLYP GSPHMTPTPW LPNRPSSSEAL20  
VMQMLKKSMT GAMTSRTGAM TSRTAAMRN 149

(2) INFORMATION ON SEQ ID NO. 366:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 80 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

PRSRSLSDLS WPRSDLSWPL SSFSWLRSWL SWPLSDLSWL RSNFSSASAL LLLSFLADLV60  
TTELGSCGES QDTRSVSAFQ 80

(2) INFORMATION ON SEQ ID NO. 367:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 160 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

VAQQPALIHG YRKAVLTPNH VEFSLRYDAV LRGPMDSDDS HGSVLRLSQA LGNVTVVQKG 60  
ERDILSNGQQ VLVCSQEGSS RRCGGQGDLL SGSLGVLVHW ALLAGPQKTN GSSPLLVAAF120  
GACSLTRQCN HQAFQKHGRS TTSDMIAEV GAAPSKLFET 160

004221 5622950

## (2) INFORMATION ON SEQ ID NO. 368:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

ILNGNQFMLK LKIWQAPYAF STRVGPDPFI THTLSPVQGA CLLLVCAGSG FKELAEGGPH 60
LGDHVGGGGG ATVLEGLVV ALPGERAGAK RGHQERAGPI CFLWSSKERP VYQDAQGARQ120
EVPLPSTPAA AAFLAAHKHL LAVGEDVALS FLDHRHVAQG LAES                      164

```

## (2) INFORMATION ON SEQ ID NO. 369:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 187 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

KSGKHRTPSA HAWVRIFPSH TRSPPSKVPV YFWSARAQVS KSLKKAAPTS AIMSEVVVER 60
PCFWKAWWLH CLVREQAPNA ATRRGLDPEV FCGPARSAQC TRTPREPDRR SPCPPHLRLL120
PSWLHTSTCW PLERMSRSPF WTTVTLPRAW LSLSTD PWLS SLSIGPLSTA SYSLLNSTWL180
GVSTAFR                                           187

```

## (2) INFORMATION ON SEQ ID NO. 370:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein

004227 09022000

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

LFLFTNHNDS GKPGCKKHQHC HQLRICDQEC HLTVTGRRQK

40

(2) INFORMATION ON SEQ ID NO. 371:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 34 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

QAEDKSETGL MRITGKLALA PPENELFHSL ADHP

34

(2) INFORMATION ON SEQ ID NO. 372:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 38 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

NSSFSGGAKA SFPVIRISPV SLSSACYRE MALLITDP

38

004221562350

## (2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

RQLFGIVSIA TLTVLAYERI IRVVHARVIN FSWAWRAITY IWLKSLAWAG APLLGWNRYI 60  
 LDVHGLGCTV DWKSKDANDS SFVLFLFLGC LVVPLGVIAH CYGHILYFHS NASLVWKIFR120  
 QFK 123

## (2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

TVHSRGPCQS DQFFLGLEGH YLHLALLTGV GRSTSPGMEQ VHPGRTRTRL HCGLEIQGCQ 60  
 RFLCAFLIS WLPGGAPGCH SPLLWPYSIF PFECFVGVED LQTIQVIKIL KYEKKLAKMC120  
 F 121

## (2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00422T" 9622960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

HPGAPPGSQE IRKAQRRNRW HPWISSPQCS LVRVRPGCTC SIPGEVLLPT PVSRARCR 58

(2) INFORMATION ON SEQ ID NO. 376:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 49 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

AFTCDFVPLC GLLEQWTTKS AMQFIKVDLV ICHPTAYGPC KPVLEANIL

49

(2) INFORMATION ON SEQ ID NO. 377:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

FCTTLWPSGA MDNQVSYAVH KSGPGYMSSN SIWSLQACFG SQYSITYRNP LESDVFGSNI60  
FSQGSNGL 68

(2) INFORMATION ON SEQ ID NO. 378:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 64 amino acids

004227 00000000

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

HITRSTFMNC IADLVVHCSR RPQSGTKSQV KAQTAPVILV VLSLHSSPLA KTGLNMKSPA60  
 PRPQ 64

(2) INFORMATION ON SEQ ID NO. 379:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 144 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

APISSNFCSE SIWGYCDQLK VSESTHVLQP FLPSILDGLI HLAAQFSSEV LNLVMTLCI 60  
 VCTVDPEFTA SMESKICPFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMRLLIP120  
 TLVSIMQAPA DKIPAGLCAT PLIS 144

(2) INFORMATION ON SEQ ID NO. 380:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 254 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

004221 9622960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

(2) INFORMATION ON SEQ ID NO. 381:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

SLSGPNANEAE DSHSGQHNAG PSRQDSCRAL CDTIDILTTV VRNTKPPLSQ LLICQAFPAV60  
AQCTLHTDDN AISAEWRRVL AGLCVSDPGT SSPVA 95

(2) INFORMATION ON SEQ ID NO. 382:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 263 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

APISSNFCSE	SIWGYCDQLK	VSESTHVLQP	FLPSILDGLI	HLAAQFSSEV	LNLVMETLCI	60
VCTVDPEFTA	SMESKICPFT	IAIFLKYSND	PVVASLAQDI	FKELSQIEAC	QGPMQMRLIP	120
TLVSSIMQAPA	DKIPAGLCAT	PIDILTTVVR	NTKPPLSQLL	ICQAFPAVAQ	CTLHTDDNAT	180
MQNGQCEGLRA	YVSVTLEQVA	QWHDEQGHNG	LWYVMQVVSQ	LLDPRTSEFT	AAFVGRLCFHD	240
PHLQGRAGTR	GESRPDFFVP	SFS				263



## (2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TLRCGGPGAG SPLASHTTVH CGPAHHATGL LVPGLTHRP ASTLRHSAWW HCHLCEGYTV60  
PQQGKLGR 68

## (2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

HIGPQALSAI LHGGIVICVK GTLCHSRESL ADEKLGKGRL CISYYCCQDI NGCRTKPCRN60  
LVCWGLHYAD QSGNQPHLHW ALTGFNLGQL LEDVLSQ 97

## (2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 140 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

004227 96022960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

(2) INFORMATION ON SEQ ID NO. 386:

(vi) ORIGIN  
(A) ORGANISM: HUMAN

DVPLLFRLPC HIPQLKVGLG SVEVGMRIEI CTGLHWLYWQ LWGVLSLVK 49

(2) INFORMATION ON SEQ ID NO. 387:

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

SECMVLRTYN HRLTRSSLDI QLSTPPHSSY GRPVFLHSLR NKGLDRGSLL S 51

(2) INFORMATION ON SEQ ID NO. 388:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 97 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

SSSPLSFCWF LPSPAASCSS SCPSGMTSWS RSGPSISGFS WLTDRAACTC GVWPSSPAPP60  
KPLPPTGLSS TPAPGLAPAA ACPSEAPINT DLMVFFP 97

(2) INFORMATION ON SEQ ID NO. 389:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 148 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GKGTMRSVLI GASEGQAAAG ARPGAGVEDR PVGGRGFGGA GELGQTPQVQ AALSVSQENP 60  
EMEGPERDQL VIPDGQEEEQ EAAGEGRNQQ KLRGEDDYNM DENEAESETD KQAALAGNDR120  
NIDVFNVEDQ KRDTINLLDQ REKRNHTL 148

(2) INFORMATION ON SEQ ID NO. 390:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 84 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

00422T" 5622960

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GPRDRLIQPS YFQRGKWGLE VTEHLAGALA PLASHRLPSS WDYRHTVTEA GPVCNSRCHL60  
QLKHSSYVMS LVTKVKLSHP EKAT 84

(2) INFORMATION ON SEQ ID NO. 391:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 59 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

CGKKCITLFL FLSPSLPLWC LRYWGSHSWG HSEATRNAS LHLAVSARTR NPQTSSQTS 59

(2) INFORMATION ON SEQ ID NO. 392:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 107 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TPRNLNFEHRSK LTQFHCVNTV SLGSTKHPIT QFCFIVWTPS RLQGHGQEV CEEVCGFLVL 60  
ALTARCKLEA FLVASEWPQL WDPQYLRHRH GREGDRNRNR VMHFFPH 107

(2) INFORMATION ON SEQ ID NO. 393:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein

00673395-122700

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

VAPAVGSPVS QAPQRQRGGQ EQKQSYAFLS TLKKRNYTFR GMLSPRSTSS PVFHDLP TKK60  
I 61

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 74 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

CNCAPSLPDF SPLHPQCGIS LVPRGTPLDL WTSRPGQEAA TRNPRPLLLK FTASVVVPDS60  
SPAPGTTSTW GGAF 74

(2) INFORMATION ON SEQ ID NO. 395:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 112 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

ATVHPACQIF PHYTPSVAYP WSPEAHPLIC GPPGLDKRLL PETPGPCYSN SQPVWLCLTP 60  
RQPLEPHPPG EGPSEWSSDT AEGRPCPYPH CQVLSAQPGS EEELEELCEQ AV 112

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 396:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

DRRSHGLLLY NLPGEQFKNM NQDPFDPLII QKSTQKYAQK YVGIH

45

## (2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

ERLSHCRSLV MLALISLCTP CTHAFSPVFY QASVSCITLK CDH

43

## (2) INFORMATION ON SEQ ID NO. 398:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

007227 967395 12700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

WIKRILIHIF KLLSREVVVKQ QSMRASISLP LLGDACPHLP MYPMHSCLLS CFLSSLSFMY60  
YTKM 64

## (2) INFORMATION ON SEQ ID NO. 399:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 77 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

HIKIEFFGQN FWEAMHPTWA DIQPELFSRG EWYQWFMAEI HSDWLESMLY QLLNILSITL60  
AYCYYIISI YRQKGHF 77

## (2) INFORMATION ON SEQ ID NO. 340:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

SSLGKTFGKQ CILHGLIFSL SCSQEESEGTG SLWLKSILIG WSLCYTSC 48

## (2) INFORMATION ON SEQ ID NO. 401:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

00422T"98224950

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

FRNPALIEPS VGSTAEIFRA FNILKMAFLS IYRGNIIVTV CKSDTQNV

48

(2) INFORMATION ON SEQ ID NO. 402:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 70 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

EQLRLNISPC RMHCFPKVLP KELYFYVLSH RTGEKCSGHC WDLIFLGMGS GLMILATGVQ60  
ENGSPGSDSW 70

(2) INFORMATION ON SEQ ID NO. 403:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 63 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

MCDFIRGICQ FSHCGSFSD F ACSSSKEARS FADFTIPQTC KFLTSSKLAL ALSSTFPFKS60  
NLC 63

(2) INFORMATION ON SEQ ID NO. 404:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 71 amino acids

00422T 5622960



- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

MGITHECVIL LGASANSLTV VPSLTLPVHH LRRLDPSLTS PFLKPVSFSL LPNWLWLFLQ60  
PFHSRAIFAK E 71

(2) INFORMATION ON SEQ ID NO. 405:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 63 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

LGDHIYNWDV NHFFSGIRAQ RHNLQGHIIY YEHTVRLFI LPSTCAEMKP KQAVGFHKSI60  
YVG 63

(2) INFORMATION ON SEQ ID NO. 406:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 88 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

004227" 5662950

## 88

HRRLHRVLR A ALRVHLRAAL AGAALPPQAA QLPERLPLSL PLLGLPADRP LLLLLQRLRG 60  
 GQFAQPLRL AALLLPCVPA VFHPHADELV LHAGDFQSQV KIFSRTQIP VAPLPGLPLH120  
 QPCFPVGEFN LCCAGKDGKL GEEGYRLCAS GH 152

## (2) INFORMATION ON SEQ ID NO. 409:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

LGFENHLREV QVHQREGEKL QAHREAVEQP EDEGAERIGR HEVFEVEGEE DGPPGGPEEA 60  
EKEEDALVAE PLVAVTQHQP ELHVDEHEEQ RVEHGVDDE 100

## (2) INFORMATION ON SEQ ID NO. 410:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 268 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

APISSNFCSE SIWGYCDQLK VSESTHVLQP FLPSILDGLI HLAAQFSSEV LNLVMETLCI 60  
VCTVDPEFTA SMESKICPFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMRLLIP120  
TLVSIMQAPA DKIPAGLCAT AIDILTTVVR NTKPPLSQLL ICQAFFPAVAQ CTLHTDDNAT180  
MQNGGECLRA YVSVTLEQVA QWHDEQGHNG LWYVMQVVSQ LLDPTTSEFT AAFVGAFFVST240  
LISKAGRELG ENLDQISSCH PSVKMAGG 268

## (2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

HIGPQALSAI LHGGIVICVK GTLCHSRESL ADEKLGKGR L CISYYCCQDI NGCRTKPCRN60

LVCWGLHYAD QSGNQPHLHW ALTGFNLGQL LEDVLSQ

97

(2) INFORMATION ON SEQ ID NO. 412:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 77 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

PPAILTEGWH EEIWSRFSPS SRPALEMRVE TKAPTAAVN SEVRGSRWL TTCITYHSPL60  
WPCSSCHWAT CSRVTDT

77

(2) INFORMATION ON SEQ ID NO. 413:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 62 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

IGFASIPPRI SGSPSILLAF YPHPPSPKLG PVLLCARETP KFRKRSIFYR GGFILDQKNK60  
KN

62

00673395-122100

## (2) INFORMATION ON SEQ ID NO. 414:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

DLIYNYYCYP SDLSFSAIDV IAISRSSHNV FNPALILMLR MEFLTSSLKE PQPPNTYTYT60  
SRIAK 65

## (2) INFORMATION ON SEQ ID NO. 415:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

LDLSPFHHVF PDPHPSFWLF TRIRHLRSWG QCYYVPGKPR NLGENQYFTG EDSSLTKKIK60  
KIKNTKKFMF LYCIPKECLY TVIILKENTS MLDI 94

## (2) INFORMATION ON SEQ ID NO. 416:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

09673395-122700

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GRRNDQLNLH IPQAGPFAGP YRLGWPLLSS GIRLPDWLVL HVSIKLKVIP WPPPGENQPH60

PASWGQWGRD FGLSEQLLEA AHD

83

(2) INFORMATION ON SEQ ID NO. 417:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

RRKASIIAFK GILLTLTQGV QSAREPILIS SSKMFLEENP WNVLKDVSGV RSSMWLAKGH60  
 LYLFPQLEFIN SCSLVSLGAE VWHIFKPVHS RIQ 93

(2) INFORMATION ON SEQ ID NO. 418:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

TLNPHKTLA KKVAVIFFCI QDSTANLVFC YKNLVSHFLL KRTRITGTHP QLHETPSFLN60  
 EHESIYVHPS THMKMLCSST GMDGIRIKPI WKLKYF 96

004227 5622960

## (2) INFORMATION ON SEQ ID NO. 419:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 68 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

YSFFFFLYQN NHLPLFFLER EEESGEEGKN AKCHFELLVH HTRGSPLMSA ASVHRPQVKE60  
RMRSSWTS 68

## (2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 60 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

KPSIHFFESC TKTIIFLYFS WSGKRRVEKK GRMQSVTLNF SFTTHVGVHS CQQPPCTGPR60

## (2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 52 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

004227 56224960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

52

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

52

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

YRYVFPTTHY GYNGVELOTV KFCFGLVSPD PPRQELPLPP YLPALKLCPI KLDTNLTGF 59

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: ORF



(A) ORGANISM: HUMAN

VTCLSLYVET NFTMITDLCN ISSLNFTIL KCLLGKLPF CSKGALHLLK PWGHTSSVAS60  
EGQILWVVGD NEVLTYVIL 79

(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

HKKTSSYSGV TVCSYDSIIR LKAGEICVQF NRTQLKGRQV GWERKLLSGG IRGNQSKTKF 60  
 -YCLQFNIIA IMCSGKHIPV LLDRVSFPFS GTKMVEGIIN PT 102

(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

SMPEQFGTQP RRPVVEGGDS SIELEPGLSS SAACNGKEMS PTRQLRRCPG SHCLTITDVP60  
VTVYATTRKP PAOSSKEMHP K 81

## (2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 62 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

GRASALACHR YRSDWASGLY ILAALSTSSS IGSSGGRGNW QQVGNYVKES PDVIISGCHR60  
 NI 62

## (2) INFORMATION ON SEQ ID NO. 428:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

REHQLLSGND FQGTSGVAWL VTSPSHYRQH WSSAQVPAQL KNLLLPLETS LAGFQIEKAY 60  
 FTENQKRLSL IPVEVNKSML STGLSTEGWN CQRNDDQMFR 100

## (2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

004227 35524960

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

NSHLNVTLLI IMLIFSISYR NQSLCLKLHRG LKNVYHSIFI

40

(2) INFORMATION ON SEQ ID NO. 430:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 31 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GGIGYKGRYL NSSNNGYNPF FHNHLGCFKA I

31

(2) INFORMATION ON SEQ ID NO. 431:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 53 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

TLPIIRDAKN QHNYQCHIQ VGILPNTTIK GRIKLONKIK KYKAFKNLTH HLK

53

(2) INFORMATION ON SEQ ID NO. 432:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 31 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

004227 9502/950

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

IALKHHPKWLW KKGLYPLFEL FRYLPLYPIP P

31

(2) INFORMATION ON SEQ ID NO. 433:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 85 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

CNIFQWGPSE HTCWTVTQIS SPEGKYFCIR GNSVLERNMF FISQIKTLSN GKLASNFFKY60  
SIFFSPLVVT GFYRSSYTV C FNSGP

85

(2) INFORMATION ON SEQ ID NO. 434:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 81 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

LLIREINQVF PLIYDAIYFS GGLQSTPVGR CKPYLLQKAN TFWSEETQFW RGICSLYLKS60

KLSLMVNWLL IFLSTVFFFP L

81

004227 5622460

## (2) INFORMATION ON SEQ ID NO. 435:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 95 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

YKSICLLEKI WFAPSNRCAL KAPTEIYCII DEGKDLVNFS YQKLVERTSC PTWLPGAQGF60  
FSEIVLRDPQ TCSPSPGATC ASSPRRQAVR SMRLS 95

## (2) INFORMATION ON SEQ ID NO. 436:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 81 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

SCAFLLLWGH SGPTWASMDP GLEQAHLHLF HLRQCGSRCQ EGLTSGPSRF LCARNERP60  
ILPPRLDPEV RAGQPSRKHT V 81

## (2) INFORMATION ON SEQ ID NO. 437:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 94 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

SRWNDSHPLL ISPLTSLKLL SSSKSHCQLP YVVLGPREPW NLAPWGGLIP AREHSCFSRD60  
TVACMGQHGP WADHVHSCFS GDTVGPHGPA WTLG 94

(2) INFORMATION ON SEQ ID NO. 438:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 91 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

HLEPHCLRWK RWRCACSSPG SMLAHVGPLC PQRSRNAHDQ PRVHAGPCRP LCPLRSRNAL60  
VPELNHPRVP GSKAPWDPEP HTEVNGNSLM S 91

(2) INFORMATION ON SEQ ID NO. 439:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 456 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

ITKTHKVDLG LPEKKKKKKV VKEPETRYSV LNDDYFADV SPLRATSPSK SVAHQAPEM 60

PLVKKKKKKK KGVSTLCEEH VEPETTLPAR RTEKSPSLRK QVFGHLEFLS GEKKNKKSPL120  
AMSHASGVKT SPDPRQGEET TRVGKKLKKH KKEKKGAQDP TAFSVQDPWF CEAREARDVG180  
DTCSVGKKDE EQAALGQKRK RKSPREHNGK VKKKKKIHQE GDALPGHSPK SRSMESPRK240  
GSKKKPVKVE APEYIPISDD PKASAKKKMK SKKKVEQPMI EEPALKRKKK KERESGVAGD300  
PWKEETDIDL EVVLEKKGNM DEAHIDQVRR KALQEEIDRE SGKTEASETR KWTGTQFGQW360  
DTAGFENEDQ KLKFLRLMGG FKNLSPSFSR PASTIARPNM ALGKKAADSL QQNLQRDYDR420  
AMSWKYSRGA GLGFSTAPNK IFYIDRNASK SVKLED 456

004227 3522360

(2) INFORMATION ON SEQ ID NO. 442:

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN  
(A) ORGANISM: HUMAN

```
VRVCFLLPRV SCYPTLSLLL FLPFQSWLLD DWLLYLLFGL HLFLCGGLRV ITYGDVFRSL 60
NFDWLLFTSF PRAALHGGPG LGVAWEGISL LVDEFFLLHL PIVFSGALPL PFLPQGCLFL120
ILLPH                                         125
```

(2) INFORMATION ON SEQ ID NO. 442:

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN  
(A) ORGANISM: HUMAN

ACPWATLLEG DVALKGETSA K 381

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 43 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

DHHNKLSLQS QTYYILLSVN GEKISPYVLW VKCCNRLGLS NLP

43

(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

MVISIFPPLL YKLIETHLLL YKLTFINTNK RLVLISOFIGH EPRNN

45

(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

GKPKNCCDEF QGKLDNPNLL QHFTHKTYGL IFSPLTDSSI

40

(A) LENGTH: 78 amino acids



(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

GVGGGALRSA ALPWRTLPLT STCSRCTKPS TAEMEHLVQS WCLLNILMLQ THDFKWPLQR60  
 RSVNKS WNPL MMKCLQLI 78

(2) INFORMATION ON SEQ ID NO. 446:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 125 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

RLRRRGWRSP FGGAPMAHIT INQYLQQVYE AIDSRDGASC AELVSFKKHPH VANPRLQMAS 60  
 PEEKCQQVLE PPYDEMFAAH LRCTYAVGNH DFIEAYKCQT VIVQSFLRAF QAHKEENWAL120  
 LSCMQ 125

(2) INFORMATION ON SEQ ID NO. 447:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 80 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

004227 5622/960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

MSCKHFIIRG FQDLLTLLW RGHLKSWVCN MRMFKRHQLC TRCSISAVDG FVHLLQVLVN60  
GNVRHGSAAE RRAPPPTPQA 80

## (2) INFORMATION ON SEQ ID NO. 448:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

RSRGFSCVQT PCHFREVTA CVISLWQQVG GLPQGRWPE MCFRSLTHHS LHTRREHHSW60  
SILRMEI 67

## (2) INFORMATION ON SEQ ID NO. 449:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

PITPYTHDVN TTPGAFSEWR FEFHVAASHT QTCHHSPHTH SRHSTAMSQK KFLVSDLKVL60

## (2) INFORMATION ON SEQ ID NO. 450:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00427 3524360

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

RATSGRSGFI KPSNLKQGTS FGSWLLNVVS GCVGNDGRFV CEKLPHGIIQI SILRMLQEW60  
SRRVCRE

67

(2) INFORMATION ON SEQ ID NO. 451:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

SASHPESRLC RGGADMQAPR GTLVFALVIA LVPVGREPSS QGSQSALQTY ELGSENVKVP 60  
IFEEDTPSVM EIEMEELDKW MNSMNRNADF ECLPTLKEEK ESNHNPSDSE S 111

(2) INFORMATION ON SEQ ID NO. 452:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

EEWALEETAK GSCVYVDLKL IKFVSSSSSV GSLSRLPQGL LLENMSAIQ V

51

(2) INFORMATION ON SEQ ID NO. 453:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids

004221 0602960

RRGVSEFLLSR QKWYHYVAAL QSPRARSLN HLLSRFFFFL RVGVSLCCPK TRPGNCWGAK60  
GIAPVPQASR VGR 73

(2) INFORMATION ON SEQ ID NO. 457:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 81 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 457:

DQPSLPFIRH KTLNLTSMAT KIIGSPETKW IDATSGIYNS EKSSNLSVTT DFSESLQSSN60  
IESKEINGIH DESNAFESKA S 81

(2) INFORMATION ON SEQ ID NO. 458:

```
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
```

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

QLISPKAFRV LILNPKKSME FMMKAMLLNQ KHLESIFFEK P

41

(2) INFORMATION ON SEQ ID NO. 459:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

IPEVASIHV SGEPIILVAI LVRLRVLCRI NGREGW

36

(2) INFORMATION ON SEQ ID NO. 460:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

NSEGFRRNQL LQIDLKIFLS CKFQKLHQST LFQVNL

36

(2) INFORMATION ON SEQ ID NO. 461:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

0042221-00000000

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

GRRNDQLNLH IPQAGPFAGP YRLGWPLLSS GIRLPDWLVL HVS IKLKVIP WPPPGENQPH60  
PASWGQWGRD FGLSEQLLEA AHD 83

(2) INFORMATION ON SEQ ID NO. 462:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 93 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

RRKASIIAFK GILLTLTQGV QSAREPILIS SSKMFLEENP WNV LKDVSGV RSSMWLAKGH60  
LYLFQLEFIN SCSLVSLGAE VWHIFKPVHS RIQ 93

(2) INFORMATION ON SEQ ID NO. 463:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 96 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

TLNPHKTLISA K KARVIFFCI QDSTANLVFC YKNLVSHFLL KRTRITGTHP QLHETPSFLN60  
EHESIYVHPS THMKMLCSST GMDGIRIKPI WKLKYP 96

004221 4622950

## (2) INFORMATION ON SEQ ID NO. 464:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

NLFTMKFLPE FSPFDTNSMH VSTFETQPNV ISVKSSLSLP SSNLPSPRVY LPFCAHLSYS60

SMLFYNCDSP GSLGAI

76

## (2) INFORMATION ON SEQ ID NO. 465:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

NQRMIEIYSN TKTERKCHST LKAANTIDHF IWLPSQESH NCKITCYCNS NVHKMAGKL 59

## (2) INFORMATION ON SEQ ID NO. 466:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

09673395-122700



(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

HATVTQMCTK WQVNSRRRQI TAWKTQGRFY RNDIWLSLEG

40

(2) INFORMATION ON SEQ ID NO. 467:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 41 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

IPLQRFSLLT SLFFVLKLDL LVVHASLSLV TVNNLPTSSN Q

41

(2) INFORMATION ON SEQ ID NO. 468:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

LSKAIYFCKK AAACINHDHS STLNKERKRF LSLTQSLPLC HSPRGWGWTA HSKLTRLAIC60  
EYFSK

65

(2) INFORMATION ON SEQ ID NO. 469:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

004227 5522960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

(2) INFORMATION ON SEQ ID NO. 470:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

(2) INFORMATION ON SEQ ID NO. 471:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

```
AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNPGPSSSLR RAFRRRELPF 60
PACHEIGLGA EAGSGPPPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120
PGVTEVTIIE KPPAERHMIS SWEQKNNCVM PEDVKNFYLM TNGFHMFTSV KLDEHIIPLG180
SMAINSISKL TQLTQSSMYS LPNAPTLDL EDDTHEASDD QPEKPHFDSR LVIFELDSN240
GSGKVCIVYK SGKPALAEDT EIWFLDRALY WHFLTDTFTA YYRLLITHLG LPQWQYAFTS300
YGISPQAKQW FSMYKPITYN TNLLTEETDS FVNKLDP SKV FKSKNKIVIP KKKGPVQ PAG360
GQKGPSGPGS PSTSSTS KSS SGSGETPPGK LRHPSFQFA
```

## (2) INFORMATION ON SEQ ID NO. 472:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

RSAGGFSSMV TSVTPGEDSR MRVMPRVFS RCGLLQPSFG DDASSSMARD RDSRAAGAGG60  
 GPDPASAPRP ISWHAGNGSS RRLKARRSDD GPGGLV 96

## (2) INFORMATION ON SEQ ID NO. 473:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

KYVSHANISI YKWRTLTLALL FSYKIPNFVI ILSGITLYCK NASYFTFKFD NVCDEL 56

## (2) INFORMATION ON SEQ ID NO. 474:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

002227 56222960

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

WIFRVCCISR EIHFYILFYI KHLDKGHLTH FKKHKCI

37

(2) INFORMATION ON SEQ ID NO. 475:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 33 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

PKGLSIKVRRL NLDTRRKRCR LLNFIIHHIH CQI

33

(2) INFORMATION ON SEQ ID NO. 476:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

HIKIEFFGQN FWEAMHPTWA DIQPELFSRG EWYWQFMAEI HSDWLESMLY QLLNILSITL60  
AYCYYYISSI YRQKGHFRNI

80

(2) INFORMATION ON SEQ ID NO. 477:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

004221" 502224960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

400

## (2) INFORMATION ON SEQ ID NO. 480:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 225 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

SSSGWRVARG SRHSSWGRRL GNLWSQLCRA LQGLPRSTSS IRWLVMWLVL VPKPRKGAV 60  
 SLCGPLFLVP GAGIIQDNLL HRVQASHTGS RQGLPRQSRL DHLLVGCSR VMAIWHLVIG120  
 TSRTMVMIVP WSMWKGIGRQ HLCTCWIPLR FKLRELPGE RSGEVLGVTH GGEGQGPFQL180  
 PDAQDILGLG IISRVYGWQI QACSVPVQAG AVAPSPCYRP RSLLR 225

## (2) INFORMATION ON SEQ ID NO. 481:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

KQRMQSSHRL HFKA RVC GGL RGRALHNRFP GGQRASRGGT EKNQPGVLPT SLSQNAVRTR 60  
 PQTWPGLSDL GMNGVTREPP EGWAEAPVEE PHTLPLSAAA AGCFFYSWAS CRHECSEARW120  
 AHAPS 125

## (2) INFORMATION ON SEQ ID NO. 482:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein

00221"56E2960

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

VAMTAKDCSI MIALSPCLQD ASSDQRPVVP SRSRFAFSV SVLDLDLKPY ESIPHQYKLD60  
GKIVNYYSKT VRAKDNVMS TRFKESEDCT LVLHKV 96

(2) INFORMATION ON SEQ ID NO. 483:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 66 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

LHCLPVCRRMP ALIKGLWSLH RGPGLPFPCL CWTLTSSPTR AFPISINWTA RSSTIIQRLY60  
VPKTTP 66

(2) INFORMATION ON SEQ ID NO. 484:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 109 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

NKAFTRIRES D MSPGWERRTI QNVFPGLNGH FHFKS VSSFL GHSTHFLHSL SRKLFVLVFN 60  
SMSPRGNPTS KGVKSKNIHN QRSPTTNI SIIQPSHYVQ VSKTLQGKS 109

0567395-12200

## (2) INFORMATION ON SEQ ID NO. 485:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

CSSIPCLQEA IPPQKGLKAK TFTTKGHPTQ QKISLSFSLH IMFKFQRHCR ERVRPCGELM60  
CNLRFP 66

## (2) INFORMATION ON SEQ ID NO. 486:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

ARPAPAGREG RGEGEATSRR CGVGHRAGPR EPAPHGAAAV RPTPGPHHHC AALSGAENYR 60  
SRHAMKLASA LRRGPALHPL PPRANRGREF WRRRHRPRGW AAASRTWRS 109

## (2) INFORMATION ON SEQ ID NO. 487:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 389 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

004427 5522/950



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```
AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNPGPPSSLR RAFRRRELPF 60
PACHEIGLGA EAGSGPPPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120
PGVTEVTIIE KPPAERHMIS SWEQNNNCVM PEDVKNFYLM TNGFHTWSV KLDEHIIPLG180
SMAINSISKL TQLTQSSMYS LPNAPTLADL EDDTHEASDD QPEKPHFDSR SVIFELDSCN240
GSGKVCLVYK SGKPALAEDT EIWFLDRALY WHFLTDTFTA YYRLILITHLG LPQWQYAFTS300
YGISPQAKQW FSMYKPITYN TNLLTEETDS FVNKLDPSKV FKSKNKIVIP KKKGPVQPAG360
GQKGPSGPGSG PSTSSTSKSS SGSGNPTRK                                     389
```

(2) INFORMATION ON SEQ ID NO. 488:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 96 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```
RSAGGFMMV TSVTPGEDSR MRVMPRVSEF RCGLLQPSPG DDASSSMARD RDSRAAGAGG60
GPD PASAPRP ISWHAGNGSS RRLKARRSDD GGPGLV                               96
```

(2) INFORMATION ON SEQ ID NO. 489:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 152 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```
LAAGRGKEEE MGFEDHGLPF LPLTHHTPPF PLSLSPLPKK KKKETFIMNQ QGFSPYQREM 60
WKELKKPPFV PNSTLPIFYA TQTLSEFWVPF LQMDLLRRII VFHVFSQPVT KINICIYNLY120
YCYIFVDNTF RWCWVIYYNL NLGISFGLPQ SC                                   152
```

09673396-32700



KGSLPPTKQG KLGQLAPGHQ GQLPTWLLPF LGFFQGFNGS LGVGEVASCL HWYWPRRWAG60  
HGGGGVNIWF ISHPAGCKPL VK 82

(2) INFORMATION ON SEQ ID NO. 495:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

RVPSPQLNKG NWANWPLVIK VNSQLGSCLS LGSSRALGTA WGWEKWLPAF TGTGPEGGQG60  
MEEGYLIISG FPTLLAVNL 79

(2) INFORMATION ON SEQ ID NO. 496:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 88 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

IQKVQYYTSP AAFVNGSLHS HWGTTVCMGR NSKCPHCGHW VGSAFCQGVC RNWLISVCQS60  
DQHTKVSAIK NVASLHPPSC YSGPSNLM 88

(2) INFORMATION ON SEQ ID NO. 497:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 98 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: stindividual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

SHTSEKRRGT REEVTPASRS SISGVKRGTV ALPSWLRMRK SFLQWEEIHF SIPVQSDFMG60  
PVLNSDCIIN TIKRDSEMGs RIHWONSKAY NTALMDPT 98

(2) INFORMATION ON SEQ ID NO. 498:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 83 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

AGYTPVSSTI RQLHQITGPR VTGWRMQGSH ILYGRDFGVL ITLAYRNKPI PADSLTKGTP60  
HPMTTMRALA VSAHAHSCTP MAV 83

(2) INFORMATION ON SEQ ID NO. 499:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 85 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

GKICEYVNFL SLRDDRMFPY FSCKENNILT YTSCRKYHLF PLYYSTMFTL LYCQAESIKN60  
VHIHFELCIL FLKKGAGLWH WAGHD 85

004221" 9602260

## (2) INFORMATION ON SEQ ID NO. 500:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

SYRLKGIGKC VFSRDHVESE QCWQTLPRKS CFSRCPCFGI SFLGRKKKSS LTIVNSISYF60  
 SFCCSNGFPP TIIPSIYVLL YSPLSPVTFE SNTPEPKF 98

## (2) INFORMATION ON SEQ ID NO. 501:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

VSSCTSNHGV RSSLSSGEHK CTERDVLVRT TKELPSLSLT QAMCTCDAE CAGVGGGHVA60  
 PPEHFLTGKL GDPLLNVFVE IRTVSFT 87

## (2) INFORMATION ON SEQ ID NO. 502:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00/00/00 00/00/00

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

TPKTLGCLLV SRVEQAQRES LGPELKEFIE PWQTGSKQPI LAAVLRRECG GQI 53

(2) INFORMATION ON SEQ ID NO. 503:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

PSGPFSSLES TLLLQQVQAA IASFLSDCNS PIREPCFYIC PPHSLNTAA RMGCLLPVCH60  
GSINSLSSGP KDSRWACSTR DTSRQPSVLG V 91

(2) INFORMATION ON SEQ ID NO. 504:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

VFIYDSLIIIP TSISSVHTVC QMFRAEPVSR ILLSDYGGFT TRPGSNSLGS KVGHSSMHR 59

(2) INFORMATION ON SEQ ID NO. 505:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual

004227 0602/950

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

DRKEWNQKID PVFSYIQSST SEFLFLNIGV LALFLKDALY LKRKLDERTG CGAVKYFRPR60  
SVYTFYRRNE VL 72

(2) INFORMATION ON SEQ ID NO. 506:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 102 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

SILGPGLCTH FIEEMKYSEV FWLPFHFCV LNLSDHTYIV LLGAVVSFIK PLACVQKFLK 60  
GNTSNAYPLL ACYACFTAI AVCFTVFVKI PLSFPLVTGK AC 102

(2) INFORMATION ON SEQ ID NO. 507:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

NNEHKMLFII TSICEISYCK TTTGLLLNSL VIVFRLEMP TLVINITYN VFLGRHFIKC60  
IMPWLLLR 68

00422T"56224960



## (2) INFORMATION ON SEQ ID NO. 508:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

LKFLQVLKFF FYSLHWIYVF LIPNMFNWDV CHSRAARQTF KSNSHTAELA FLLTQKFRKL60  
TVTVT 65

## (2) INFORMATION ON SEQ ID NO. 509:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

GPRAHWPLPN TMLEPKRANM GPEYNGDIFM FQPFNLTCLL LSFPPISSNL FOLTYYLQGI  
ITSSYRIPSS LMSCPQKY 78

## (2) INFORMATION ON SEQ ID NO. 510:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

004227 55552950

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

SLKLLGFLDV ENTPCARHSI LYGSLGSVVA GFGHFLTSE YLYFLFLYVL KKAFLYIMNY60  
FFF 63

(2) INFORMATION ON SEQ ID NO. 511:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 53 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

SFVKWSPNLK LGNYEEKIA RYLLRSACRS AVGLVTIGSK VLLQWQILWP LSG 53

(2) INFORMATION ON SEQ ID NO. 512:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 43 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

ICCRACHHWK QGPTSVADLV AFEWLKTTTL HRAGAMHRHP SLP 43

(2) INFORMATION ON SEQ ID NO. 513:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 37 amino acids

004221 5522450

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

QALQQIYRQT LTDTGQFSLL RNFLVLSWVT ILQNFTT

37

(2) INFORMATION ON SEQ ID NO. 514:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 228 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

TGGARARRPL SAVARPARSS DPLRSAPLGP APPVNMIRCG LACERCRWIL PLLLSAIAF 60  
 DIIALAGRGW LQSSDHGQTS SLWWKCSQEG GGSGSYEEGC QSLMEYAWGR AAAAMLFCGF120  
 IILVICFILS FFALCGPQML VFLRVIGLL ALAAVFQIIS LVIYPVKYTQ TETLHANRAV180  
 TYIYNWAYGF GWAATIILIG CAFFFCCLPN YEDDLLGNAK PRYFYTSA 228

(2) INFORMATION ON SEQ ID NO. 515:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 94 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

004227 5522450

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

DPLPPPSWEH FHHSEDVWPW SLDCNQPRPA SAMMSKAMAL SRSRGRIQRQ RSQARPQRIM60  
 LTGGAGPSGA ERSSEERAG RATAESGLRA RAPP 94

## (2) INFORMATION ON SEQ ID NO. 516:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 208 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

TLPKNGFKVA WRNSFFFWSP SQQQRFSPTE IPKLGRCEV PGLGIAQKVI FVVGEAAEEE 60  
 GTADQDNRG C PPKAVGPVID VSDSTVGMKG EGLGLVHG V YQGDDLEHSS QGKETSNNHSQL20  
 EDKHLGSTEG EEGEDETDHQ DDEATEEHGS RCSTPRVLHE ALTALLVGPA AAALLGAFFP180  
 QRGRLAVVAR LQPAAAGQRD DVEGDGAE 208

## (2) INFORMATION ON SEQ ID NO. 517:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 204 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

PSCPPPEMKKE LPVDSCLPRS LELHPQKMDP KRQHIQLLSS LTECLTVDP L SASVWRQLYP 60  
 KHLSQSSLLL EHLSSWEQI PPKVQKSLQE TIQSLKLTNQ ELLRKGSSNN QDVVTCDMAC120  
 KGLLQQVQGP RLPWTRLLLL LLVFAVGFLC HDLRSHSSFQ ASLTGRLLRS SGFLPASQQA180  
 CSKFTPTVCK VTGWLGEKCR FGVP 204

002227-55554950

(2) INFORMATION ON SEQ ID NO. 518:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 90 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

PEVMAQEAYS EDQQQQEEPR PGQPRTLNL QALAGHVTG DDILVVTATL PQQLLVGKLE60  
GLNGFLORLL YLLGNLLPGA EOVLQKAGL 90

(2) INFORMATION ON SEQ ID NO. 519:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

GTPKRHFSPN QPVTLQTVGV NLEHACWLAG KKPDDRSNRP VREAWKELCD RRSWHRKPTA60  
KTSSNRRSRV QGSRGP 76

(2) INFORMATION ON SEQ ID NO. 520:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 355 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

FRHSMNGCEK DSSSTDSANE KPALIPREKK ISILEEPSKA LRGVTGPNIE KSVKDLQRCT 60  
VSLTRYRVMI KEEVDSSVKK IKAFAELHN CIIDKEVSLM AEMDKVKEEA MEILTARQKK120  
AEELKRLTDL ASQMAEMQLA ELRAEIKHFV SERKYDEELG KAARFSCDIE QLKAQIMLCG180  
EITHPKNNYS SRTPCSSLLP LLNAHAATSG QSNFNRKSS THNKPSEGKA ANPKMVSSLP240  
STADPSHOTM PANKQNGSSN QRRRFNPQYH NNRLNGPAKS QGSGNEAEPL GKGNSRHEHR300  
RQPHNGFRPK NKGGAKNQEA SLGMKTPEAF AHSEKPRRRQ ARCRTPREGQ GPFRG 355

(2) INFORMATION ON SEQ ID NO. 521:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 120 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

NQNVKNRGTQ KKCLPSVEKL PNPPWGQKNA TVKTPNRKLT PERPLALPRC PAACLPSGL 60  
FRMGRGLGGL HPQGSLLIFG TAFVFGPEAV VRLSSVFVAA VALSQWLGF I PTALRLGRPI120

(2) INFORMATION ON SEQ ID NO. 522:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 116 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

RAVRISMASS LTLISISAIN TSLSMQLCN SAKAALIFFT ELSTSSLIMT RYLVRETQVR 60  
CKSETDFSIF GPVTPRSAFE GSSSIEIFFS RGIRAGFSLA ESVDLSFSQ PFMLCR 116

004227 56224950

(2) INFORMATION ON SEQ ID NO. 523:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 130 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

RRQRKAEPGA CALGRVGSEC IPEPGARRTA QAAGLRVS VG AANTKVRELK HFRFLGLLRS 60  
CRSEMEVDAP GVDGRDGLRE RRGFSEGG RQ NFDVRPQSGA NGLPKHSYWL DLWLFILFDV120  
VVFLFVYFLP 130

(2) INFORMATION ON SEQ ID NO. 524:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

ISANSKWQKI HKEKHHHIEK DEKPEVQPVG VFGKPICPRL RPHIEVLPPS LAKASPLPET60  
ISTINTRCVH LHLAPAAS 78

(2) INFORMATION ON SEQ ID NO. 525:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

(2) INFORMATION ON SEQ ID NO. 526:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

(2) INFORMATION ON SEQ ID NO. 527:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

(2) INFORMATION ON SEQ ID NO. 528:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 102 amino acids



- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

RNHAKIQLPM QAPQSLILSS QFCCQATVVW RLVGCCPCCN EWEEVDSGMV ETFTSSSPAT 60  
GIPPRPVLCC GGRFKSKLL FEVGFAVWFK CMMLLRGKAI QG 102

(2) INFORMATION ON SEQ ID NO. 531:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004221 3622360

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

```

CCTGGAAACA AGATCCAAAC CCAAGTGACC CCGCCGGAAA GTGACCCAGT CAGGTTTAAA 60
AATTCCAACA AACCAGCGTG AACAAATAGA CCGACCAACC AAATATACAA TCCGTCAAAA 120

TACATTCACT TCCACTACGA AACCCCAACA AAGGGTGTGA ATGCCGCCC AGGAGAGACG 180
GTTTTGGTTT CATCAAGTGT GTGGATCGTG ATGTTTCGTAT GTTCTTCCAC TTCAGTGAAA 240
TTCTGGATGG GAACCAGCTC CATATTGCAG ATGAAGTAGA GTTTACTGTG GTTCTGATA 300
TGCTCTCTGC TCAAAGAAAT CATGCTATTA GGATTAAAAA ACTTCCAAG GGCACGGTTT 360
CATTTTCATT CCATTCAGAT CACCGTTTTT TGGGCACGGT AGAAAAAGAA GCCACTTTTT 420
CCAATCCTAA AACCCTAGC CCAAATAAAG GCAAAGAGAA GGAGGCTGAG GATGGCATT 480
TTGCTTATGA TGAAGTGGG GTGAACTGA CTATTGCTTT TCAAGCCAAG GATGTGGAAG 540
GATCTACTTC TCCTCAAATA GGAGATAAGG TTGAATTTAG TATTAGTGAC AAACAGAGGC 600
CTGGACAGCA GGTGCAACT TGTGTGCGAC TTTTAGGTCG TAATTCTAAC TCCAAGAGGC 660
TCTTGGGTTA TGTGGCAACT CTGAAGGATA ATTTTGGATT TATTGAAACA GCCAATCATG 720
ATAAGGAAAT CTTTTTCCAT TACAGTGAGT TCTCTGGTGA TGTGATAGC CTGGAAGTGG 780
GGGACATGGT CGAGTATAGC TTGTCCAAAG GCAAAGGCAA CAAAGTCAGT GCAGAAAAAG 840
TGAACAAAAC AACTCAGTG AATGGCATT  CTGAGGAAGC TGATCCCACC ATTTACTCTG 900
GCAAAGTAAT TCGCCCCCTG AGGAGTGTTG ATCCAACACA GACTGAGTAC CAAGGAATGA 960
TTGAGATTGT GGAGGAGGGC GATATGAAAG GTGAGGTCTA TCCATTTGGC ATCGTTGGGA 1020
TGGCCAACAA AGGGGATTGC CTGCAGAAAG GGGAGAGCGT CAAGTTCCAA TTGTGTGTCC 1080
TGGGCCAAAA TGCACAACT ATGGCTTACA ACATCACACC CCTGCGCAGG GCCACAGTGG 1140
AATGTGTGAA AGATCAGTTT GGCTTCATTA ACTATGAAGT AGGAGATAGC AAGAAGCTCT 1200
TTTTCCATGT GAAAGAAGTT CAGGATGGCA TTGAGCTACA GGCAGGAGAT GAGGTGGAGT 1260
TCTCAGTGAT TCTTAATCAG CGCACTGGCA AGTGCAGCGC CTGTAATGTT TGGCGAGTCT 1320
GTGAGGGCCC CAAGGCTGTT GCAGCTCCTC GACCTGATCG GTTGGTCAAT CGCTTGAAGA 1380
ATATCACTCT GGATGATGCC AGTGCTCCTC GCCTAATGGT TCTTCGTCAG CCAAGGGGAC 1440
CAGATAACTC AATGGGGTTT GGTGCAGAAA GAAAGATCCG TCAAGCTGGT GTCATTGACT 1500
AACCACATCC ACAAAGCACA CCATTAATCC ACTATGATCA AGTTGGGGGG AATCTGGTGA 1560
AGGGTTCTGA ATATCTCCCT CTTTCATCCCT CCCGAAATCT GGAATACTTA TTCTATTGAG 1620
CTATTACACC AGTTTTAACA CCTTCCTCGT GTTATGTTTA AAAAAATAAA TAAATTTAAG 1680
AAAACCATTT TAAATAATGA AAAGTTGG

```

09673395.12200

## (2) INFORMATION ON SEQ ID NO. 532:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2128 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227 5652950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

CTGTATCCTA ATTTCTTGGT GAATGAACTC ATTCTTAAAC AGAAGCAAAG ATTTGAGGAA 60  
 AAGAGGTTCA AATTGGACCA CTCAGTGAGT AGCACCAATG GCCACAGGTG GCAGATATTT 120  
 CAAGATTGGT TGGGAACTGA CCAAGATAAC CTTGATTTGG CCAATGTCAA TCTTATGTTG 180  
 GAGTTACTAG TGCAGAAGAA GAAACAACCTG GAAGCAGAAT CACATGCAGC CCAACTACAG 240  
 ATTCCTTATGG AATTCCTCAA GGTGCAAGA AGAAATAAGA GAGAGCAACT GGAACAGATC 300  
 CAGAAGGAGC TAAGTGTTTT GGAAGAGGAT ATTAAGAGAG TGAAGAAAT GAGTGGCTTA 360  
  
 TACTCTCCTG TCAGTGAGGA TAGCACAGTG CCTCAATTTG AAGCTCCTTC TCCATCACAC 420  
 AGTAGTATTA TTGATTCCAC AGAATACAGC CAACCTCCAG GTTTCAGTGG CAGTTCTCAG 480  
 ACAAAGAAAC AGCCTTGGTA TAATAGCACG TTAGCATCAA GACGAAAACG ACTTACTGCT 540  
 CATTTTGAAG ACTTGGAGCA GTGTTACTTT TCTACAAGGA TGTCTCGTAT CTCAGATGAC 600  
 AGTCGAACTG CAAGCCAGTT GGATGAATTT CAGGAATGCT TGTCCAAGTT TACTCGATAT 660  
 AATTCAGTAC GACCTTTAGC CACATTGTCA TATGCTAGTG ATCTCTATAA TGGTTCCAGT 720  
 ATAGTCTCTA GTATTGAATT TGACCGGGAT TGTGACTATT TTGCGATTGC TGGAGTTACA 780  
 AAGAAGATTA AAGTCTATGA ATATGACACT GTCATCCAGG ATGCAGTGGA TATTCAATAC 840  
 CCTGAGAATG AAATGACCTG CAATTGCGAA ATCAGCTGTA TCAGTTGGAG TAGTTACCAT 900  
 AAGAACCTGT TAGCTAGCAG TGATTATGAA GGCAGTGTTA TTTTATGGGA TGGATTACCA 960  
 GGACAGAGGT CAAAGGTCTA TCAGGAGCAT GAGAAGAGGT GTTGGAGTGT TGACTTTAAT1020  
 TTGATGGATC CTAAACTCTT GGCTTCAGGT TCTGATGATG CAAAAGTGAA GCTGTGGTCT1080  
 ACCAATCTAG ACAACTCAGT GGCAAGCATT GAGGCAAAGG CTAATGTGTG CTGTGTTAAA1140  
 TTCAGCCCCCT CTTCCAGATA CCATTTGGCT TTCGGCTGTG CAGATCACTG TGTCCACTAC1200  
 TATGATCTTC GTAACACTAA ACAGCCAATC ATGGTATTCA AAGGACACCG TAAAGCAGTC1260  
 TCTTATGCAA AGTTTGTGAG TGGTGAGGAA ATTGTCTCTG CCTCAACAGA CAGTCAGCTA1320  
 AAACGTGTGA ATGTAGGGAA ACCATACTGC CTACGTTTCT TCAAGGGTCA TATCAATGAA1380  
 AAAAACTTTG TAGGCCTGGC TTCCAATGGA GATTATATAG CTTGTGGAAG TGAAAATAAC1440  
 TCTCTCTACC TGTACTATAA AGGACTTTCT AAGACTTTGC TAACTTTTAA GTTTGATACA1500  
 GTCAAAAGTG TTCTCGACAA AGACCGAAAA GAAGATGATA CAAATGAATT TGTTAGTGCT1560  
 GTGTGCTGGA GGGCACTACC AGATGGGGAG TCCAATGTGC TGATTGCTGC TAACAGTCAG1620  
 GGTACAATTA AGGTGCTAGA ATTGGTATGA AGGGTTAACT CAAGTCAAAT TGTACTTGAT1680  
 CCTGCTGAAA TACATCTGCA GCTGACAATG AGAGAAGAAA CAGAAAATGT CATGTGATGT1740  
 CTCTCCCCAA AGTCATCATG GGTTTTGGAT TTGTTTTGAA TATTTTTTTC TTTTTTCTT1800  
 TTCCCTCCTT TATGACCTTT GGGACATTGG GAATACCCAG CCAACTCTCC ACCATCAATG1860  
 TAACCTCATG GACATTGCTG CTCTTGGTGG TGTTATCTAA TTTTTGTGAT AGGGAAACAA1920  
 ATTCTTTTGA ATAAAAATAA ATAACAAAAC AATAAAAGTT TATTGAGCCA CAAAAAAA1980  
 AAAAAAAAAA AAAAAAAAAA ACAAAGAGA AAACAAAGGT TACGAAGTAG CATATGTGAA2040  
 CTATAATGTA ACAGTGAATA ATTTGTAAAG TTCGTATTTT CCAACCTCTT TGGGAATTAC2100  
 ACATATCAAT ATAAACAAAA TATAAGT 2128

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 533:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2640 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227" 502222950

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

CTAGCAAGCA GGTAAACGAG CTTTGTACAA ACACACACAG ACCAACACAT CCGGGGATGG 60  
 CTGTGTGTTG CTAGAGCAGA GGCTGATTAA ACACTCAGTG TGTTGGCTCT CTGTGCCACT 120  
 CCTGGAAAT AATGAATTGG GTAAGGAACA GTTAATAAGA AAATGTGCCT TGCTAACTGT 180  
 GCACATTACA ACAAAGAGCT GGCAGCTCCT GAAGGAAAAG GGCTTGTGCC GCTGCCGTTT 240  
 AAACCTGTCA GTCAACTCAT GCCAGCAGCC TCAGCGTCTG CCTCCCCAGC ACACCCTCAT 300  
 TACATGTGTC TGTCTGGCCT GATCTGTGCA TCTGCTCGGA GACGCTCCTG ACAAGTCGGG 360  
 AATTTCTCTA TTTCTCCACT GGTGCAAAGA GCGGATTTCT CCCTGCTTCT CTTCTGTCAC 420  
 CCCCCTCCT CTCCCCCAGG AGGCTCCTTG ATTTATGGTA GCTTTGGACT TGCTTCCCCG 480  
 TCTGACTGTC CTTGACTTCT AGAATGGAAG AAGCTGAGCT GGTGAAGGGA AGACTCCAGG 540  
 CCATCACAGA TAAAAGAAAA ATACAGGAAG AAATCTCACA GAAGCGTCTG AAAATAGAGG 600  
 AAGACAACT AAAGACCAG CATTGAAGA AAAAGGCCTT GAGGGAGAAA TGGCTTCTAG 660  
 ATGGAATCAG CAGCGGAAAA GAACAGGAAG AGATGAAGAA GCAAAATCAA CAAGACCAGC 720  
 ACCAGATCCA GGTCTAGAA CAAAGTATCC TCAGGCTTGA GAAAGAGATC CAAGATCTTG 780  
 AAAAGCTGA ACTGCAATC TCAACGAAGG AAGAGGCCAT TTTAAAGAAA CTAAAGTCAA 840  
 TTGAGCGGAC AACAGAAGAC ATTATAAGAT CTGTGAAAGT GGAAAGAGAA GAAAGAGCAG 900  
 AAGAGTCAAT TGAGGACATC TATGCTAATA TCCCTGACCT TCCAAAGTCC TACATACCTT 960  
 CTAGGTTAAG GAAGGAGATA AATGAAGAAA AAGAAGATGA TGAACAAAAT AGGAAAGCTT 1020  
 TATATGCCAT GGAAATTTAA GTTGAAAAAG ACTTGAAGAC TGGAGAAAGT ACAGTTCTGT 1080  
 CTTCCAATAC CTCTGGCCAT CAGATGACTT TAAAAGGTAC AGGAGTAAAA GTTTAAGATG 1140  
 ATGGGCAAAA GTCCAGTGA TTCAGTAAAG TGCTAATCAC AAGTTGGAGG TCAATGGCAC 1200  
 CGATGGCCTG GCACCAAGTTG AAGTAGAGGA ACTTCTAAGA CAAGCCTCAG AGAGAACTC 1260  
 TAAATCCCCA ACAGAGTATC ATGAGCCTGT ATATGCCAAT CCCTTTTACA GGCCTACAAC 1320  
 CCCACAGAGA GAAACGGTGA CCCCTGGACC AAACCTTCAA GAAAGGATAA AGATTTAAAC 1380  
 TAATGGACTG GGTATTGGTG TAAATGAATC CATACACAAT ATGGGCAATG GTCTTTCAGA 1440  
 GGAAAGGGGA AACAACTTCA ATCACATCAG TCCCATTCCG CCAGTGCCCTC ATCCCCGATC 1500  
 AGTGATTCAA CAAGCAGAAG AGAAGCTTCA CACCCCGCAA AAAAGGCTAA TGACTCCTTG 1560  
 GGAAGAATCG AATGTCATGC AGGACAAAGA TGCACCCTCT CCAAAGCCAA GGCTGAGCCC 1620  
 CAGAGAGACA ATATTGGGA AATCTGAACA CCAGAATTCT TCACCCACTT GTCAGGAGGA 1680  
 CGAGGAAGAT GTCAGATATA ATATCGTTCA TTCCCTGCCT CCAGACATAA ATGATACAGA 1740  
 ACCGGTGACA ATGATTTTCA TGGGGTATCA GCAGGCAGAA GACAGTGAAG AAGATAAGAA 1800  
 GTTTCTGACA GGATATGATG GGATCATCCA TGCTGAGCTG GTTGTGATTG ATGATGAGGA 1860  
 GGAGGAGGAT GAAGGAGAAG CAGAGAAACC GTCCTACCAC CCCATAGCTC CCCATAGTCA 1920  
 GGTGTACCAG CCAGCCAAAC CAACACCACT TCCTAGAAAA AGATCAGAAG CTAGTCCTCA 1980  
 TGA AACACA AATCATAAAT CCCCCACAA AAATTCCATA TCTCTGAAAG AGCAAGAAGA 2040  
 AAGCTTAGGC AGCCCTGTCC ACCATTCCCC ATTTGATGCT CAGACAACTG GAGATGGGAC 2100  
 TGAGGATCCA TCCTTAACAG CTTTAAGGAT GAGAATGGCA AAGCTGGGAA AAAAGGTGAT 2160  
 CTAAGAGTTG TACCACCTAT ATAAACATCC TTTGAAGAAG AAACTAAGAA GCATTTGCAA 2220  
 ATTTCTCTTC TGGATATTTT GTTTATTTTT TCTGAAGTCC AAAAAATTAT CATTACAGTG 2280  
 TACCATATTA AGCCATGTGA ATAAGTAGTA GTCATTATTT GTGAAAAATT CCCAAAAAGC 2340  
 TGGGGAAAAC AAATGTGTAA CTTTCCAGT TACTTGACAC GATTCAGTGG GGGAAAACCA 2400  
 GCATTTTTTA TTCTATTGAT ACCAAAGCAT TTCTAATAAG AGCTTGTTAA ATTTAAGAAT 2460  
 AAAGTTATTT AAAATATTCT GAGTATAGTA TATTAAGTGG CATTGTAATT TTGATGATAC 2520  
 AAAGATTGAA AGATCATAGG AAAGCATTGC CCTTCATCAC AGAAGTATTC AACTCTGACA 2580  
 AATAAATATG TCATCCTGAA TTAATAATGC CTTAATAAAA GTACATCCTC CTGCTAAAAA 2640

00227 555499

## (2) INFORMATION ON SEQ ID NO. 534:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1245 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

```

TGCAGCGCGT GCGTGCTGCG CTACTGAGCA GCGCCATGGA GGACTCTGAA GCACTGGGCT 60
TCGAACACAT GGGCCTCGAT CCCC GGCTCC TTCAGGCTGT CACCGATCTG GGCTGGTCCG 120
GACCTACGCT GATCCAGGAG AAGGCCATCC CACTGGCCCT AGAAGGGAAG GACCTCCTGG 180
CTCGGGCCCC CACGGGCTCC GGAAGACGG CCGCTTATGC TATTCGATG CTGCAGCTGT 240
TGCTCCATAG GAAGGCGACA GGTCCGGTGG TAGAACAGGC AGTGAGAGGC CTTGTTCTTG 300
TTCCTACCAA GGAGCTGGCA CGGCAAGCAC AGTCCATGAT TCAGCAGCTG GCTACCTACT 360
GTGCTCGGGA TGTCCGAGTG GCCAATGTCT CAGCTGCTGA AGACTCAGTC TCTCAGAGAG 420
CTGTGCTGAT GGAGAAGCCA GATGTGGTAG TAGGGACCCC ATCTCGCATA TTAAGCCACT 480
TGCAGCAAGA CAGCCTGAAA CTTCGTGACT CCCTGGAGCT TTTGGTGGTG GACGAAGCTG 540
ACCTTCTTTT TTCCTTTGGC TTTGAAGAAG AGCTCAAGAG TCTCCTCTAG TCACTTGCCC 600
CGGATTTACC AGGCTTTTCT CATGTCAGCT ACTTTTAACG AGGACGTACA AGCACTCAAG 660
GAGCTGATAT TACATAACCC GGTTACCCTT AAGTTACAGG AGTCCCAGCT GCCTGGGCCA 720
GACCAGTTAC AGCAGTTTCA GGTGGTCTGT GAGACTGAGG AAGACAAATT CCTCCTGCTG 780
TATGCCCTGC TCAAGCTGTC ATTGATTCGG GGCAAGTCTC TGCTCTTGT CAACACTCTA 840
GAACGGAGTT ACCGGCTACG CCTGTTCTTG GAACAGTTCA GCATCCCCAC CTGTGTGCTC 900
AATGGAGAGC TTCCACTGCG CTCCAGGTGC CACATCATCT CACAGTTCAA CCAAGGCTTC 960
TACGACTGTG TCATAGCAAC TGATGCTGAA GTCCTGGGGG CCCCACGTCA ACGGGCAATG1020
CGACCCCGGC GACGAGCCAA AACGGGGACA ATGGCTCTC GATTCCTGGA ACGCACGGTC1080
GTGGCCCTGG GGCAC TAGAC CTTCCACCAT CGTGTCTGCA TGTGCTCAAC TTTTGATCTT1140
CCCCCCCCAAC CCCTGAGGCC TAACATCCAT CGAGCTTGGC AGGACAGCAA CGCGCTAACA1200
ACCCAGGGCA TAGGTCTTAA CCTTTGGTGC TTTCCACGG AGGCG 1245

```

096499-1370

## (2) INFORMATION ON SEQ ID NO. 535:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 822 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

AAGATCGGTC TTTGTCCTTA TCCTTATCCT TATTCTAATG GCAGTTAGAT GCNNTTCTTT 60
AGAGGGGGCA ATGAGACAGC CAGGTGGGAA GGGGTCCCCA GAGAACTCC AGCCTGCACA120
CTGGGAGGAG TGTGCACTGG GGTGAAGCCA CCGGAAGTTT GCGCCATCTC CAGTGGGGAA180

GAGCCCAGCC CCTCCTCTTC CTGGGTGGGA AACTGCGATT CAACTGCCA GGTGGGAAGT240
CCATGGGCAG GAAACAGGCT CTCGNTTTC TAAGAGTCTC TGTTTCCCCC TTTTTCCTT300
TATGCCTAAT TAATAAATTC CATTTCCTC ACCCTTCAA CAGCCTGTGA GCCTAAATTT360
TTGTGGCCAT GGGACAGACA AGGACCCCGT CTTAGCTGA ACTAAGGAGA AAGTCCCCAA420
ACAATGGGAA GAAAGGCAGG GAGTAGACAT CCAATTCCT GCGGTGGATT GTGGAGGGGT480
ACCATGGTTC TGACCATGAT TGTATCAGGA GCTGTGTTGC AGGAAGTCTC AGGAATGAAG540
TTGATAGCTT TCTTTCCATC ACATGATGAC TGAAAGACG AAGGCATCTA ATGAGTTAGA600
GTCACACCAT CTCATGCCTG TATACTATCA AACAACCTTT GGAAGCTAG CCTTGGTTGG660
GAAAACATCA TTTCTTAAT GAATGCCTGG ATGCAAGCAA AGTCTCATTC TTGATCATGA720
TGAGGTTTAC CATGTCTTCT TGACAGGATC CTGCAAACAA ACCCACAAAT GCTACTATGA780
CATGCAACTC CATGGTTAAT TCCTTGGATA GCAAATAGCT CG 822

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## (2) INFORMATION ON SEQ ID NO. 536:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

0967395.122700



(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN

(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

AGTTTCGGCAC	AGGGGGAGGA	ACCTGGCCCT	GGGAGGAGGC	TGTTGCGTGC	TCCTAGAGAA	60
TCCCGTTCTG	AAGGGAAGAG	CATGTTTGCG	GGCGTCCCCA	CCATGCGTGA	GAGCTCCCCC	120
AAACAGTACA	TGCAGCTCGG	AGGCAGGGTC	TTGCTGGTTC	TGATGTTTAT	GACCCCTCCTT	180
CACTTTGACG	CCAGCTTCTT	TTCTATTGTC	CAGAACATCG	TGGNGCAGAN	GCTCTGATGA	240
TTTTNAGTGG	CCATTGGTTC	TAAAACCAAG	CTGGCTGCTT	TGACTCTTGT	TGTGTGGGCTC	300
TTTGCCATCA	ACGTATATTT	CAACGCCTTC	TGGACCATTG	CAGTCTACAA	NGCCCCATGA	360
TGACTTCCNT	GAATATACG	NTTCTTCCAG	ACCATGTCGG	TGATTGGGGG	CTTGCTCCTG	420
GNTGGNTGGC	CCTGGGCCCT	NGGGGGTGTC	TCATGGATG	AGAAGAAGAA	GGAGTGGTAA	480
CAGTCACAGA	TCCCTACCTG	CCTGGCNTNA	AGACCCNGTN	GGCCGTCAAG	GNACTGGNTT	540
CNGGGGTGGA	TTCAACNAAA	ANCTGNCCAG	CTTTTATGT	ATCCTCTTCC	CTTCCCCCTCC	600
CTTGGTAAAG	GCACAGATGT	TTTGAGAANC	TTTATTTGCA	GAGACACCTG	AGAATNCGAT	660
GGNCTCAGTC	TGCTCTGGAG	CCACAGTCTG	GCGTCTGACC	CTTCAGTNGC	AGGCCNAGCC	720
TGGCANGCTG	GNAAGCCNTC	CCCCNACGCC	GAGGCTTTTG	GNAGTGAANC	AGNCCCCTCT	780
NGGNCTGTGG	CATNCTCAGT	CNTATTTTTT	GAGTTTTTTT	GTGGGGGTAN	NCAGGAGGGG	840
GCCTTCAAGC	TGTACTGTGA	NGCAGACGCA	NATTGGTATTA	TCATTCAAAG	CAGTCTCCCT	900
CTTNATTTGT	AAGTTTNACA	TTTTTNNAGC	GGAAACTACT	AAATTATTTT	GGGNTGGTTC	960
AGCCAAACCT	CAAAACAGTT	AATCTCCCNT	GGNTTTNAAA	ATCACACCAG	TGGNCTTTTNG	1020
ATGTTGTTTC	TGCCCCGCAT	TNGTATTTTA	TAGGNNAATA	GTGAAAACAT	TTAGGGNACA	1080
CCCAANAGAA	TGATNGCAGT	ATTAAAGGGG	TGGTAGAAGC	TGCTGTTTAT	GATAAAAGTC	1140
ATCGGTCAGA	AAATCAGCTT	GGATTNGGTG	CCAAGTGNNN	TTTTATTGGG	TAACACCCTG	1200
GGAGTTTTAG	TAGCTTGAGG	CAAGGTGGAG	GGGCAAGAAG	TCCTTGGGGA	AGCTGCTGGT	1260
CTGGGTNGCT	NGCTGGCCTC	CAAGCTGGCA	GTGGGAAGGG	CTAGTGNAGA	CCACACANGG	1320
GGTAGCCNAG	AGCAGCAGCA	CCCTGCAANG	CCAGCCNTGG	CCNAGCTNNG	CTCNAGACCA	1380
GCNTTCCCAG	ANGCCGCAGN	CCGCTGTNNG	GGCANGGGGG	TGNTGGCAGG	AGCTCCCNCAG	1440
CACNTNGNAG	ACCCACGGAC	NTCAACCCAG	TTNACCTCAC	ATGGGGCCNT	TTTNCNTGAGC	1500
AAGGTCTNCG	AAAGCGCAGG	CCGCCCTGGN	CTGAGCAGCA	CCGCCCTTTC	CCAGCTGCAC	1560
TCGCCCTGTG	GACAGCCCCG	ACACACCANC	TTTCTNNGAG	GCTGTCGCTC	ACTCAGATTG	1620
TCCGTTTGCT	ATGCCGAATG	CAGCCAAAAN	TTCTTTTTTA	CAATTGTGA	TGCCTTACCG	1680
ATTTGATCTT	AATCCTGTAT	TTAAAGTTTT	CTAACACTGN	NCCTTAAACT	GTGTTTCTCT	1740
TTTTGGGGGA	GCTTAACTGC	TTGTTGCTCT	CTGTCGTCTN	GCACCATAGT	AAATGCCACA	1800
AGGTTAGTCG	AACACTCTC	TGGCCCCTAG	ACCTATCTGG	GGCAGGCTG	GCTCAGNCTG	1860
TCTNCCANGG	GCTGCTGCGG	CCGAGCCCCG	AGCCTGCCTC	CCCTTGGGNC	CTCTCATCCA	1920
TTGGNCTCTG	CAGGGCANGG	GGTGAGGCAG	GTTTCTNNGC	TCATAAGTGC	TTTTNNGAAG	1980
TCACCTACCT	TTTTAACACA	GCCGAACTAN	GTCCCAACGC	GNTTGTGAAA	TATTTCCCTN	2040
GGTAGCCTAC	TTNCCTTANC	CCCCGAANTA	TTGGTAAGAT	CGAGCAATGG	NNCTTCAGGA	2100
NCATNGGGTT	CTCTTCTCCT	GTGATCATTN	CAAGTGCTCA	CTGCNATNGA	ANGACTNNGC	2160
TTGNTCNTCA	GTGTTTCNAA	CCTNCACCAG	GGCNTGTCTC	TTGGTCCACN	ACCTCGCTCC	2220
CTGTTAGTCG	CGTATACAG	CCCCNATCN	AAATGACCTT	GGCCNAGATN	CACNGGTTTC	2280
TCTGTGGTNC	AAGGTTGGTT	GGCTGATTGG	TGGAAANGTN	AGGGTNGNAC	CNAAANGGAG	2340
GNCCACGTGA	NGCAGNTCNA	GCACCANNGT	TNCTGCANCC	AGCAGCNGCC	TCCGTNCCTA	2400
GTGGGTGTTN	CCTNGTTTCN	TNCTGGCCCC	NTGGGTNNGG	CTNAGGGNCC	TGATTGGGGN	2460
AANGATGCCT	TTGNCANGGG	AGGGGAGGAN	TAAGTGGGAT	CTACCNAANT	TNGATTCTGG	2520
CAAAACAANT	TTCTAAGANT	TTTTTTTGCTT	TATGTGGGNA	AACAGATCTA	AATCTCATTT	2580
TATGCTGTAT	TTTATATCNT	TNAGTTGTGT	TTGAAAACNG	TTTNTGATTT	TTGGAAACAC	2640
ATCAAAATAA	ATAATGGCGT	TTGTTGTAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2700
AAA						2700

## (2) INFORMATION ON SEQ ID NO. 537:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2664 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

CTCCCAGGGA GTGCTGAGTA GTGATGGTGT CTGGAGGGTC AAATCCATTC CCAATGGCAA 60  
 AGGTTCCCTCA CCACTCCCCA CCGCTACAAC TCCAAAACCA CTTATCCCTA CAGAGGCCAG 120  
 CATCAGGGTC TGGGGCACGA GCGGCACGAG CCATCTCCAT CCCCAGGAGCA TCTGTATGAT 180  
 TCAGAAGTAC AACCACGATG GGGGAAGCAGG TCGGCTGGAG GCTTTTAGCC AAGGGGAAAG 240  
 TGTCTTAAAG GAACCCAAGT ACCAGGAAGA GCTGGAGGAC AGGCTGCATT TCTACGTGGA 300  
 GGAATGTGAC TACTTGCAAG GCTTCCAGAT CCTGTGTGAC CTGCACGATG GCTTCTCTGG 360  
 GGTAGGCGCG AAGGCGGCAG AGCTGCTACA AGATGAATAT TCAGGGCGGG GAATAATAAC 420  
 CTGGGGCCTG CTACCTGGTC CCTACCATCG TGGGGAGGCC CAGAGAAACA TCTATCGTCT 480  
 ATTAACACA GCTTTTGGTC TCGTGCACCT GACTGCTCAC AGCTCTCTTG TCTGCCCTT 540  
  
 GTCCTTGGGT GGGAGCCTGG GCCTGCGACC CGAGCCACCT GTCAGCTTCC CTTACCTGCA 600  
 TTATGATGCC ACTCTGCCCT TCCACTGCAG TGCCATCCTG GCTACAGCCC TGGACACAGT 660  
 CACTGTTTCT TATCGCCTGT GTTCTCTCC AGTTTCCATG GTTCATCTGG CTGACATGCT 720  
 GAGCTTCTGT GGGAAAAGG TGGTGACAGC AGGAGCAATC ATCCCTTTCC CTTGGCTCC 780  
 AGGCCAGTCC CTTCTGATT CCCTGATGCA GTTTGGAGGA GCCACCCCAT GGACCCCACT 840  
 GTCTGCATGT GGGGAGCCTT CTGGAACACG TTGCTTTGCC CAGTCAGTGG TGCTGAGGGG 900  
 GTATAGACAG AGCATGCCAC ACAAGCCACA GAACCAAGG GACACCTCCA CCCTCTGCCC 960  
 TTCATGCATG TACCACTGGG GAAGAAATCT TGGCTCAGTA TTTACAACAG CAGCAGCCTG1020  
 GAGTCATGAG TTCTTCCCAT CTGCTGCTGA CTCCCTGCAG GGTGGCTCCT CTTACCCCC1080  
 ACCTCTTCTC AAGCTGCAGT CCACCGGGTA TGGTTCTGGA TGGTTCCCC AAGGGAGCAG1140  
 GTCCTCTGTT TCCCTCTCCC TTCCACAGCA GTGGAGAGCA TCCCAGTGTT TGGGGCACTG1200  
 TGTTCTCTT CGTCCCTGCA CCAGACCTTG GAAGCCTTGG CCAGAGACCT CACCAAACTC1260  
 GACTTGCGGC GCTGGGCCAG CTTCATGGAT GCTGGAGTGG AGCACGATGA CGTAGCAGAG1320  
 CTGCTGCAGG AGCTACAAAG CCTGGCCCAG TGCTACCAGG GTGGTGACAG CCTCGTGGAC1380  
 TAAAGTTCCC AGTGTGGGAG AAAGGAGCTA GTTTGCAATA AAAACAGCTG GATGCAGGAG1440  
 CCCAGTGTCT TCATGCAGAG GAGCTCAATG TCGCGGGACT AGCTACACCA ACATATGCAC1500  
 TTTTACATT TAGAAACACT GTGATTAGAC CACAGAACAA TAAATATGTG CCATCAGACC1560  
 AAAAAAAGT AGAGAAAGGA GCTGAACTCC ACTCTCGATG CTATTTACAG AGGACATCTG1620  
 TAAAGTCTTC ATAAAAGACC TTGAATGATG CCTAGGATGG CAGAGCCCCT GGGTCTACT1680  
 CCATCCTCCA GCCTTTGTCC TTGTCTTGGC CTCCTGCTCT CCAGATCTGT AAAGTGGGCT1740  
 CAAGGACTGT ACAAGCAGAG TACAACCTACC CCCTCCCCGG TGCCAGGGCG CTTGTTGGGT1800  
 TTGGTCTGT GTAGATGATT CCCAGAGTCT CATTCATCCA GCTCCTCTTC AGACAGAAGG1860  
 TCCCCATGGT CAGACAGCTG GTCTGCATTG CTGGTACTGG TTGCATCATC CTCATCCTCA1920  
 GAGCTGGCTT CACAGGCAGT GTGGAAGAGC TGCATGAGTT CTCGAAAACG GTGGGAACC1980  
 TCAGCAGGGG TCTTATTTCC CAGCTGCTGG GAGATGATGT TGAAGGTCTG TGGCTGTGCC2040  
 CCTTGCTCCT GGCACATGGT GAGGATCACA CGGTCAGCTT CCCTTGTTCCA CAGGACAACC2100  
 TTTTCCCCAG TGGAGCTGAC CTTGCTGTTG TTGGCACACA CCGTAGCTTC TGCGGCTTT2160  
 GGCTGCTGCT CCCCCTCTGG ACCCTTGGCC TGTGTTCCAC TGTCTTTAGC CAAACCCCT2220  
 CTAGGGGCTT TGGGAGAAGT CTCTGAGGTG TCAATTCTTG ATGGAGATTG ATGGACAGGG2280  
 CACGTCCTGT CTCTTGTCTT CACCCTAGCT CTGCTTGAGG GCAGCCATCT CTCTTGAGTG2340  
 TCTGGTTTCC CGGACACATG TCTTCTCCCT GCATCTCTGG TCTTTGAGGA AACAGGACTC2400  
 AGGAAGGAAG CAGGGGGTTC CACGGTACCA GGCAATTTCT CAGTTTCTGA TGCATCCCAG2460  
 ACCAGCATCA AAGCCTCTGA CTCACTCACT GCCTTTTGGC CCTCCCTCTC TTTCTGAAGT2520  
 CTGGGGGATG CCTTGGGGCA GGAGCGAACC TCAGGCCCAA CCTGGTTTCT CTTAACAGTG2580  
 TACAGTACAG CTCCAGTTGT GGGGGGAAAT TGAGGAGTCT CTGGTGAATG AGGTGGTGGG2640  
 CCATCCAGGA GGAGCCGTTT TGTA 2664

004227 3622950

## (2) INFORMATION ON SEQ ID NO. 538:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3888 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.12300

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

GAATTCCTCGC CCGGACTGAC GGAGCCCCT GCGGTGCGGG CGTTGGCGCG GGCACGGAGG 60  
 ACCCGGGCAG GCAGCGCAAG CGACCCCGAG CGGAGCCCCG GAGCCATGGC CCTGAGCGAG 120  
 CTGGCGCTGG TCCGCTGGCT GCAGGAGAGC CGCCGCTCGC GGAAGCTCAT CCTGTTCATC 180  
 GTGTTCTCTG CGCTGCTGCT GGACAACATG CTGCTCACTG TCGTGGTCCC CATCATCCCA 240  
 AGTTATCTGT ACAGCATTAA GCATGAGAAG AATGCTACAG AAATCCAGAC GGCCAGGCCA 300  
 GTGCACACTG CCTCCATCTC AGACAGCTTC CAGAGCATCT TCTCCTATTA TGATAACTCG 360  
 ACTATGGTCA CCGGGAATGC TACCAGAGAC CTGACACTTC ATCAGACCGC CACACAGCAC 420  
 ATGGTGACCA ACGCGTCCGC TGTTCCTTCC GACTGTCCCA GTGAAGACAA AGACCTCCTG 480  
 AATGAAAACG TGCAAGTTGG TCTGTTGTTT GCCTCGAAAAG CCACCGTCCA GCTCATCACC 540  
 AACCCCTTCA TAGGACTACT GACCAACAGA ATTGGCTATC CAATTCCTCAT ATTTGCGGGA 600  
 TTCTGCATCA TGTTTGTCTC AACAATTATG TTTGCCCTTCT CCAGCAGCTA TGCCTTCCTG 660  
 CTGATTGCCA GGTGCTGCA GGGCATCGGC TCGTCTGCT CCTCTGTGGC TGGGATGGGC 720  
 ATGCTTGCCA GTGTCTACAC AGATGATGAA GAGAGAGGCA ACGTCATGGG AATCGCCTTG 780  
 GGAGGCCTGG CCATGGGGGT CTTAGTGGGC CCCCCCTTCG GGAGTGTGCT CTATGAGTTT 840  
 GTGGGGAAGA CGGCTCCGTT CCTGGTGCTG GCCGCCCTGG TACTCTTGA TGGAGCTATT 900  
 CAGCTCTTTG TGCTCCAGCC GTCCCGGGTG CAGCCAGAGA GTCAGAAGGG GACACCCCTA 960  
 ACCACGCTGC TGAAGGACCC GTACATCCTC ATTGCTGCAG GCTCCATCTC CTTTGCAAAC1020  
 ATGGGCATCG CCATGCTGGA GCCAGCCCTG CCGATCTGGA TGATGGAGAC CATGTGTTCC1080  
 CGAAAGTGGC AGCTGGGCGT TGCCTTCTTG CCAGCTAGTA TCTCTTATCT CATTGGAACC1140  
 AATATTTTTG GGATACTTGC ACACAAAATG GGGAGGTGGC TTTGTGCTCT TCTGGGAATG1200  
 ATAATTGTTG GAGTCAGCAT TTTATGTATT CCATTTCCAA AAAACATTTA TGGACTCATA1260  
 GCTCCGAAC TGGAGTTGG TTTTGCAAAT GGAATGGTGG ATTCGTCAAT GATGCCTATC1320  
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 GATGTGGCAT TTTGTATGGG GTATGCTATA GGTCTTCTG CTGGTGGTGC TATTGCAAAG1440  
 GCAATTGGAT TTCCATGGCT CATGACAATT ATTGGGATAA TTGATATTCT TTTTGCCCTT1500  
 CTCTGCTTTT TTCTTCGAAG TCCACCTGCC AAAGAAGAAA AAATGGCTAT TCTCATGGAT1560  
 CACAACAGCC CTATTAAAAC AAAAAATGAC ACTCAGAATA ATATCCAGTC ATATCCGATA1620  
 GGTGAAGATG AAGAATCTGA AAGTGACTGA GATGAGATCC TCAAAAATCA TCAAAGTGT1680  
 TAATTGTATA AAACAGTGTT TCCAGTGACA CAACTCATCC AGAACTGTCT TAGTCATACC1740  
 ATCCATCCCT GGTGAAAGAG TAAAACCAA GGTATTATT TCCCTTCCAT GGTTATGGTC1800  
 GATTGCCAAC AGCCTTATAA AGAAAAAGAA GCTTTTCTAG GGGTTTGTAT AAATAGTGTT1860  
 GAAACTTTAT TTTATGTATT TCATTTTATT AAATATCATA CAATATATTT TGATGAAATA1920  
 GGTATTGTGT AAATCTATAA ATACTTGAAT CCAAACCAA TATAATTTT TAACTTACAT1980  
 TAACAAACAT TTGGGCAAAA ATCATATTGG TAATGAGTGT TAAAAATTAA AGCACACATT2040  
 ATCTCTGAGA CTCTTCCAAC AAAGAGAAA TAGAATGAAG TCTGAAAAAC AGAATCAAGT2100  
 AAGACAGCAT GTTATATAGT GACACTGAAT GTTATTTAAC TTGTAGTTAC TATCAATATA2160  
 TTTATGCGTT AAACAGTAG TTCTCTCAAG TGTAAGGAC AAGAACTTGT GTCAGTTATC2220  
 TTTTGAATCC ATAAATCTTA GCTGGCATT GTTTTCTATG TAATCACCTA CCTAGAGAGA2280  
 GTTGTAATT ATATGTTAAC ATGTTATCTG GTTGGCAGCA AACACTAAAG CCAATAAAGG2340  
 AAAACAGTA AATGTTCCGA AAGCAGAGAA AAGCAACCAA ACATATTGTT ATGAACTAAA2400  
 AGCTTTCCCT TTAAGATGCA TACTTGTCTT ACTGGATGAA GAAATTTGAG GGTACATGTA2460  
 CCTTATACTG TCAAGGTTGT TTAACATGA TAAGGTTAAT CGCCATCTAC TTCAAGTTTT2520  
 AGAAAAGGAA ACAAGAAGCT AAAAACAGCT GCTCTGACTT TAATATCTGA CTATATCTTT2580  
 GATCTGTTT CAGGTATCC AAGTGTTTT TAGGAATATA TTTATTTTAG GTTGTCTGAA2640  
 ACTACTATTT TTTAGACTCC TGAAAGTTGT TCACATCAAT GTGAAGACAA ATTTTAAATG2700  
 AAAATGAAGA ATGAAATTAT GTCTTGAATC ATATATTAAG AAGTAAAAAT AATAGTGATC2760  
 AGGCAGAAAA GAAAAATGGA ACATCTAAAA ATGTATGTGC TAACTATATC ATCCAGTGTG2820  
 CAGTGTGTG TATTTTCTA AGCATGACAA CATTGATGTG CCTTTTCAGT GTAACAGCAA2880  
 ATACTGTTAG TGAACATTGT CAATTTATGT CATTGTGTTA AGAGATATGA CTGGAGTGTG2940  
 CAGTGTGGAA TGTCTCTAAT ACTACTTGAG AATCCTGCAG TTCTATAATC ATAAACAAAA3000  
 ATTACTTAGT TTCGTTAAGC TAAGATTGTG TTTGTGTTAA CTTTCGACATC AAGGAGCAAA3060  
 GAACTTTAGA ACAGACTCCT CAATCTTGTG ACTTTCTTAT TCTCTAGGAA AGTAACACTT3120  
 CGTTTCATGA AGCTTTTCTG TGGGGCTTCG ATTATTTCAA GTCTGGTTTC TAAGTCAGT3180  
 GTGTTTGAAG CAAACGAAC TCCAATCAG TTATTTGGCA TTGGGCAACT TGGCCAAGTC3240  
 TGCTACTTTG GAAGATGGCT CTGGAGGAAA CTCTCATATG GCTAAAAAGG CAGGCTAGTT3300  
 TCTTACTTCT ACAGGGGTAG AGCCTTAAAA AAGAACGTGC TACAAATTGG TTCTCTTTGA3360  
 GGGTTTCTGG TTCTCCCTGC CCCCATAACC ATATACTTTA TTGCAATTTT ATTTTTCCT3420  
 TTACGGCTCT GTGTCTTTCT GCAAGAAGGC CTGGCAAAGG TATGCCTGCT GTTGGTCCCT3480  
 CGGGATAAGA TAAAATATAA ATAAAACCTT CAGAACTGTT TTGGAGCAAA AGATAGCTTG3540

TACTTGGGGA AAAAAATTCT AAGTTCTTTT ATATGACTAA TATTCTTGGT TAGCAAGACT3600  
GGAAAGAGGT GTTTTTTTAA AATGTACATA CCAGAACAAA GAACATACAG CTCTCTGAAC3660  
ATTTATTTTT TGAACAGAGG TGGTTTTTAT GTTTGGACCT GGTAATACAG ATACAAAAAC3720  
TTTAATGAGG TAGCAATGAA TATTCAACTG TTTGACTGCT AAGTGTATCT GTCCATATTT3780  
TAGCAAGTTT ACTTAATAAA TCTTCTGAAC CATGTTTTGT GCCTGTTTGT ATTCCTTTAT3840  
AAACCAAATG TTGTTGGAAT AAAATACATA AGGTATCATT TTGACCGT 3888

(2) INFORMATION ON SEQ ID NO. 539:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

004227" 5622/960

AACACCTCTT	GGCTGTCTGC	TGTCCAGGGA	GTCCCACTC	CCTTCATTAT	AGCCTTGCTC	60
AGAGTGCAGC	GGCAGGCCTG	GGGATGGCCT	CGGGAGAGGG	ACCACAGAGC	ACCAGCCTGC	120
ATGGAACTTC	CTTCCTCACT	CAGCTTCCCA	CGTTGCCAGC	TGGGACAGGG	GAGATGGAGT	180
AATTTTGCTG	TGGAAAGACT	TCACGTCTTG	CCGAATGAAA	GTCCCGCCTG	TCTGTACACG	240
TGATGCCCGT	GCAGCTGTCT	GAGCACCCGG	AATGGAATGA	GTCTATGCAC	TCCCTCCGGA	300
TCAGTGTGGG	GGGCTTCTCT	GTGCTGGCGT	CCATGACCAA	GGCCGCGGAC	CCCCGCTTCC	360
GCCCCGCTG	GAAGGTGATC	CTGACGTTCT	TTGTGGGTG	TGCCATCCTC	TGGGTGCTCT	420
GCTCCACCG	CCCGGCCCCC	GGCAGGCCCC	CCACCAACA	TGCACACAAC	TGGAGGCTCG	480
GCCAGGCGCC	CGCCAACCTG	TACAATGACA	CCTACCCCTT	GTCTCCCCCA	CAAAGGACAC	540
CGGTGGGAT	TCGGTATCGA	ATCGCAGTTA	TCGCAGACCT	GGACACAGAG	CCAACCGCCC	600
AAGACGAAAA	CACCTGGCGC	AGCGACCTGA	AAAAGGGCTA	CCTGACCCTG	TCAGACAGTG	660
GGGACAAGGT	GGCCGTGGAA	TGGGACAAAG	ACCATGGGGT	CCTGGAGTCC	CACCTGGCGG	720
AGAAGGGGAG	AGGCATGGAG	CTATCCGACC	TGATTGTTTT	CAATGGGAAA	CTCTACTCCG	780
TGGATGACCG	GACGGGGGTC	GTCTACCAGA	TCGAAGGCAG	CAAAGCCGTG	CCCTGGGTGA	840
TTCTGTCCGA	CGCGACGGTC	ACCGTGGAGA	AAGGCTTCAA	GGCCGAATGG	CTGGCAGTGA	900
AGGACGACGC	TCTGTACGTG	GGCGGCTTGG	GCAAGGAGTG	GACGACCACT	ACGGGTGATG	960
TGGTGAACGA	GAACCCGGAG	TGGGTGAAGG	TGGTGGGCTA	CAAGGGCAGC	GTGGACCACG	1020
AGAACTGGGT	GTCCAACCTA	AACGCCCTGC	GGGCTGCTGC	CGGCATCCAG	CCGCCAGCTA	1080
ACCTCATCCA	TGAGTCTGCC	TGCTGGAGTG	ACACGCTGCA	GCGCTGGTTC	TTCTGCCGCT	1140
GCCGCGCCAG	CCAGGAGCGC	TACAGCGAGA	AGGACGACGA	GCGCAAGGGC	GCCAACCTGC	1200
TGCTGAGCGC	CTCCCTTGAC	TTCGGCGACA	TCGCTGTGAG	CCACGTCGGG	GCGGTGGTCC	1260
CCACTCACGG	CTTCTCGTCC	TTCAAGTTCA	TCCCCAACAC	CGACGACCAG	ATCATTGTGG	1320
CCCTCAAATC	CGAGGAGGAC	AGCGGCAGAG	TCGCCCTCCT	CATCATGGCC	TTACGCTGGT	1380
ACGGGGCGTT	CCTGTTGCCG	GAGACCAAGA	TCGGAAGCGT	GAAATACGAA	GGCATCGAGT	1440
TCATTTAACT	CAAAACGGAA	ACACTGAGCA	AGGCCATCAG	GACTCAGCTT	TTATAAAAAC	1500
AAGAGGAGTG	CACTTTTGTT	TTGTTTTGTT	CTTTTTGGAA	GTGTGCCTGG	GTGGAGGTC	1560
TGGACAGGGA	GCCAGTCCC	GGGCCCCATA	GTGGTGCGGG	CACTGGACCC	CCGGGCCCA	1620
CGGAGGCCGC	GGTCTGAACT	GCTTTCCATG	CTGCCATCTG	GTGGTGATTT	CGGTCACCTT	1680
AGGCATTGAC	TCAAGGCCTG	CCTAAGCTGG	TGGGTCGTTT	CTTCCATCCG	ACCTCGTTTC	1740
TTTTCTTTCC	TATGTTCTTT	TGTTCACTGA	ATATCCCTAG	AGCTCCTACC	ATATGTCAGG	1800
CCCTATGCCT	CACCCTGAGA	ACGCAGTGAG	CATGAGGTGG	ACCTGTTTGC	TGGGAACCCG	1860
AGGTCACCCC	CTTTTCTTCC	CAAACCTGGT	GCCTTGGAAG	AATCAGGTCC	AGCCCTGAAG	1920
ATCCTTGGGG	AAGAAAATGT	TTATGTTGCA	GGGTATTGCA	TGGTCACGAG	TGAGGGGCAG	1980
GCCCCGTTGG	GACACATCTG	CCCACAGCTG	CACAGGCCAG	GGGCACAGGC	ACATCTGTTG	2040
GTTCTCAGGC	CTCAGATAAA	ACCATCTCCG	CATCATATGG	CCAGTGACCG	CTTTCTCCCT	2100
TCAAGAAAAA	TCTGTGGCTG	TGCAGTACTT	TGAAGTTTTA	ATTATTAACC	TGCTTTAATT	2160
AAAGCAGTTT	CCTTCTTAT	AAAGTGGAA	CACCAAACT	TATCACACAG	AGCACAGTCC	2220
TGTAGTTACC	GACCCCGCTC	CAGCAGTGGC	GGAGATTGTA	AGGAAGCGGT	GGCGGCTGGT	2280
GAAGCAAGTC	TCACATGTGC	GCGTTCTTGG	CCAATGGATA	CAAAGATAAA	GAAATAGTTG	2340
CCTTTTTCTA	GGAAGTGTCA	GAAATCCTCA	TGCCCTTCAA	GACTTCTGTG	AATGACTTGA	2400
ATTTTTTATT	CCCTGCCTAG	GGTCTGTGAA	CGAGGCCTGT	CTCTTCCCTG	GGGTTTCTTT	2460
CCATGGCCTT	TATTTCTCCT	CTTCCAGTGG	GAGTTTTGCA	GGCTCTTCTC	TGTGGAAACT	2520
TCACGAGCGT	TGGCTGGGCC	TCGGCTTCGC	TGGAGTGATC	TCCAGGGTGA	AGGCAGAGTG	2580
GGATTTGAGA	CCCAGGTTAG	GCACGACCCA	GGCTGAGAAG	GGACGTTTCC	ATCATTACAA	2640
GTGCCCTCCC	CACAGCAACT	ACCTCACCCC	GACCCCCACC	CTCACTCCTA	CCCCACCCCG	2700
CGATCGTCAG	GGGTGCCACG	GTGGGCCGGA	GGGTGCCCGG	TCTGGCTGTC	CCTGTGCCGG	2760
TCCCTCACAA	ACCTCTCCCC	CTTTGAAACT	CAAAGCAGAC	TGCGAGGAGG	GCAGGAGGAG	2820
GGGACCCCTC	TCTCATGGTT	GTCTCTTTCC	CCCGCTATGT	CATAGGTAGT	GAGGAAGCGG	2880
AAGGAAGTGA	ACGCTGAATG	TGACGCATTT	CTGAAGAGCT	CAGCTGTCAC	CGGGCATAGC	2940
CTGGAAGCCC	CAAGTCTGTT	CTGACTTTGC	CTGGCTGTCT	CCTTGACCCG	CCTCCTAGAT	3000
CATTGTCCTT	GATGTCCAGG	CTGGGTCATT	TAAAATAGAG	ATGCAATCAG	GAAGGTTGGG	3060
GGACTTGGGA	CTGTGGCTGA	ATTGAGACCT	TGCTGATGTA	TTCATGTCAG	CACCTGAGTC	3120
ACAGCCCAGG	TGCCCGGAAG	CAGCCTCTTC	GCATAGGCAG	TGATTTGCGA	TTACTTTAAA	3180
GCTCACCTTT	TTTCTTCCCC	TCTCTGTTCC	CTGCTGTCAG	CATAATGATT	GTGTTCTTTC	3240
CCATATGGAT	CCATCTGTTT	TGTAAACAA	AAAGCGTCTG	AGGGAGTGTA	AAAAACAGAT	3300
GGAT						3300

## (2) INFORMATION ON SEQ ID NO. 540:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 863 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

CAGGATTGAA ACAAGATGGC GGGTTCGTGG TGAGAAGCCG TCAAGGAGTA GAAATTGGTA 60  
 TGCTTAGAAG CAGATTCTAA AAGCAGTTTC TCTTCAGAAC ATCTTTTTTC ATACCACTTG120  
 ATAAGCATCT TGAAACACCA TGGCTGTAGC TGCAGTAAAA TGGGTGATGT CAAAGAGAAC180  
 TATCTTGAAA CATTTATTTC CAGTCCAAAA TGGAGCTTTA TATTGTGTTT GTCATAAATC240  
 TACGTATTCT CCTCTACCAG ATGACTATAA TTGCAACGTA GAGCTTGCTC TGACTTCTGA300  
 TGGCAGGACA ATAGTATGCT ACCACCCTTC TGTGGACATT CCATATGAAC ACACAAAACC360  
 TATCCCTCGG CCAGATCCTG TGCATAATAA TGAAGAAACA CATGATCAAG TGCTGAAAAC420  
 CAGATTGGAA GAAAAAGTTG AACACCTTGA GGAAGGACCT ATGATAGAAC AACTTAGCAA480  
 AATGTTCTTT ACTACTAAGC ACCGTTGGTA TCCTCATGGA CGGTATCACA GATGTCGTAA540  
 GAATCTGAAT CCTCCAAAAG ACAGATGATG CGGAGGTTCC TGGGGGAATC AAAGAGAAAT600  
 GTGCCTCATT TGCCATTTGA GAAAATGCAG TCTGGTGTAT TCAGTAATAT ATAGTAAAGT660  
 AATAATGATA AAATATCTTT TCATATATTA GAATGTGTAC TTTTATATAA AGTAATTCTG720  
 GATTTGACAT TCTCATTTAG AGAGACCTAT TCCTTTTTTC GTTTTCTATT TTAGTGTTC780  
 ATTTATGTGC GGTCTCCAAT TTAGGACTTT TCCATAGTGC CAAAGCCATA CATATTCAGT840  
 AGAACATCAA TAAAAAAAAA AAA 863

0067398-12700



## (2) INFORMATION ON SEQ ID NO. 541:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

ACCGACGGCC GCCCCTTTTC GTCTTTTTTTT TTTTACATT TCAAATATAT TTTATTACTT 60  
TCCATCTTAG AAAGAATATG AAACCTGCAT GCAATGCTAA TGGTTTCTGA CATGTACATA 120  
GCATATAACA CAGCAGTACA ATGCGGCATA TACTGGGGGG CAGTGTGTGG AGGGGGCGTT 180  
CTTAAGGGTA TATGTACAGA GGAAAGGGCG CATGGTCATC TTAGCTTTTCG AAAGAGGACT 240  
GCACTGTTTA ACATTGAAGA ATTACATGGG GAATCACAAA TATATTGCTT TAGTACTGCA 300  
TGTTCTGTTG TGGTGAGGGA AAGAAACATG CTTTGAAGGT TTTCCCTTGT CAACAGAATG 360  
TGTGTCTGTA GCTGTGTATT GCGCATGTAT TCATATATTT TTAAGTTTTT TCCTAAGGTT 420  
TTTGCTGACA GTGTTGGGAA CCTCACATGC TTCTGAAGCA TTAAATATTG AACCTGTGAA 480  
CCTTTCAGAA ATCCTCAGGT TGGGAAAGAC CCCACACCTT CTTTAAGGAT CATTGTGCTC 540  
GCCATCACAG GATCTTGGA ATGTTTCTTA GGGTGTGTAA AAATTAACCA GGGGGGAATG 600  
AAGCACATTT TTCTGGCAAC CAAACTTGAG TTCCTCAGAG AACAGATGCA GAGAGACCTG 660  
CTCCTGCTTG CCCGGCTACA GGGGCCACTG TGGAGTCACA CTGAGGCTGT GACCGGCCAT 720  
AAGCCCAGGA GAGCCCGTGG CAGCTGTGCC GAGGCGCCAG GACCTCTAAG CGGAAGCTTC 780  
CCAAGCTAGG AATGGAGCAA CACTGCAATG AAATGTGTCC ACCAAGCTCA TTGTTCTCCTC 840  
CGGGCGCTTA TAAAGCTCAG ATGTATAGTG ACGTATGGAC AAATACAAAA AAAAAAAAAA 900  
AAAAAAAAAA AAAAAAAGCC TTTCTTTCTC ACAGGCATAA GACACAAATT ATATATTGTT 960  
ATGAAGCACT TTTTACCAAC GGTCAGTTT TACATTTTAT AGCTGCGTGC GAAAGGCTTC1020  
CAGATGGGAG ACCCATCTCT CTTGTGCTCC AGACTTCATC ACAGGCTGCT TTTTATCAA1080  
AAGGGGAAAA CTCATGCCCT TCCTTTTAA AAAATGCTTT TTTGTATTG TCCATACGTC1140  
ACTATACATC TGAGCTTTAT AAGCGCCCGG GAGGAACAAT GAGCTTGGTG GACACATTT1200  
ATTGCAGTGT TGCTCCATTC CTAGCTTGGG AAGCTTCCGC TTAGAGGTCC TGGCGCCTCG1260  
GCACAGCTGC CACGGGCTCT CCTGGGCTTA TGGCCGGTCA CAGCCTCAGT GTGACTCCAC1320  
AGTGGCCCT GTAGCCGGGC AAGCAGGAGC AGGTCTCTCT GCATCTGTTT TCTGAGGAAC1380  
TCAAGTTTGG TTGCCAGAAA AATGTGCTTC ATTCCCCCTT GGTTAATTTT TACACACCCT1440  
AGGAAACATT TCCAAGATCC TGTGATGGCG AGACAAATGA TCCTTAAAGA AGGTGTGGGG1500  
TCTTTCCCAA CCTGAGGATT TCTGAAAGGT TCACAGGTTT AATATTTAAT GCTTCAGAAG1560  
CATGTGAGGT TCCCAACACT GTCAGCAAAA ACCTTAGGAG AAAACTTAAA AATATATGAA1620  
TACATGCGCA ATACACAGCT ACAGACACAC ATTCTGTTGA CAAGGGAAAA CCTTCAAAGC1680  
ATGTTTCTTT CCTCACCAC AACAGAACAT GCAGTACTAA AGCAATATAT TTGTGATTCC1740  
CCATGTAATT CTTCAATGTT AAACAGTGCA GTCCTCTTTC GAAAGCTAAG ATGACCATGC1800  
GCCCTTTCTT CTGTACATAT ACCCTTAAGA ACGCCCCCTC CACACACTGC CCCCAGTAG1860  
TACGCAGGCA TTGGTACCGG CTGGTGTAA AATGGCTATG GGACATGGTC AGGAAACCAT1920  
TTAGGCATTG GCATTGAGGG TTCCATAATC CGTTTCTAAG GA 1962

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 542:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1772 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```

TGGGCGCTGT AGTCCGGCCG GAACCTGTTT GCGACCCCGA GTCCCATGAC ACCGCTTCTC 60
CTCACACCCC AGTCCGCAGT GCCCCTCCCC AGCCTCGGCC GGGCCTCCCG GGAGCCGGGC 120
GTGGCGTTCC AGCTAGTGAG CCGTTTCTCC CCTGGGCTCG GAGGCGGAAG CTTGAGGGGC 180
GCGGGGAGGA GCTTCGCGTG CGGGGTGAAC GCCCGCTCTA CGTGCTCGTT CTCTTCGCGA 240
CCGCTGCGCG CGAGCCCCGT GTCCCCACGG CGGGCAGCAG CGCCGGCGGC GGC GGCTGAA 300
CGCGGAGGGG GCGGAGGGAG CCCGCGGCGG CGGCAGCAGC TACAGCGAAA TGGCGGAGAC 360
CGTGGCTGAC ACCCGGCGGC TGATCACCAA GCCGCAGAAC CTGAATGACG CCTACGGACC 420
CCCCAGCAAC TTCCTCGAGA TCGATGTGAG CAACCCGCAA ACGGTGGGGG TCGGCCGGGG 480
CCGCTTCACC ACTTACGAAA TCAGGGTCAA GACAAATCTT CCTATTTTCA AGCTGAAAGA 540
ATCTACTGTT AGAAGAAGAT ACAGTGACTT TGAATGGCTG CGAAGTGAAT TAGAAAGAGA 600
GAGCAAGGTC GTAGTTCCCC CGCTCCCTGG GAAAGCGTTT TTGCGTCAGT TCCTTTTAGA 660
GGAGATGATG GAATATTTGA TGACAATTTT ATTGAGGAAA GAAAACAAGG GCTGGAGCAG 720
TTTATAAACA AGGTCGCTGG TCATCCTCTG GCACAGAACG AACGTTGTCT TCACATGTTT 780
TTACAAGATG AAATAATAGA TAAAAGCTAT ACTCCATCTA AAATAAGACA TGCCTGAAAT 840
TTGGCAAGAA GGGGCAAAAA CGTGACTATT AATGATTGAT AAGCACCAGT GAAGAAGTTC 900
TAACTTTTAG CATGCTGCAC AGAAACTGGT ATAACATGCC TTCAGTATAC TAACACTCAT 960
ATGCTCAGTT TTGTTTTGTT TTGGCAGTTG ACAAGAAGTT AATTTGCTTT AGTAAAAATC1020
CCTCATTCCA GCCTTTCTAT ATAAATAGCT CTTTCTTGCT GTTTTAATGT GGTGCACACT1080
ATAGCCTCAC AAACCTGTTA TTCCAGTGTA ATCTGCAGTG TCGTAACTAA AGTTACTGGC1140
TTGGTCTTAT TTGCACAGTT TTTGCGTCTT GTTTGCTTCT TGCATCTGAT TAACTAGAAT1200
ATTTCTCTTT CCCCCTTTTA ATTTGTGATG TCACTTGACC CCATTTATGT GTAGGAGCAC1260
TACACCATTG GTTTCCAATA CTGCACACAT AAGATACATA CTTGTGTGCA GAAAGTATCT1320

TCCTCCAGGC TTGTAATACC CTTACATGG AAGATTAATG AGGGAAATCT TTATATTCTG1380
TATAAAAAACA AAAGCAAATT TATATACTAA AATCATTGT CTAAAAATTT AAGTTGTTTT1440
CAAATAAAAAA TTAAATGCA TTTCTGATAT GCACTGATTG TGTTCCTCC AGCTTTTTTT1500
GCTCTCTATG AGTGACTACT TAAGTCACTT GTTGAGAGGG ATTATTTACT AATTATATAC1560
TTCTCATTCC TGTAACCTCA TTCCCTTTAA ACAGTGGTGA TATCAAATAT ACTTCCATCC1620
ATTGAATGGG GTATTTTAA CAACAACAAA AGTGATATAC TAAAAAATGT ATTGCTTAAG1680
GCTTATTGAA TCATTTTGAA GCACCTTGTG TATTTGAAAA CTGCTTTATA ATCTCATTTA1740
TAAAAAGGAC TTTCAAAGAT AAAACCAAAA AA

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1772

004227 56226950

## (2) INFORMATION ON SEQ ID NO. 543:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

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CTCGTGCGGT GATGTTGAGC AGAAGATACA ATTCAAAAGA GAAACAGCCA GTTTGAAACT 60
GTTACCCAC CAGCCCCGAA TTGTGGAGAT GAAGAAAGGA AGCAATGGCT ATGGTTTCTA 120
TCTGAGGGCA GGCTCAGAAC AGAAAGGTCA AATCATCAAG GACATAGATT CTGGAAGTCC 180
AGCAGAGGAG GCTGGCTTGA AGAACAATGA TCTGGTAGTT GCTGTCAACG GCGAGTCTGT 240
GGAAACCCTG GATCATGACA GTGTGGTAGA AATGATTAGA AAGGGTGGAG ATCAGACTTC 300
ACTGTTGGTG GTAGACAAAG AGACGGACAA CATGTACAGA CTGGCTCATT TTTCTCCATT 360
TCTCTACTAT CAAAGTCAAG AACTGCCCCA TGGCTCTGTC AAGGAGGCTC CAGCTCCTAC 420
TCCCCTTCT CTGGAAGTCT CAAGTCCACC AGATACTACA GAGGAAGTAG ATCATAAGCC 480
TAAACTCTGC AGGCTGGCTA AAGGTGAAAA TGGCTATGGC TTTCCTTAA ATGCGATTTC 540
GGGTCTGCCA GGCTCATTCA TCAAAGAGGT ACAGAAGGGC GGTCTGCTG ACTTGGCTGG 600
GCTAGAGGAT GAGGATGTCA TCATTGAAGT GAATGGGGTG AATGTGCTAG ATGAACCTA 660
TGAGAAGGTG GTGGATAGAA TCCAGAGCAG TGGGAAGAAT GTCACACTTC TAGTCTGTGG 720
AAAGAAGGCC TATGATTATT TCCAAGCTAA GAAAATCCCT ATTGTTCCCT CCCTGGCTGA 780
TGCCAGTTGA CAGCCCTGCA GGTTCATAAG AAGGAATAGT GGTGGAGTCA AACCATGACT 840
CGCACATGGC AAAAGAACGG GCGGCTATTG CAGACGGCTA ATTTATGCTT AACTTAGGAA 900
GAGATAAGGT TCCTTGAGCA CCAAAGATGA TTCATAACTC TGTATAGGTG ACAGCTGCTT 960
ATAAAAGCAT CTTAGCAGAT AAGCCTATTA AAATTGTGCT TTTGTAACA 1009

```

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 544:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2834 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

002227 36664360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

CACCTTTGCGG	GCGGCACTTT	TTCCAGGTTG	TTAATCCAGC	TAATGGAGAA	GGATAGATGC	60
ACGCTACTTG	GTTTAGAAAA	AAAAACAAAA	ATGAGCAAAC	GAGACGCCCC	TTCCGTTTTTA	120
TGATAACTAA	GCTGCAGGGA	AATAAATCGG	CTGGCCCTAC	TGCAATCTAC	TGCACTCGAG	180
AAACATCACA	GAAAATTCTT	TGATTTATCT	TAATAGTGAC	AAGTGAGCCT	GCTTCTGTCA	240
ATTACTGAAG	CTATAAGGAG	ATTTTTTAAA	AATTAAACTT	CAACACAATG	AGGTGTTGCC	300
ACATCTGCAA	ACTTCCTGGG	AGAGTAATGG	GGATTGAGT	GCTTCGATTA	TCTTTGGTGG	360
TCATCCTCGT	ATTATTACTG	GTAGCTGGTG	CTTTGACTGC	CTTACTTCCC	AGTGTTAAAG	420
AAGACAAGAT	GCTCATGTTG	CGTAGGGAAA	TAAATCCCCA	GGGCAAGTCC	ACCATTGACT	480
CCTTTACTCT	CATAATGCGA	ACGTGACACA	GAAACAGATCT	CTTTATTGAAA	CTTTTAAATC	540
ATTATCAGGC	TGTACCAAAT	CTGCACAAAG	TGATTGTGGT	ATGGAACAAT	ATTGGAGAGA	600
AGGCACCAGA	TGAGTTATGG	AATTCTCTAG	GGCCCCACCC	TATCCCTGTG	ATCTTCAAAC	660
AACAGACAGC	AAACAGGATG	AGAAATCGAC	TCCAGGTCTT	TCCTGAACTG	GAAACCAATG	720
CAGTGTGAT	GGTAGATGAT	GACACACTCA	TCAGCACCCC	AGACCTTGTT	TTTGCTTTCT	780
CAGTTTGGCA	GCAATTTCCCT	GATCAAATTG	TAGGATTTGT	TCCTAGAAAAG	CACGTCTCTA	840
CTTCATCAGG	TATCTACAGT	TATGGAAGTT	TTGAAATGCA	AGCACCAGGG	TCTGGAAATG	900
GTGACCAGTA	CTCTATGGTG	CTGATTGGAG	CCTCATTTCT	CAATAGCAAA	TATCTTGAAT	960
TATTTTCAGAG	GCAACCTGCA	GCTGTCCATG	CTTTGATAGA	TGATACTCAA	AACTGTGATG	1020
ATATTGCCAT	GAATTTTATC	ATTGCCAAGC	ATATTGGCAA	GACTTCAGGG	ATATTTGTGA	1080
AGCCTGTAAA	CATGGACAAT	TTGGAAAAAG	AAACCAACAG	TGGCTATTCT	GGAATGTGGC	1140
ATCGAGCTGA	GCACGCTCTG	CAGAGGTCTT	ATTGTATAAA	TAAGCTTGTT	AATATCTATG	1200
ATAGCATGCC	CTTAAGATAC	TCCAACATTA	TGATTTCCCA	GTTTGGTTTT	CCATATGCCA	1260
ACTACAAAAG	AAAAATATAA	AAGTAAAACA	AACAAAAACA	AACCTGAAAA	CTGCTTGGCA	1320
TTTGAGTAGC	TTCTCCATGC	TATGTATTTT	TTTAAGCAAC	ATCATGAATT	TTATCTACTC	1380
CAGAAGTCTC	TACAATAGAA	AAAAAAGTGC	AGTGCTTTCTA	GGATATAAAA	TTCACTATTAC	1440
TTTTGAAAGC	CAAGAAGTTG	GTCTTATCCA	GTTAGGTTCT	CTTATGAAGA	GTTTTCTATCC	1500
AGGGATAATA	CTCCTTGGTC	AGTGATTTTA	TTGTTTACAT	CCTGAGACTG	TTCTACAGTT	1560
TCTTTGACTC	CTGGCATTTG	CCTTAAGGAC	CTATAGCAAG	CTGTTTCTAG	GATCAGAAAC	1620
TCAAGAGAGG	CATTTCTCTG	CTTTTTCACT	AAAGGTCAGT	TGTTTTAATT	TGAAACCTGA	1680
AATGCCTCTT	TAGCAAAAGC	CTGTGGTATG	GGGTAAAGCC	ATGTAAGAAG	AGAATAGTCT	1740
CAGTCACATA	TGAAGAGGAA	AATTTGCAGC	TGCCAGTGCT	TTCTTGTGG	CCCTGCCAAC	1800
CAGCTCTTCC	AGGACGAACT	CAGTCCAGCA	TGGTTTTGAT	GTAACCATCC	ATGCTTTTAT	1860
TTTTGTTAAG	TCTTTTGTGA	CTGGGACAGT	TAATTTTAGT	AGCTGAAGAA	CGCTAGTTTG	1920
TTTGCTTGAT	ATTTGTGAAC	ATTTACTGCA	TGGATCACAA	AACAATATAC	CCTGTATTTTC	1980
TTTACCGCCA	CTTATATGCA	GCAAGGAGTA	AATGTGTTAC	TAGATTTCGGG	TAGTGCATTT	2040
TGTCACGTAA	CTTGACCTTG	AGAAGTGACA	TTAATTCTTA	TATTTTACAT	AATGTATGTG	2100
TTGTTTAAGA	AATGTATAAA	AAACCTGAAA	AAAATGAGTA	AGAACTGGCA	GAAGTTAAAA	2160
CCCTTTGTAT	CAAAAGATCT	TTATTGGTAG	AGCACTGGTT	ATCTTCTGGA	TACTAAAAAG	2220
TTGTATTACA	AAGCCAAACA	CTTGCATTCA	CAACTTTAAA	AAAAGATCCA	AGGAACTATT	2280
CATAATGATG	AAATTCCAAC	TACATACAAG	GAGGAGAAAA	TAAGAACCCA	GTCATAACAG	2340
AGGAATTCTA	TAGGAGTCTG	CATCAATTCA	TTCTTAAGGT	TGCCTACTCT	CTGTTATGTG	2400
AATTAGCGTC	TGTGTTTCAC	CCATTGTCTG	TGTTTAGTCC	TTGTTTACCA	CTAAGGCAAG	2460
GAATTCTTAA	CTAGGCCTCT	GTTTACCAAC	TTCTCTTTCT	CCTCCTTTCC	CTCTATTCC	2520
TCCTTCTCCT	CTTCCTTCTT	ATATAATGCT	AGTATATTCT	CAAAATGCA	AAGCTGTGAG	2580
AATATTAAAA	TAATCATGGC	TAATGTTCCA	ATAATGAGGT	CTTTGTGCAT	TTAGTTCCGC	2640
ATATGATGGT	FTTTTTTTTA	CATTAAAGAG	TATATGTGTC	TTAATGCAGT	CAGATTGTAA	2700
AAAAACAAAA	CAAGAAACT	AAGAATCTTA	CTAAAAATCG	ATAATGTCAG	TTATCTGTTT	2760
TGTCCAATAT	TGGTAGTACT	TTTTTGCCCT	TTATGATTCC	TCTAGCAGAT	AAATAAAAGA	2820
AACTTTTGCC	ATCC					2834

## (2) INFORMATION ON SEQ ID NO. 545:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2319 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

AACGTCATTG GTAACAGCAA GTCCCAGACA CCAGCCCCCA GTTCCGAAGT GGTTTTGGAT 60  
TCAAAGAGAC AAGTTGAGAG AGAGGAAACC AACCATGAGA TCCAGGAGGG GAAAGAAGAG 120  
CCTCAGAGGG ACAGGCTGCC GCAGGAGCCA GGCCGGGAGC AGGTNGTGGA AGACAGACCT 180  
GTAGGTGGAA GAGGCTTCGG GGGAGCCGGA GAATGGGGCC AGACCCACCA GGTGCAGGCT 240  
GCCCTGTGAG TGAGNCCAGG AAAATCCAGA GATGGAGGGC CCTGAGCGAG ACCAGCTTGT 300  
CATCCCCGAC GGACAGGAGG AGGAGCAGGA AGTGCCGGG GAAGGGAGAA ACCAGCAGAA 360  
ACTGAGAGGA GAAGATGACT ACAACATGGA TGAAAATGAA GCAGAATCTG AGACAGACAA 420  
GCAAGCAGCC CTGGCAGGGA ATGACAGAAA CATAGATGTT TTTAATGTTG AAGATCAGAA 480  
AAGAGACACC ATAAATTTAC TTGATCAGCG TGAAAAGCGG AATCATACAC TCTGAATTGA 540  
ACTGGAATCA CATATTTTAC AACAGGGCCG AAGAGATGAC TATAAAATGT TCATGAGGGA 600  
CTGAATACTG AAAACTGTGA AATGTACTAA ATAAAATGTA CATCTGAANG ATGATTATTG 660  
TGNAATTTT AGTATGCACT TTGTGTAGGA AAAAATGGNA ATNGGTCTTT TAAACAGCTT 720  
TTGGGGGGNT ACTTTNGGAA GTGTCTNAAT AANGGTGTCA CNAATTTTGG GNTAGTANGG 780  
TATTTGCTGA GNAAGNNTTT AACACCAAAA CTNGGAACAT AGTTCTCCTT CAAGTGTTGG 840  
CGACANCGGG NNGCTTCCTG ATTCTGGAAT ATAACCTTGT GTAAATTAAC AGCCACCTAT 900  
AGAAGAGTCC ATCTGCTGTG AAGGAGAGAG AGAGAACTCT GGGTTCCTGC GTCCTGTCCA 960  
CGTGCTGTAC CAAGTGCTGG TGCCAGCCTG TTACCTGTTT TCACTGAAAA GTCTGGCTAA1020  
TGCTCTTGAG TAGTCACTTC TGATTCTGAC AATCAATCAA TCAATGGNCC TAGANGCACT1080  
GACTGTTAAC ACAAACGTCA CTAGNCAAAG TAGNCAACNA GCTTTAAGTC TAAATACAAA1140  
GCTGTTCTGT GTGAGAATTT TTTAAAAGGC TACTTGTATA ATAACCCTTG TCATTTTTTAA1200  
TGTACAAAAC GCTATTAAGT GGCTTAGAAT TTGAACATTT GTGGNTCTTT ATTTACTTTG1260  
CTTNCGTGTG TGGGCAAAGC AACATCTTCC CTAATATAT ATTACCAAGA AAANGCAAGA1320  
AGCAGATTAG GNTTTTTGAC NNAAAACANA ACAGGCCNNA AAAGGGGGCN TGNACCTGGA1380  
GCAGAGCATG GTGNAGAGGC AAGGCATGNA GAGGGCAAGT TTGTTGTGGA CAGATCTGTG1440  
CCTACTTTAT TACTGGAGTA AAANGAAAAC AAAGTTNCAT TGATGTGCGNA AGGATATATA1500  
CAGTGTTNAG AAATTNNAGG NACTNGTTTN AGAAAAACAG GAATACNNAA TGGNTTGNNT1560  
TTTATCATAN GTGNTACACA TTTAGCTTGT GGNTAAATNG ACTCACAAAA CTGANTTTTA1620  
AAATCAAGTT AATGTGAATT TTGAAAATTA CTAATTAATC CTAATTCACA ATAACAATGG1680  
CATTAAAGTT TGACTTGAGT TGGTTCTTAG TATTATTTAT GGTAATAGG CTCTTACCAC1740  
TTGCNAAATA ACTGGNCCAC ATCATTAATG ACTGACTTCC CNAGTAANG CTCTTAAGG1800  
GGTAAGTNAG GAGGATCCAC AGGATTTGAG ATGCTAAGGC CCCAGAGATC GTTTGATNCC1860  
AACCTCTTA TTTTCNAGAG GGGAAAATGG GGCCTNAGNA AGTTACANGA GCATCNTNAG1920  
CNTGGTGCGC TGGNCACCCC NTGGCCNTCN ACACNAGACT CCCNGAGTAG CTGGGANCTA1980  
CAGGCACACA GTCACGAGC CAGGCCNTG TTTGCAATTC ACGTTGCCNA CCTNCCAACN2040  
TTAAACATTN CTTACATATG GATGTCCTTA GTCACTAAG GTTAAANCTT TNCCCAACCA2100  
GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC TCTTCTAANG TCCTCTTCCA2160  
GCCTCACTTT GAGTCCTCCT TNGGGGTTGA TNNNAGGAAT TTTCTCTTGC TTTCTCAATA2220  
AAGTCTCTAT TCATCTCATG TTTAATTTGT ACGCATAGAA TTGCTGAGAA ATAAATGTT2280  
CTGTTCAACT TANNNNNAAA AAAAAAANAA AAAAAAAA 2319

0963395-122700

## (2) INFORMATION ON SEQ ID NO. 546:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2456 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

TGCAACTGTG CACCCAGCTT GCCAGATTTT TCCCCATTAC ACCCCCAGTG TGGCATATCC 60  
 TTGGTCCCCA GAGGCACACC CTTGATCTG TGGACCTCCA GGCCTGGACA AGAGGCTGCT 120  
 ACCAGAAACC CCAGGCCCTT GTTACTCAA TTCACAGCCA GTGTGGTTGT GCCTGACTCC 180  
 TCGCCAGCCC CTGGAACCAC ATCCACCTGG GGAGGGGCCT TCTGAATGGA GTTCTGACAC 240  
 CGCAGAGGGC AGGCCATGCC CTTATCCGCA CTGCCAGGTG CTGTCGGCCC AGCCTGGCTC 300  
 AGAGGAGGAA CTCGAGGAGC TGTGTGAACA GGCTGTGTGA GATGTTTCAGG CCTAGCTCCA 360  
 ACCAAGAGTG TGCTCCAGAT GTGTTGGGGC CCTAACTTGG CACAGAGTCC TGCTCCTGGG 420  
 AAAGGAAAGG ACCACAGCAA ACACCATTCT TTTTGCCGTA CTTCTAGAA GCACTGGAAG 480  
 AGGACTGGTG ATGGTGGGAG GGTGAGAGGG TGCCGTTTTT CTGCTCCAGC TCCAGACCTT 540  
 GTCTGCAGAA AACATCTGCA GTGCAGCAA TCCATGTCCA GCCAGGCAAC CAGCTGCTGC 600  
 CTGTGGCGTG TGTGGGCTGG ATCCCTTGAA GGCTGAGTTT TTGAGGGCAG AAAGCTAGCT 660  
 ATGGGTAGCC AGGTGTTACA AAGGTGCTGC TCCTTCTCCA ACCCCTACTT GGTTTCCCTC 720  
 ACCCAAGCC TCATGTTTAT ACCAGCCAGT GGGTTCAGCA GAACGCATGA CACCTTATCA 780  
 CCTCCCTCCT TGGGTGAGCT CTGAACACCA GCTTTGGCCC CTCCACAGTA AGGCTGCTAC 840  
 ATTCAGGGGC AACCCTGGGC TCTATCATTT TCCTTTTTTG CCAAAAGGAC GACGTAGATA 900  
 GGTGAGCCCT GAGCACTAAA AGGAGGGGTC CCTGAAGCTT TCCCACTATA GTGTGGAGTT 960  
 CTGTCCCTGA GGTGGGTACA GCAGCCTTGG TTCCTCTGGG GGTGAGAAT AAGAATAGTG1020  
 GGGAGGGAAA AACTCCTCCT TGAAGATTTC CTGTCTCAGA GTCCCAGAGA GGTAGAAAGG1080  
 AGGAATTTCT GCTGGACTTC ATCTGGGCAG AGGAAGGATG GAATGAAGGT AGAAAAGGCA1140  
 GAATTACAGC TGAGCGGGGA CAACAAAGAG TTCTTCTCTG GGAAAAGTTT TGTCTTAGAG1200  
 CAAGGATGGA AAATGGGGAC AACAAAGGAA AAGCAAAGTG TGACCCTTGG GTTTGGACAG1260  
 CCCAGAGGCC CAGCTCCCCA GTATAAGCCA TACAGGCCAG GGACCCACAG GAGAGTGGAT1320  
 TAGAGCACAA GTCTGGCCTC ACTGAGTGGA CAAGAGCTGA TGGGCCTCAT CAGGGTGACA1380  
 TTCACCCAG GGCAGCCTGA CCACTCTTGG CCCCTCAGGC ATTATCCCAT TTGGAATGTG1440  
 AATGTGGTGG CAAAGTGGGC AGAGACCCC ACCTGGGAAC CTTTTTCCCT CAGTTAGTGG1500  
 GGAGACTAGC ACCTAGGTAC CCACATGGGT ATTTATATCT GAACCAGACA GACGCTTGAA1560  
 TCAGGCACTA TGTTAAGAAA TATATTTATT TGCTAATATA TTTATCCACA AATGTGGTCT1620  
 GGTCTTGTGG TTTTGTCTG TCGTGAAGT CACTCAGGGT AACACGTCA TCTCTTTCTA1680  
 CATCAAGAGA AGTAAATTAT TTATGTTATC AGAGGCTAGG CTCCGATTCA TGAAAGGATA1740  
 GGGTAGAGTA GAGGGCTTGG CAATAAGAAC TGGTTTGTA GCCCCTAAAA GTGTGGCTTA1800  
 GTGAGATCAG GGAAGGAGAA AGCATGACTG GATTCTTACT GTGCTTCAGT CATTATTATT1860  
 ATACTGTTCA CTTACACAT TATCATACTT CAGTGACTCA GACCTTGGGC AAATACTCTG1920  
 TGCCTCGCTT TTTAGTCCA TAAAATGGGC CTACTTAATA GTTGTTCAG GACTTACATG1980  
 AGATAATAGA GTGTAGAAAA TATGTTCCAA AGTGGAAGT TTTATTAGT GATAGAAAAC2040  
 ATCCAAACCT GTCACAGAGC CCATCTGAAC ACAGCATGGG ACCGCCAACA AGAAGAAAGC2100  
 CCGCCCGGAA GCAGCTCAAT CAGGAGGCTG GGCTGGAATG ACAGCGCAGC GGGGCCTGAA2160  
 ACTATTATA TCCCAAAGCT CCTCTCAGAT AAACACAAAT GACTGCGTTC TGCCTGCACT2220  
 CGGGCTATTG CGAGGACAGA GAGCTGGTGC TCCATTGGCG TGAAGTCTCC AGGGCCAGAA2280  
 GGGGCCTTTG TCGCTTCCTC ACAAGGCACA AGTTCCCCTT CTGCTTCCCC GAGAAAGGTT2340  
 TGGTAGGGGT GGTGGTTAG TGCCTATAGA ACAAGGCATT TCGCTTCCTA GACGGTGAAA2400  
 TGAAAGGGAA AAAAAGGACA CCTAATCTCC TACAAATGGT CTTTAGTAAA GGAACC 2456

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 547:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2218 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

GAGGAAAAAG AACAAATGAAC AGCAACGATC TTGACTGTGC AACTCAGACA TTCCTGCAGA 60  
 AAAGACATAT GTTGCTTTAC AAGAAGGCCA AAGAACTATG GGGCCTTCCC AGCATTTGAC 120  
 TGTTCATTGC ATAGAATGAA TTAAATATCC AGTTACTTGA ATGGGTATAA CGCATGAATG 180  
 TGTGATTTTA TTAGGGGCAT CTGCCAATTC TCTCACTGTG GTTCCTTCTC TGACTTTGCC 240  
 TGTTCATCAT CTAAGGAGGC TAGATCCTTC GCTGACTTCA CCATTCCTCA AACCTGTAAG 300  
 TTTCTCACTT CTTCCAAAT GGCTTTGGCT CTTTCTTCAA CCTTTCCATT CAAGAGCAAT 360  
 CTTTGCTAAG GAGTAAGTGA ATGTGAAGAG TACCAACTAC AACAATTCTA CAGATAATTA 420  
 GTGGATTGTG TTGTTTGTG AGAGTGAAGG TTTCTTGGCA TCTGGTGCCT GATTAAGGCT 480  
 TGAGTATTAA GTTCTCAGCA TATCTCTCTA TTGTCTTGAC TTGAGTTTGC TGCATTTTCT 540  
 ATGTGCTGTT CGTGACTTGG AGAACTTAAA GTAATCGAGC TATGCCAACT TGGGGTGGTA 600  
 ACAGAGTACT TCCCACCACA GTGTTGAAAG GGAGAGCAAA GTCTTATGGA TAAACCCTCC 660  
 TTTCTTTTGG GGACACATGG CTCTCACTTG AGAAGCTCAC CTGTGCTGAA TGTCCACATG 720  
 GTCATAAAC ATGTTATCCT TAAACCCCCC GTATGCCTGA GTTGAAAGGG CTCTCTCTTA 780  
 TTAGGTTTTC ATGGGAACAT GAGGCAGCAA ATCTATTGCT AAGACTTTAC CAGGCTCAAA 840  
 TCATCTGAGG CTGATAGATA TTTGACTTGG TAAGACTTAA GTAAGGCTCT GGCTCCCAGG 900  
 GGCATAAGCA ACAGTTTCTT GAATGTGCCA TCTGAGAAGG GAGACCCAGG TTATGAGTTT 960  
 TCCTTTGAAC ACATTGGTCT TTTCTCAAAG TTCCTGCCTT GCTAGACTGT TAGCTCTTTG 1020  
 AGGACAGGGA CTATGTCTTA TCAATCACTA TTATTTTCCT GTTACCTAGC ATGGGACAAG 1080  
 TACACAACAC ATATTGTGT AGTCTTCTAA AAGACTCCTC TGATTGGGAG ACCATATCTA 1140  
 TAATTGGGAT GTGAATCATT TCTTCAGTGG AATAAGAGCA CAACGGCACA ACCTTCAAGG 1200  
 ACATATTATC TACTATGAAC ATTTTACTGT GAGACTCTTT ATTTTGCCTT CTACTTGCGC 1260  
 TGAAATGAAA CCAAAACAGG CCGTTGGGTT CCACAAGTCA ATATATGTTG GATGAGGATT 1320  
 CTGTTGCCTT ATTGGGAAC GTGAGACTTA TCTGGTATGA GAAGCCAGTA ATAAACCTTT 1380  
 GACCTGTTT AACCAATGAA GATTATGAAT ATGTTAATAT GATGTAAATT GCTATTTAAG 1440  
 TGTAAAGCAG TTCTAAGTTT TAGTATTTGG GGGATTGGTT TTTATTATTT TTTTCTTTT 1500  
 TGAAAAATAC TGAGGGATCT TTTGATAAAG TTAGTAATGC ATGTTAGATT TTAGTTTTCG 1560  
 AAGCATGTTG TTTTCAAAT ATATCAAGTA TAGAAAAAGG TAAAACAGTT AAGAAGGAAG 1620  
 GCAATTATAT TATCTCTCTG TAGTTAAGCA AACACTTGTT GAGTGCCTGC TATGTGCACG 1680  
 GCATGGGCCC ATATCTGTGA GGAGCTTGTC TAATTATGTA GGAAGCAATA GATCTCGGTA 1740  
 GTTACGTATT GGGCAGATAC TTAGTGTATG AATGAAAGAA CATCACAGTA ATCACAATAT 1800  
 CAGAGCTGAG TTATCCCCAG TGTAAGCTTCG TTGGGGATTC CAGTTTCTGG GAACGAGAGT 1860  
 TAGGGCCATT TTATTTAAAA GAAACTCCCG GTTGAGACCG GTTCTTATGA ACCTCTGAAA 1920  
 CGTACAAGCC TTCACAAGTT TAACTAAATT GGGATTAATC TTTCTGTAGT TATCTGCATA 1980  
 ATTCTTGTTT TTCTTTCCAT CTGGCTCCTG GGTGACAAT TTGTGGAAAC AACTCTATTG 2040  
 CTACTATTTA AAAAAATCA GAAATCTTTC CCTTTAAGCT ATGTTAAATT CAAACTATTG 2100  
 CTGCTATTCC TGTTTTGTCA AAGAATTATA TTTTCAAAA TATGTTTATT TGTTTGATGG 2160  
 GTCCCAGGAA AACTAATAA AAACCACAGA GACCAGCCCC AAAAAAAAAA AAGTTTTG 2218

09673395-12200



## (2) INFORMATION ON SEQ ID NO. 548:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2196 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

CGGCGCGATG	CGCGGAGACC	CCC GCGGGGG	CGGCGGCGGC	CGTGAGCCCC	GATGAGGCCC	60
GAGCGTCCCC	GGCGCGCGGG	CAGCGCCCCC	GGCCCGATGG	AGACCCCGCC	GTGGGACCCA	120
GCCCGCAACG	ACTCGCTGCC	GCCCACGCTG	ACCCCGGCCG	TGCCCCCCTA	CGTGAAGCTT	180
GGCCTCACCG	TCGTCTACAC	CGTGTCTAC	GCGCTGCTCT	TCGTGTTTCT	CTACGTGCAG	240
CTCTGGCTGG	TGCTGCGTTA	CCGCCACAAG	CGGCTCAGCT	ACCAGAGCGT	CTTCCTCTTT	300
CTCTGCCTCT	TCTGGGCCTC	CCTGCGGACC	GTCCTCTTCT	CCTTCTACTT	CAAAGACTTC	360
GTGGCGGCCA	ATTGCTCAG	CCCCTTCGTC	TTCTGGCTGC	TCTACTGCTT	CCCTGTGTGC	420
CTGCAGTTTT	TCACCCTCAC	GCTGATGAAC	TTGTACTTCA	CGCAGGTGAT	TTTCAAAGCC	480
AAGTCAAAAT	ATTCTCCAGA	ATTACTCAA	TACCGGTTGC	CCCTCTACCT	GGCCTCCCTC	540
TTCATCAGCC	TTGTTTTCT	GTTGGTGAAT	TTAACCTGTG	CTGTGCTGGT	AAAGACGGGA	600
AATTGGGAGA	GGAAGGTTAT	CGTCTCTGTG	CGAGTGGCCA	TTAATGACAC	GCTCTTCGTG	660
CTGTGTGCCG	TCTCTCTCTC	CATCTGTCTC	TACAAAATCT	CTAAGATGTC	CTTAGCCAAC	720
ATTTACTTGG	AGTCCAAGGG	CTCCTCCGTG	TGTCAAGTGA	CTGCCATCGG	TGTCACCGTG	780
ATACTGCTTT	ACACCTCTCG	GGCCTGCTAC	AACCTGTTCA	TCCTGTCTAT	TTCTCAGAAC	840
AAGAGCGTCC	ATTCTTTTGA	TTATGACTGG	TACAATGTAT	CAGACCAGGC	AGATTGGAAG	900
AATCAGCTGG	GAGATGCTGG	ATACGTATTA	TTTGGAGTGG	TGTTATTTGT	TTGGGAACTC	960
TTACCTACCA	CCTTAGTCGT	TTATTTCTTC	CGAGTTAGAA	ATCCTACAAA	GGACCTTACC	1020
AACCCTGGAA	TGGTCCCCAG	CCATGGATTC	AGTCCCAGAT	CTTATTTCTT	TGACAACCTT	1080
CGAAGATATG	ACAGTGATGA	TGACCTTGCC	TGGAACATTG	CCCCTCAGGG	ACTTCAGGGA	1140
GGTTTTGCTC	CAGATTACTA	TGATTGGGGA	CAACAAACTA	ACAGCTTCCT	GGCACAAAGCA	1200
GGAACCTTTC	AAAGACTCAA	CTTTGGATCC	TGACAAACCA	AGCCTTGGGT	AGCATCAGTT	1260
AACAGTTTTA	TGGACGATTC	CTCAGATGAA	AAGCTTCAGA	AAAGCATAGT	GACAGCTGAA	1320
TTTTTAGGGC	ACTTTTCCTT	AAGAAATAGA	ACTTGATTTT	TATTTGTTAC	AGGTTTCCAA	1380
TGGCCCCATA	GGAATAAGCA	ATAATGTAGA	CTGATAAACC	CTTATTTTAG	TACTAAAGAG	1440
GGAGCCTTGC	TATTTTCAGT	GGTATAATTT	AAACTTTTTT	AAGAAAATCT	GTACTTTTAT	1500
AAAGATGTAT	TTTGATAAAC	TTAAATAATA	ATGCTAAAGT	ATACTAGGGT	TTTTTTTTCT	1560
TGAGAATGTT	ACTGCAATCA	TGTTGTAGTT	TGCACAGACT	TTTATGCATA	ATTCACTTTA	1620
AAAATATAGA	ATATATGGTC	TAATAGTTTT	TTAAAGCTTT	TGGACTAAAG	TATTCACAA	1680
ATCTTACCTC	TTTAGGTCAC	TGATGGTCAC	TCCGATTCTG	AGTGCCACAT	TGGTAGACTC	1740
CTAAAATACA	GTTGACAACT	TAGCCAATTG	CAACTCCAGT	GTTGATAATT	AAAATGAAAT	1800
GGTAAAGCAG	CAGACTGTAA	GGTCTTTAGA	GATTTTTTTT	TTAAGGTTCA	GGCCGTAGGT	1860
TCCTCAAGGA	ATCTCTTAAG	TTTTGCCCAA	AGACTGGTAC	TTCTTTTCAG	TAGGGCGCTA	1920
ATGTATACAC	ATTAATGATA	AGTTGATAAC	ATTAAAAATG	TAGCTGACTT	ATCCTATTAA	1980
ACCTCCTCTG	CTATGTTTAC	AGAACCCCCA	TAACCTTTTT	TCAGCCTAAT	GAAATCTAAT	2040
ATGCATTACC	TCAGGGCCAC	ATCAAGAATA	CACCCCTTTC	CGAACTCACT	GAATGTTTCA	2100
TACATTCAAG	GAGAAAATAA	GAGGGTCCAT	AAAGGGCATT	AATAACAAAT	ACCCCAAGCC	2160
GTTGAGCTAA	GACTATGTGG	AATCCTAATA	GTTTTT			2196

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 549:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 701 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

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AATTAAATA AATAGAAACA TACGGAGATT CTTTATGTT GGATTTATTA TACCCTCCAC 60
CATTTTGGTC CCTGAAAAGG GAAAAGATAC ACGGTCGAGT AGTACAGGTA TGTGTTTCCC120
ACTACACATT ATGGCTATAA TGGAGTTGAA TTGCAAACAG TAAAATTTTG TTTTGGATTG180

GTTTCCCCTG ATCCCCCAG ACAGGAGCTT CCTCTCCCAC CCTACCTGCC TGCCCTTAAG240
TTGTGTCCTA TTAAACTGGA CACAAATCTC ACCGGCTTTT AGTCTAATAA TTGAATCATA300
GCTACACACA GTGACACCAG AATAGCTACT TGTTTTTTTA TGTTACCAGT GAGTAACTTG360
TTTATCCTTG TATGTAGAAA CTAATTTTAC CATGATCACA GATCTGTGTA ACATCTCTAG420
TTTGAATTC CACACAATTT TAAAATGTCT ACTAGAAAAC TTACACCTTT TTGTTCCAAG480
GTGCTCTTCA TCTATAAAC CGTGGGCATA CTTCAGTGTT CTTCTGAGGC CAAATTTTGT540
GGGTCGTGGG GGACAATTTT GTATTAACAT ACGTTATTTT GTAATTCATT CTCCAAATTT600
GAAGCTTTAT TAAAGGTATT CTATTTCCAC TGGCTTCCCT TAACTTGAAT AAAATTTACT660
CCCAGTGCCG TGGCTCATGC CTGCTGCAAT CCCAGCCCTT T 701

```

## (2) INFORMATION ON SEQ ID NO. 550:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2214 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

00673396.12700

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GCTAAAGAGG AGGATGCTAT ACTTTTCTAA ATGGCAAGAG ATGGGGGAGAG AAGGGGATTA 60  
 AGAGTTGACC CGCAACCTCC CGGTGGATTG TTTGTTCTTA CCAGATCTCT TGGCCACTCC 120  
 CCTATTCTGA AGTCGTCTTG GCTCTCTTGA CTGCTCCCCT ATTCTGAAGT CGTCTTGGCT 180  
 CTCTTGACTA CTCCCCTATT CTGAAGTCGT CTTGGCTCTC CTGACTACAC TATTTCAAGG 240  
 AATGATCACC AAGACACACA AAGTAGACCT TGGGCTCCCA GAGAAGAAAA AGAAGAAGAA 300  
 AGTGGTCAAA GAACCAGAGA CTCGATACTC AGTTTTTAAAC AATGATGATT ACTTTGCTGA 360  
 TGTTTCTCCT TTAAGAGCTA CATCCCCCTC NTAAGAGTGT GGCCCATGGG CAGGCACCTG 420  
 AGATGCCTCT AGTGAAGAAA AAGAAGAAGA AAAAGAAGGG TGTCAGCACC CTTTGCGAGG 480  
 AGCATGTAGA ACCTGAGACC ACGCTGCCTG CTAGACGGAC AGAGAAGTCA CCCAGCCTCA 540  
 GGAAGCAGGT GTTTGGCCAC TTGGAGTTCC TCAGTGGGGA AAAGAAAAAN TAAGAAGTCA 600  
 CCTCTAGCCA TGTCCCATGC CTCTGGGGTG AAAACCTCCC CAGNACCCNT AGACAGGGTG 660  
 AGGAGGAAAC CAGAGTTGGC AAGAAGCTCA AAAAANCACA AGAAGGAAAA AAAGGGGGNC 720  
 CCAGGACCCC ACNAGCCTTC TCGGTCCAGG ACCCTTGGTT CTGTGAGGCC AGGGAGGCCA 780  
 GGGATGTTGG GGACACTTGC TNCAGTGGGG AAGAAGGATG AGGAACAGGC AGCCTTGGGG 840  
 NCAGAAACGG AAGNCGGAAG AGCCCCAGAG AACACAATGG GAAGGTGAAG AAGAAAAAAA 900  
 AAATCCACCA GGAGGGAGAT GCCCTCCAG GCCACTCCAA GCCCTCCAGG TCCATGGAGA 960  
 GCAGCCCTAG GAAAGGAAGT AAAAAGAAGC CAGTCAAAGT TGAGGCTCCG GAATACATCC1020  
 CCATAAGTGA TGACCCTAAG TCCTCCGCAA AGAAAAAGAT GAAGTCCAAA AAGAAGGTAG1080  
 AGCAGCCAGT CATCGAGGAG CCAGCTCTGA AAAGGAAGAC GAGGAAGAAG AGGAAAGAGA1140  
 GTGGGGTAGC AGGAGACCTT TGGAGGGAGG AAACAGACAC GGACTTAGAG GTGGTGTGG1200  
 AAAAAAAGG CAACATGGAT GAGGCGCACA TAGACCAGGT GAGGCGAAAG GCCTTGCAAG1260  
 AAGAGATCGA TCGCGAGTCA GGCAAAACGG AAGCTTCTGA AACCAGGAAG TGGACGGGAA1320  
 CCCAGTTTGG CCAGTGGGAT ACTGCTGGTT TTGAGAACGA GGACCAAAAA CTGAAATTTTC1380  
 TCAGACTTAT GGGTGGCTTC AAAAACCTGT CCCCTTCGTT CAGCCGCCCC GCCAGCACGA1440  
  
 TTGCAAGGCC CAACATGGCC CTCGGCAAGA AGGCGGCTGA CAGCCTGCAG CAGAATCTGC1500  
 AGCGGGACTA CGACCGGGCC ATGAGCTTGG AAGTACAGCC GGGGAGCCGG CTTGCGGTGT1560  
 TCTCCACCGC CCCCAACAAG ATCTTTTACA TTGACAGGAA CGCTTCCAAG TCAGTCAAGC1620  
 TGGAAGATTA AACTCTAGAG TTTTGTCCCC CAAAACCTGC CACAATTGCT TTGATTATTC1680  
 CATTTATGCT GGAGATTACA AATTTTTTTT GGTGAACAAA TCAGATCTTG GTGAGGACCT1740  
 CGAGCAGTAA GATATAAATA ACTCCCNATA AGCTTAGNCG TTCCAGTAA TGGAACACTA1800  
 GGCATAAANT GGTTTATTNC AGTTGTGCAA ATGAAAGCCA TCTGACAGTT GGCTNCACAT1860  
 TGAACACCTG TGGAGATTAA GGACGAGGAC AACTATATTG ATGGGCTTGG ATGAACTGGG1920  
 GCAGGGCAGC TCATATTTTC GGAGCCAGGA GAACGAGTGA GTGCTAAAC CTCCTGTTTT1980  
 CTGTGTTAAA CATTCCGTCC CTGTTTGAGA CATCAGTATG TACAGTTAAC TTTTGTGAG2040  
 TGTTTAGCAG GTACTAGGGA CATACTAGTG TTTTCCTTAA TGTATTTAAT CTTCATAATT2100  
 ATGAAATGGG TGCTATTATT AGCCCCATCT TATAGATGAG GCAACTGAGG TTCAGGGATA2160  
 AAGTAATAAA ATTGCCTGGG GTCACCCAGC CACTAAAAAA AAAAAAAAAA AAAA 2214

0967395-12700

## (2) INFORMATION ON SEQ ID NO. 551:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

GCGCGGCCGG CGCCTGCGGG GCGAGAGGGT CGGGGCGAAG GGAAGCTAC GTCCCGGAGG 60  
 TGCGGTGTGG GGCACCGGGC GGGGCGCGG GAACCGGCGC CCCACGGAGC TGCTGCTGTC 120  
 AGACCAACCC CGGGCCCCCA TCATCACTGC GCCGCGCTTT CAGGCGCCGA GAACTACCGT 180  
 TCCCGGCATG CCATGAAATT GGCCTCGGCG CTGAGGCGGG GTCCGGCCCT CCACCCGCTC 240  
 CCGCCGCGCG CGAATCGCGG TCGCGAGCCA TGGAGGAGGA GGCATCGTCC CCGGGGCTGG 300  
 GCTGCAGCAA GCCGCACCTG GAGAAGCTGA CCCTGGGCAT CACGCGCATC CTAGAATCTT 360  
 CCCAGGTGT GACTGAGGTG ACCATCATAG AAAAGCCTCC TGCTGAACGT CATATGATTT 420  
 CTTCCTGGGA AAAAAAGAAT AACTGTGTGA TGCCTGAAGA TGTGAAGAAC TTTTACCTGA 480  
 TGACCAATGG CTTCCACATG ACATGGAGTG TGAAGCTGGA TGAGCACATC ATTCCACTGG 540  
 GAAGCATGGC AATTAACAGC ATCTCAAAAC TGA CTGAGT CACCCAGTCT TCCATGTATT 600  
 CACTTCCTAA TGCACCCACT CTGGCAGACC TGGAGGACGA TACACATGAA GCCAGTGATG 660  
 ATCAGCCAGA GAAGCCTCAC TTTGACTCTC GCAGTGTGAT ATTTGAGCTG GATTCATGCA 720  
 ATGGCAGTGG GAAAGTTTGC CTTGTCTACA AAAGTGGGAA ACCAGCATTG GCAGAAGACA 780  
 CTGAGATCTG GTTCCTGGAC AGAGCGTTAT ACTGGCATT TCTCACAGAC ACCTTTACTG 840  
 CCTATTACCG CCTGCTCATC ACCACCTGG GCCTGCCCCA GTGGCAATAT GCCTTCACCA 900  
 GCTATGGCAT TAGCCACAG GCCAAGCAAT GGTTCAGCAT GTATAAACCT ATCACCTACA 960  
 ACACAAACCT GCTCACAGAA GAGACCGACT CCTTTGTGAA TAAGCTAGAT CCCAGCAAAG1020  
 TGTTTAAGAG CAAGAACAAG ATCGTAATCC CAAAAAGAA AGGGCCTGTG CAGCCTGCAG1080  
 GTGGCCAGAA AGGGCCCTCA GGACCCTCCG GTCCCTCCAC TTCCTCCACT TCTAAATCCT1140  
 CCTCTGGCTC TGGAAACCCC ACCCGGAAGT GAGCACCCCT CCCTCCAAC CTCTACCAGC1200  
  
 TCCAGAGTGG TGGTTTCCAT GCACAGATGG CCCTAGGGGT GACCTCCAGT TTTGCGTGTG1260  
 GACCGTAGGC CTCTTTCTAG TTGAATGACC AAAATTGTAA GGCTTTTAGT CCCACCGACA1320  
 TTAGCCAGGC TCGTAGTGAG GCCTCCAGAG CAGGTTGTGC TGTCCCCTGC CTCTGGAAGC1380  
 AATGGGGAAT GTGGAATCAA GACAATGCCC AAAAAATTTT TAATGCAGCT GGTC 1434

0962395-12700

## (2) INFORMATION ON SEQ ID NO. 552:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

```

CCCCGAGAAG GTGGAGGGAG ACGAGAAGCC GCCGAGAGCC GACTACCCCTC CGGGCCCCAGT 60
CTGTCTGTCC GTGGTGGATC TAAGCCTCAT CTGTATCCTC TTGTGATGGC GTGAAGGAAA 120
GCCATGGCAG ATTTCCAGCC TGGTGATGCT GTACAGAACA CAGGTGGCCT GCTTCCATGC 180
CTCCTCAGCT TCAAGAAACT AGAATGAACC GAAGCATTCC TGTGGAGGTT GATGAATCAG 240
AACCATACCC AAGTCAGTTG CTGAAACCAA TCCCAGAATA TTCCCCGGAA GAGGAATCAG 300
AACCACCTGC TCCAAATATA AGGAACATGG CACCCAACAG CTTGTCTGCA CCCACAATGC 360
TTCACAATTC CTCCGGAGAC TTTTCTCAAG CTCACTCAAC CCTGAAACTT GCAAATCACC 420
AGCGGCCTGT ATCCCGGCAG GTCACCTGCC TGCACACTCA AGTTCTGGAG GACAGTGAAG 480
ACAGTTTCTG CAGGAGACAC CCAGGCCTGG GCAAAGCTTT CCCTTCTGGG TGCTCTGCAG 540
TCAGCGAGCC TGCCTCTGAG TCTGTGGTTG GAGCCCTCCC TGCAGAGCAT CAGTTTTTCAT 600
TTATGGAAAA ACGTAATCAA TGGCTGGTAT CTCAGCTTTC AGCGGCTTCT CCTGACACTG 660
GCCATGACTC AGACAAATCA GACCAAAGTT TACCTAATGC CTCAGCAGAC TCCTTGGGCG 720
GTAGCCAGGA GATGGTGCAA CGGCCCCAGC CTNCACAGGA ACCGAGCAGG CCTGGATCTG 780
CCAACCATAG ACACGGGATA TGATTCCCAG CCCCAGGATG TCCTGGGCAT CAGGCAGCTG 840
GAAAGGCCCC TGNCCCTCAC CTCCGTGTGT TACCCCCAGG ACCTCCCCAG ACCTCTCAGG 900
TCCAGGGAGT TCCCTCAGTT TGAACCTCAG AGGTATCCAG CATGTGCACA GATGCTGCCT 960
CCCAATCTTT CCCCACATGC TCCATGGAAC TATCATTACC ATTGTCCTGG AAGTCCCGAT1020
CACCAGGTGC NCATATGGCC ATGACTACCC TCGAGCAGCC TACCAGCAAG TGATCCAGCC1080
GGCTCTGCCT GGGNCAGCCC CTNNGCCTGG AGCCAGTGTG AGAGGCCTGC ACCCTGTGCA1140
GAANNNGTTA TCCTGAATTA TCCCAGCCCC TGGGACCAAG AAGAGAGGCC CGCACAGAGA1200
GACTGTCTCT TTCCGGGGCT TCCAAGGCAC CAGGACCAGC CACATCACC GACACCTAAT1260
AGAGCTGGTG CTCCGTGGGA GTCCTTGGAG TGGCTGCAG AGCTGAGACC ACAGGTTCCC1320
CAGCCTCCGT CCCCAGCTGC TGTGCCTAGA CCCCCTAGCA ACCCTCCAGC CAGAGGAACT1380
CTAAAAACAA GCAATTTGCC AGAAGAATTG CGGAAAGTCT TTATCACTTA TTCGATGGAC1440
ACAGCTATGG AGGTGGTGAA ATTCGTGAAC TTTTGTGTTG TAAATGGCTT CCAAAGTGA1500
ATTGANCANT ATTTGAGGAT AGAATCCGAG GCATTGATAT CATTNAAATG GATGGAGCGC1560
TACCTTANGG GATAAGACCG TGATGATAAT CGTAGCAATC AGCCCCNAAA NTACAAANNC1620
AGGACGTNGG NAAGGNCGCT GANGTCNGCA GCTGGACGAG GATGAGCATG GCTTACATAC1680
TAAGTACATT CATCGAATGA TGCAGATTGA GTTCATAAAA CAAGGAAGCA TGAATTTTCAG1740

ATTCATCCCT GTGCTCTTCC CAAATGCTAA GAAGGAGCAT GTGCCCACCT GGCTTCAGAA1800
CACNTCATGT CTACAGCTGG CCCAAGAATN AAAAAAACA TCCTGCTGCG GCTGCTNGAG1860
AGAGGAAGAG TATGTGGCTC CTCCACGGGG GCCTCTGCCC ACCNCTTCAG GTGGTTCCCT1920
TGTGANCACC GTTCATCCCC AGATCACTGA GGCCNAGGCC ATGTTTGGGN GCCTTGTCT1980
GNACAGCATT CTGGCTGAGG CTNNGTCCGT AGCANNTCC TGGCTGGTTT TTNTTCTGTT2040
CCNTCCCCGA NGAAGCCCTC TGGNNCCCCC ANGGAAACCT GTTGTGCAGA GCTCTTCCCC2100
GGAGACCTCC NACACANCCC TGGNCTTTGA AGTGGAGTCT GTGNACTGNC TCTGCATTNC2160
TCTGCTTTTN AAAAAACCA TTGCAGGTGN CCAGTGTCCT ATATGTTNCC TCCTNGACAG2220
NTTTGATGTN GTNCCATTCT NGGGCCTCTC AGTGCTTAGC AAGTAGATAA TGTAAGGGAT2280
GTNGGCAGCA AATGGAAATG ACTACAAACA CTCTCCTATC AATCACTTCA GGCTACTTTT2340
ATGAGTTAGC CAGATGCTTG TGTATCCTCA NGACCAAACT GATTTCATGA CAAATAATAA2400
AATGTTTACT CTTTGTGAAA AAAAAAAAAA AAAA

```

2434

0963395-12200

## (2) INFORMATION ON SEQ ID NO. 554:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

ACTAACCCAG AGTTGTGGCA TTATTAATTA TCACTGGTCT TCTTAATCGT AAAACGGGGG 60  
 ACCCCAGAGG CAAGGAAATT TCCATTACCC TATATTGGGC TTAAACTTAA AGGAGTATAT 120  
 CCACTATCAA GAGCTTAGTA CAAAGGCTGG GGTGAAGTTA CATTATACCT GGGCGTTTTA 180  
 CCATACCAGG GACCCACCT CAACAATGAC TGTGGAAGAC CAAAGGAGAT ACCTAGGTTC 240  
 AGATTATAAT AAATCACCCA GCACCACCTG AATGTATTAT CCACAAAGAT ATAGCAATAA 300  
 TAAAGGTTAT ATATACATAT ATTTATCTTG GTAACCTGAG GGCTAAAAAC GTGGAATACG 360  
 ATAATTCTTC TCAAGAGGTC CATCTGTAAG AAAGGGACCC AAAAGGACAG TGTTTGTGTT 420  
 GCATAAAATA TGGGTAAAGT GGAGTTGGGA ACAAAGGGTG GTTCTTTTAG CTCTTCCAC 480  
 ATCTCTCTTT GATAAGGACT GAAACCCTGT TGATTCATGA TAAACGTTTC CTTTTTTTTT 540  
 TTTTTTGGCA GCGGGGAGAG GGAAAGAGGA GGAAATGGGG TTTGAGGACC ATGGCTTACC 600  
 TTTCTGCCTT TTGACCCATC ACACCCCAT TCCCTCCTCT TCCCTCTCCC CGCTGCCAAA 660  
 AAAAAAAAAA AGGAAACGTT TATCATGAAT CAACAGGGTT TCAGTCCTTA TCAAAGAGAG 720  
 ATGTGGAAG AGCTAAAGAA ACCACCCTTT GTTCCCACT CCACTTTACC CATATTTTAT 780  
 GCAACACAAA CACTGTCTTT TTGGGTCCCT TTCTTACAGA TGGACCTCTT GAGAAGAATT 840  
 ATCGTATTCC ACGTTTTTAG CCCTCAGGTT ACCAAGATAA ATATATGTAT ATATAACCTT 900  
 TATTATTGCT ATATCTTTGT GGATAATACA TTCAGGTGGT GCTGGGTGAT TTATTATAAT 960  
 CTGAACCTAG GTATATCCTT TGGTCTTCCA CAGTCATGTT GAGGTGGGCT CCCTGGTATG 1020  
 GTAAAAAGCC AGGTATAATG TAACTTCACC CCAGCCTTTG TACTAAGCTC TTGATAGTGG 1080  
 ATATACTCTT TTAAGTTTAG CCCCAATATA GGGTAATGGA AATTCCTGC CCTCTGGGTT 1140  
 CCCCATTTTT ACTATTAAGA AGACCAGTGA TAATTTAATA ATGCCACCAA CTCTGGCTTA 1200  
 GTTAAGTGAG AGTGTGAAC GTGTGGCAAG AGAGCCTCAC ACCTCACTAG GTGCAGAGAG 1260  
 CCCAGGCCTT ATGTTAAAAT CATGCACTTG AAAAGCAAAC CTTAATCTGC AAAGACAGCA 1320  
 GCAAGCATT TACGGTCATC TTGAATGATC CCTTTGAAAG TTTTGTGGT 1380  
 TTTAAATCA AGCCTGAGGC TGGGTGGAAA CAGGTAGCCT ACACACCCCA AATTGGGGGT 1440  
 GGTCCCGGGG GAATGTT 1457

09673395.12200

## (2) INFORMATION ON SEQ ID NO. 555:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 741 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

```

CCTCCTAAAA GACTGGGAAA GCAGCTTTGG GCTTTGGGTC CTCCTAAAAA AACCAAGGCG 60
GATGACTTGG GGTTTGGATC CCCTTCGGAT GTCACTCGAA AAAGCCTTAG CAGACCTGAT120
TGAGAAGGAA CTGTCCCGTT CAAAGACCAA CCTTCCCTTT CGCCCCACAT CTCTTCAGAA180
CTCCTCTTCA CACACTACAA CCGCCAAAGG TCCCAGGCTC TGGATTCTTG CATCCTGCTG240
CAGCTACAAA TGCCAATTCT CTAAATAGTA CCTTTTCAGT CTTGCCCCAG AGGTTCCTC300
AATTTTCAGCA GCACCGAGCG GTTTATAATT CATTGAGTTT TCCAGGCCAG GCAGCCCGCT360
ATCCTTGGAT GGCCTTTCCA NCGCAATAGC ATCATGCNAC TTGAACCACA CAGCAAACCC420
CACCTCAAAT AGTAATTTCT TGGACTTGAA TCTCCCGCCA CAGCACAACA CAGGTCTGGG480
AGGGATCCCT GTAGCAGGGG AAGAAGAGGT GAAGGTTTCG ACCATGCCAC TGTCAACCTC540
TTCCCATTTCA TTACAACAAG GACAGCAGCC TACAAGTCTC CACACTACTG TGGCCTGACA600
ACAGAACTGA GAGGAGAGGA TTAGACTCTG GGGTGCTTGC ATGGGCAACT GGATTTTTC660
ATGATTCTCTT TATGATTTTG CTTTTAATGT ATACACCCAG AAGAGCCAAT ATAAACGTTC720
CTCATGCCTA AAAAAAAAAA A

```

741

## (2) INFORMATION ON SEQ ID NO. 561:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 470 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

004227" 5622960

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

TDQPNIQSVK IHSPLRNPN KGCECPRRD GFGFIKCVDR DVRMFFHFSE ILDGNQLHIA 60  
 DEVEFTVVPD MLSAQRNHAI RIKKLPGKTV SFHSHSDHRF LGTVEKEATF SNPKTTSPPNK120  
 GKEKEAEDGI IAYDDCGVKL TIAFAQKDVE GSTSPQIGDK VEFSISDKQR PGQQVATCVR180  
 LLGRNSNSKR LLGYVATLKD NFGFIETANH DKEIFFHYSE FSGDVSLEL GDMVEYSLSK240  
 GKGNKVSARE VNKTHSVNGI TEEADPTIYS GKVIRPLRSV DPTQTEYQGM IEIVEEGDMK300  
 GEVYPFGIVG MANKGDCLQK GESVKFQLCV LGQNAQTMAY NITPLRRATV ECVKDQFGFI360  
 NYEVGDSKKL FFHVKEVDG IELQAGDEVE FSVILNQRTG KCSACNVWRV CEGPKAVAAP420  
 RPDRLVNRLK NITLDDASAP RLMVLRQPRG PDNSMGFGAE RKIRQAGVID 470

(2) INFORMATION ON SEQ ID NO. 562:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 126 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

LNAILNFFHM EKELLAISYF IVNEAKLIFH TFHCGPAQGC DVVSHSLCIL AQDTQLELDA 60  
 LPFLQAIPFV GHPNDKAWID LTFHIALLN LNHSVLVSLC WINTPQGANY FARVNGGISF120  
 LSNAIH 126

(2) INFORMATION ON SEQ ID NO. 563:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 85 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

KSHTSCNLLS RPLFVTNTKF NLISYLRRSR SFHILGLKSN SQFHPTVIIS NNAILSLLLF60  
 AFIWASGFRI GKSGFFFYRA QKTVI 85

004227 562 492



## (2) INFORMATION ON SEQ ID NO. 564:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 549 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

LYPNFLVNEL ILKQKQRFEE KRFKLDHSVS STNGHRWQIF QDWLGTDDQN LDLANVNLML 60  
 ELLVQKKKQL EAESHAAQLQ ILMEFLKVAR RNKREQLEQI QKELSVLEED IKRVEEMSG120  
 YSPVSEDSTV PQFEAPSPSH SSIIDSTEYS QPPGFGSSQ TKKQPWYNST LASRRKRLTA180  
 HFEDLEQCYF STRMSRISDD SRTASQLDEF QECLSKFTRY NSVRPLATLS YASDLYNGSS240  
 IVSSIEFDRD CDYFAIAGVT KIKVYDYDT VIQDAVDIHY PENEMTCNSK ISCISWSSYH300  
 KNLLASSDYE GTVILWDGFT GQRSKVYQEH EKRCWSVDFN LMDPKLLASG SDDAKVKLWS360  
 TNLDNSVASI EAKANVCCVK FSPSSRYHLA FGCADHCVHY YDLRNTKQPI MVFKGHRKAV420  
 SYAKFVSGEE IVSASTDSQL KLWNVGKPYC LRSFKGHINE KNFVGLASNG DYIACGSENN480  
 SLYLYYKGLS KTLTTFKFDV VKSVLDKDRK EDDTNEFVSA VCWRALPDGE SNVLIAANSQ540  
 GTIKVLELV 549

## (2) INFORMATION ON SEQ ID NO. 565:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 132 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

TLYFVYIDMC NSQRGWEIRT LQIIHCYIIV HICYFVTFVF SEVFFFFFFF FFCGSINFYC 60  
 FVIYFYSKEF VLSLQKLDNT TKSSNVHGVT LMVESWLGIP NVPKVIKEGK EKKKKIFKTN120  
 PKPMMTLGRD IT 132

## (2) INFORMATION ON SEQ ID NO. 566:

## (i) SEQUENCE CHARACTERISTIC:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

(2) INFORMATION ON SEQ ID NO. 567:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

SANHKLEVNG	TDGLAPVEVE	ELLRQASERN	SKSPTEYHEP	VYANPFYRPT	TPQRETVT	PG 60
PNFQERIKIK	TNGLGIGVNE	SIHNMGNLS	EERGNNFNHI	SPIPPVPHPR	SVIQQAEKL	120
HTPQKRIMTP	WEESNVMDQK	DAPSPKRLS	PRETIFGKSE	HQNSSPTCQE	DEEDVRYNIV	180
HSLPPDINDT	EPVTMIFMGY	QQAEDSEEDK	KFLTGYDGGI	HAELVVIDDE	EEEEDEGEAEK	240
PSYHIAPHS	QVYQPAKPTP	LPRKRSEASP	HENTNHKSPH	KNSISLKEQE	ESLGSPVHHS	300
PEDAQTGDG	TEDPSLTALR	MRMAKLGGKV	I			331

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

LSLTSMEEA ELVKGRQLQAI TDKRKIQEEI SQKRLKIEED KLKHQHLKKK ALREKWLLDG 60  
ISSGKEQEEM KKQNQQDQHQ IQVLEQSILR LEKEIQDLEK AELQISTKEE AILKKLKSIE120  
RTTEDIIIRSV KVEREERAEE SIEDIYANIP DLPKSYIPSR LRKEINEEKE DDEQNRKALY180  
AMEIKVEKDL KTGESTVLSS NTSGHQMTLK GTGVKV 216

(2) INFORMATION ON SEQ ID NO. 569:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 132 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

LEKLHICFPQ LFGNFSQIMT TTYSHGLIWY TVMIIFWTSE KINKISRREI CKCFLVSSSK 60  
DVYIGGTTLR SPFFPALPFS SLKLLRMDPQ SHLQLSEHQM GNGGQGCLSF LLALSEIWNF120  
CGGIYDLCFH ED 132

(2) INFORMATION ON SEQ ID NO. 570:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 199 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

NEVTPWSFEWW WTKLTFFFPL ALKKSSRVSS SHLPRIYQAF LMSATFNEDV QALKELILHN 60  
PVTLLKQESQ LPGPDQLQQF QVVCETEEDK FLLLYALLKL SLIRGKSLLF VNTLERSYRL120  
RLFLEQFSIP TCVLNGELPL RSRCHIISQF NQGFYDCVIA TDAEVLGAPR QRAMRPRRA180  
KTGTMASRFL ERTVVALGH 199

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 571:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 195 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

QVRRAALLSS AMEDSEALGF EHMGLDPRLL QAVTDLGWSR PTLIQEKAIP LALEGKDLLA 60  
 RARTGSGKTA AYAIPMLQLL LHRKATGPVV EQAVRGLVLV PTKELARQAQ SMIQQLATYC120  
 ARDVRVANVS AAEDSVSQRA VLMEKPDVVV GTPSRILSHL QQDSLKLKRD LELLVVDEAD180  
 LLFSFGFEEE LKSL 195

## (2) INFORMATION ON SEQ ID NO. 572:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

DIGHSDIPST VGSQLLNHGL CLPCQLLGRN KNKASHCLFY HRTCRLPMEQ QLQHRNSISG60  
 RLPGARAGPS QEVLPF 76

## (2) INFORMATION ON SEQ ID NO. 573:

- (i) SEQUENCE CHARACTERISTIC:

00673395-122700



LIRCLRLESH HVMERKLSTS FLRLPATQLL IHIWSEPWYP STIHARKLDV YSLPFFPLFG60  
DELLSSAEDG VLVCPMATKI 80

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

LLPLLLLLLIH GDTPXGPGPX XQEQAQNHRH GLEEXRISXK SCMGXVDWNG PEGVEIYVDG 60  
 KEPHNKSQSS QLGFKTNGHX KSSEXVXHDV LDNRKEAGVK VKEGHEHQNQ QDPASELHVL120  
 FGGALTHGGD ARKHALPFT GFSRSTOOPP PRARELPCLR T 161

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 160 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

QTDNLSEKQP XGKXVCRGCP QGECSWERAV LLXPGRPALS XTLLXKXAPC EVNVVXVRGS 60  
XXCXGAPAXT PXPXQKXAAS AXAGLEXSXA XAGXAGCCCX GLPXVWSXLA LPTASLEASX120  
XPRPAASPRP SCPSTLPOAT KTPRVLPNKX XLGTXSXLIF 160

## (2) INFORMATION ON SEQ ID NO. 579:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 437 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

SQGVLSDDGV WRVKSIPNGK GSSPLPTATT PKPLIPTEAS IRVWGTSGTS HLHPRSICMI 60  
 QKYNHDGEAG RLEAFSQGES VLKEPKYQEE LEDRLHIFYE ECDYLQGFQI LCDLHDGFSG120  
 VGAKAAELLQ DEYSGRGIIT WGLLPGPYHR GEAQRNIYRL LNTAFGLVHL TAHSSLVCPL180  
 SLGGSLGLRP EPPVSFPYLH YDALTLPFHCS AILATALDTV TVPYRLCSSP VSMVHLADML240  
 SFCGKKVVTG GAIIPFP LAP GQSLPDSLMLQ FGGATPWTPL SACGEPGTR CFAQSVVLRG300  
 YRQSMPHKPQ NQRDTSTLCP SCMYHWGRNL GSVFTTAAAW SHEFFPSAAD SLQGGSSLPP360  
 PLLKLQSTGY GSGWFPQGSR SSVSLSLPQQ WRASQCLGHC VPLRPCTR PW KPWPETSPNS420  
 TCGAGPASWM LEWSTMT 437

## (2) INFORMATION ON SEQ ID NO. 580:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 277 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

TERLLLDGPP PHSPETPQFP PTTGAVLYTV KRNVGPEVR SCPKASPRLO KEREQKAVS 60  
 ESEALMLVWD ASETKLPQT VEPPASFLSP VSSKTRDAGR RHVSGKPDQ ERWLPSSRAR120  
 VKTRDRTCPV HESPSGIDTS ETSPKAPRG LAKDSGTQAK GPEGEQQPKA AEATVCANNS180  
 KVSSTGEKVV LWTREADRVI LTMCEQGAQ PQT FNIIISQQ LGNKTPAEVS HRFRELMQLF240  
 HTACEASSED EDDATSTNSA DQLSDHGDLL SEEELDE 277

## (2) INFORMATION ON SEQ ID NO. 581:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 172 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

FPESHSSSSSS SDRRSPWSDS WSALLVLVAS SSSSELASQA VWKSCMSSRK RWETSAGVLF 60  
 PSCWEMMLKV CGCAPCSWHM VRITRSASLV HRTTFSPVEL TLLLLAHTVA SAAFGCCSPS120  
 GPLACVPLSL AKPPLGALGE VSEVSIPDGD SWTGHVLSLV FTLALLEGSH LS 172

(2) INFORMATION ON SEQ ID NO. 582:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 549 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

EFPPGLTEPT AVRALARARR TRAGSASDPE RSPGAMALSE LALVRWLQES RRSRKLILFI 60  
 VFLALLLDNM LLTVVVPPIIP SYLYSIKHEK NATEIQTARP VHTASISDSF QSIFSYYDNS120  
 TMVTGNATRD LTLHQATATQH MVTNASAVPS DCPSEDKDLL NENVQVGLLF ASKATVQLIT180  
 NPFIGLLTNR IGYPIPIFAG FCIMFVSTIM FAFSSSYAFL LIARSLQGIG SSCSSVAGMG240  
 MLASVYTDDE ERGNVMGIAL GGLAMGVLVG PPFGSVLYEF VGKTAPFLVL AALVLLDGAI300  
 QLFVLQPSRV QPESQKGTPL TTLLKDPYIL IAAGSISFAN MGIAMLEPAL PIWMMETMCS360  
 RKWQLGVAFL PASISYLIGT NIFGILAHKM GRWLCALLGM IIVGVLSILCI PFPKNIYGLI420  
 APNFGVGFAN GMVDSSMMPI MGYLVDLRHV SVYGSVYAI DVAFCMGYAI GPSAGGAIK480  
 AIGFPWLMTI IGIIDILFAP LCFFLRSPPA KEEKMAILMD HNCPIKTKMY TQNNIQSYPI540  
 GEDEESED 549

(2) INFORMATION ON SEQ ID NO. 583:

- (i) SEQUENCE CHARACTERISTIC:



- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

YLLSHWNQYF WDTCTQNGEV ALCSSGNDNC WSQHFMYSIS KKHLWTHSSE LWSWFCKWNG 60  
GFVNDAYHGL PRRPAARVRL WECVRHCGCG ILYGVCYRSF CWWCYCKGNW ISMAHDNYWD120  
N 121

(i) SEQUENCE CHARACTERISTIC:

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

DGGSVHWPGR LDFCSILLML NAVQITWDDG DHDSEQHVVO QQRQEHDEQD ELPRAAALLQ 60  
PADQRQLAQG HGSGAPLGVA CAACPGPPCP RQRPHRSGLR QSGREF 106

(i) SEQUENCE CHARACTERISTIC:

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

KSRLSVTLMP	VQLSEHPewn	ESMHSLRISV	GGLPVLASMT	KAADPRFRPR	WKVILTFffVG	60
AAILWLLCSH	RPAPGRPPTH	NAHNWRLGQA	PANWYNDTYP	LSPPQRTPag	TRYRIAVIAD120	
LDTEPTAQDE	NTWRSDLKKG	YLTLSDSGDK	VAVEWDKDHG	VLESHLAEKG	RGMELSDLIV180	
FNGKLYSDDE	RTGVVYQIEG	SKAVPWVILS	DGDGTVEKGF	KAEWLAVKDE	RLYVGGLGKE240	
WTTTIGDvVN	ENPEWVKVG	YKGSVDHENW	VSNYNLALRA	AGIQPPANLI	HESACWSDTL300	
QRWFFLPrrA	SQERYSEKDD	ERKGANLLLS	ASPDGFDIAV	SHVGAVVPTH	GFSSFKFIPN360	
TDDQIIIVALK	SEEDSGRVAS	YIMAFtLDGR	FLLPETKIGS	VKYEGIEFI		409

(A) LENGTH: 249 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

KLSPDGLAQ	FRFELNELDA	FVFHASDLGL	RQQEAPVQRE	GHDVGGDSAA	VLLGFEGHND	60
LUVGVGDELE	GREAVSGDHR	PDVAHSDVAE	VRGGAQQQVG	ALALVLLAV	ALLAGAARQE	120
EPALQRVTPA	GRLMDEVSWR	LDAGSSPQGV	VVGHPVLVVH	AALVAHLLHP	LRVLVHHITR	180
SGRPLLAQAA	HVQTLVLHCQ	PFGLEAFLHG	AVAVGNQHPG	HGFAAFDLVD	DRPVIHGEV2	240
FIENNVQVG						

(A) LENGTH: 157 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

LEFFIPCLGS VNEACLFPGV SFHGLYFSSS SGSFAGSSLW KLHERWLGLG FAGVYSRVKA 60  
EWDLRPRLGT TQAEKGRFHH SQCPPHSNYL TPTPTLTPTP PRDRQGCHGG PEGAGSGCPC120  
AGPSOTSPPL KLKHSCEEGS EEGPLSHGCL FPPLCHR 157

## (2) INFORMATION ON SEQ ID NO. 588:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

NTMAVAAVKW VMSKRTILKH LFPVQNGALY CVCHKSTYSP LPDDYNCNVE LALTS DGRTI 60  
 VCYHPSVDIP YEHTKPIPRP DPVHNNEETH DQVLKTRLEE KVEHLEEGPM IEQLSKMFFT120  
 TKHRWYPHGR YHRCRKNLNP PKDR 144

## (2) INFORMATION ON SEQ ID NO. 589:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes.

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

IRQTAFSQMA NEAHFSLIPP GTSASSVFWR IQILTTSVIP SMRIPTVLSS KEHFAKLFYH 60  
 RSFLKVENFF FQSGFQHLIM CFFIIMHRIW PRDRFCVFIW NVHRRVVAYY CPAIRSQSKL120  
 YVAIIIVW 128

## (2) INFORMATION ON SEQ ID NO. 590:

- (i) SEQUENCE CHARACTERISTIC:

004221 588 12200



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

## (2) INFORMATION ON SEQ ID NO. 593:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

## (2) INFORMATION ON SEQ ID NO. 594:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

TPALRARS LR DRCARAPCPH GGQQRRRRL NAEGAEGARG GGSSYSEMAE TVADTRRLIT 60  
 KPQNLNDAYG PPSNFLEIDV SNPQTVGVGR GRFTTYEIRV KTNLPFIKFK ESTVRRRYSD120  
 FEWLRSELER ESKVVVPPLP GKAFRLQFLL EEMMEYLMTI LLRKENKGWS SL 172

## (2) INFORMATION ON SEQ ID NO. 595:

004227 006739 00700

- SAAGCQPRSP PFCSCCRRR GLPPPPPSA AAAGAAARRG DTGLARSGRE ENEHVERAFT 60  
PHAKLLPAPL KLPPPPSPGEK RLTSWNATPG SREARPLGR GTADWGVRRS GVMGLGVANR120  
FRPDYSA 127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

[illegible]

```
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

(2) INFORMATION ON SEQ ID NO. 598:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

KGWRSDFTVG GRQRDQHVQ TGSFFSISLL SKSRTAQWLC QGGSSSYSHF SGSLKSTRYY60  
RGSRS 65

(2) INFORMATION ON SEQ ID NO. 599:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 63 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

AEDTIQKRNS QFETVTPPAP NCGDEERKQW LWFLSEGRRL TERSNHQGHR FWKSSRGGWL60  
EEQ 63

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

KLNFNTMRCC	HICKLPGRVM	GIRVLRLSLV	VILVLLLVAG	ALTALLPSVK	EDKMLMLRRE	60
IKSQGKSTMD	SFTLLIMQTYN	RTDLLLLKLN	HYQAVPNLHK	VIVVWNNIGE	KAPDELWNSL	120
GHPIPIVIFK	QQTANRMRNR	LQVFPELETN	AVLMVDDDTL	ISTPDLVFAF	SVWQQFPDQI	180
VGFVPRKHVS	TSSGIYSYGS	FEMQAPGSGN	GDQYSMVLIG	ASFFNSKYLE	LFQRQPAAVH	240
ALDDTQNCDD	DIAMNFIIAK	HIGKTSGIFV	KPVNMDNLEK	ETNSGYSGMW	HRAEHALQRS	300
YCINKLVNIY	DSMPLRYSNI	MISQGFPPYA	NYKRKI			336

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes.

- (vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

```

HALKILQHYD  FVPWFSICQL  QKKNIKVKQT  KTNLKTAWHL  SSFSMLCIFL  SNIMNFIYSR  60
SLYNRKKS AV  LLGYKIHITF  ESQEVGLIQL  GLLMKS FHPG  I                               101

```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids  
(B) TYPE: Protein



(vi) ORIGIN  
(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

PLSFLMYKTL LSGLEFEHLW XFIYFAXVCG QSNIFPKYIL PRKXKKQIRX FDXKXNRPKK 60  
 GAXTWSRAWX RGKAXRGQVC CGQICAYFIT GVKXKQXSID VXRIYTVXRN XRXFXKNNRN120  
 ) TXWXXFYHXX YTFSLWXNXL TKLXFKIKLM 150

## (2) INFORMATION ON SEQ ID NO. 605:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 108 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

LDFKXQFCES IXPQAKCVXX MIKXXPXXIP VFLKXVPXIS XHCIYPXDIN XTLSFSFYSSN 60  
 KVGTDLSTTN LPSXCLASXP CSAPGXXPLX XPVXFVKXP NLLAFSW 108

## (2) INFORMATION ON SEQ ID NO. 606:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 203 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

GPSALVHSVR PDLCSNPLSC GSLACMAYTG ELGLWAVQTQ GSHFAFPLLS PFSILALRQN 60  
 FSQRRTLCCP RSAVILPFLP SFHPSSAQMK SSRNSSFLPL WDSETGNLQG GVFPSPFLFLF120  
 STPRGTAAV PTSGTELHTI VGKLQGPLLL VLRAHLCYWS FWQKRKMIEP RVAPECSSLT180  
 VEGPKLVFRA HPRREVIRCH AFC 203

09673995-12700

## (2) INFORMATION ON SEQ ID NO. 607:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 154 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

EVROKEWCLL WSFPFPGAGL CAKLGPQHIW STLLVGARPE HLTQPVHTAP RVPPLSQAGP 60  
TAPGSADKGM ACPLRCQNSI QKAPPQVDVV PGAGEESGTT TLAVNLSNRG LGFLVAASCP120  
GLEVHRSRGV PLGTDMPHW GCNGEKSGKL GAQL 154

## (2) INFORMATION ON SEQ ID NO. 608:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 123 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

CGVLSLRWVQ QPWFLWGLRI RIVGREKLLL EDFLSQSPRE VERRNFCWTS SGQRKDGMMKV 60  
EKAELQLSGD NKEFFSGKSF VLEQGWKMG TKEKQSVTLG FGQPRGPAPQ YKPYRPGTHR120  
RVD 123

## (2) INFORMATION ON SEQ ID NO. 609:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 88 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

00422T"56224960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

88

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

80

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

71

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 395 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

APMRPERPRP RGSAPGPMET PPWDPARNDS LPPTLTPAVP PYVKLGTLTVV YTVFYALLFV 60  
 FIYVQLWLVL RYRHKRLSYQ SVFLFLCLFW ASLRTVLFSE YFKDFVAANS LSPFVFWLLY120  
 CFPVCLQFFT LTLMNLYFTQ VIFKAKSKYS PELLKYRLPL YLASLFISLV FLLVNLTCAV180  
 LVKTGNWERK VIVSVRVAIN DTLFVLCVAVS LSICLYKISK MSLANIYLES KGSSVCQVTA240  
 IGVTVILLYT SRACYNLFIL SFSQNKSVHS FDYDWNVSD QADLKNQLGD AGYVLFQVVL300  
 FVWELLPTTL VVYFFVRNP TKDLTNPGMV PSHGFSRPSY FFDNPRRYDS DDDLAWNIAP360  
 QGLQGGFAPD YYDWGQQTNS FLAQAGTLQR LNFGS 395

(2) INFORMATION ON SEQ ID NO. 613:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 213 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

ARCAETPAGA AAHVSPDEAR ASPAARQRPR PDGDPVAVGPS PQLAALAHAD PGRAPLREAW 60  
 PHRRHLRVLRL AALRVHLRAA LAGAALPPQA AQLPERLPLS LPLLGLPADR PLLLLLQRLR120  
 GGQFAQPLRL LAALLLPCVP AVFHPHADEL VLHAGDFQSQ VKIFSRTITQI PVAPLPLGLPL180  
 HQPCFPVGEF NLCCAGKDGK LGEEGYRLCA SGH 213

(2) INFORMATION ON SEQ ID NO. 614:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

004227 5627950

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

LGFEHNLREV QVHQREGEKL QAHREAVEQP EDEGAERIGR HEVFEVEGEE DGPQGGPEEA 60  
EKEEDALVAE PLVAVTQHQP ELHVDEHEEQ RVEHGVDDGE AKLHVGGHGR GQRGRQRVVA120  
GWVPRRGLHR AGGAAARP GT LGPHRGSRPP PPRGSPRIA P 161

(2) INFORMATION ON SEQ ID NO. 615:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 102 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

HKKTSSYSGV TVCSYDSIIR LKAGEICVQF NRTQLKGRQV GWERKLLSGG IRGNQSKTKF 60  
YCLQFNSIIA IMCSGKHIPV LLDRVSFPFS GTKMVEGIIN PT 102

(2) INFORMATION ON SEQ ID NO. 616:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 86 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

VTCLSLYVET NFTMITDLN ISSLNHFTIL KCLLENLHLF VPRCSSSIKP WAYFSVLLRP60  
NEVGRGGQFC INIRYFVIHS PNLKLY 86

09673305-122700

## (2) INFORMATION ON SEQ ID NO. 617:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

RMLIQNCPPR PTKFGLRRTL KYAHGFIDEE HLGTKRCKFS SRHFKIVWKF KLEMLHRSVI60  
 MVKLVSTYKD KQVTHW 76

## (2) INFORMATION ON SEQ ID NO. 618:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 378 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

SRCRFCCRLS AAFLPRAMLG LAIVLAGRLN EGDREFLKPPI SLRNFSFWSS FSKPAVSHWP 60  
 NWVPVHFLVS EASVLPDSRS ISSCKAFRLT WSMCASSMLP FFSNTTSKSV SVSSLQGSPA120  
 TPLSFLFFLV FLFRAGSSMT GCSTFFLDFI FFFAEDLGSS LMGMYSGAST LTGFFLLPFL180  
 GLLSMDLEGL EWPGRASPSW WIFFFFFFTFP LCSLGLFRLP FLXPRLPVPH PSSPLXQVSP240  
 TSLASLASQN QGSWTEKAXG VLGPPFFPSC XFLSFLPTLV SSSPCLXVLG RFSPQRHGTW300  
 LEVTSXFFFS PLRNSKWPNT CFLRLGDFSV RLAGSVVSGS TCSSQRVLTP FFFFFFFFTR360  
 GISGACPWAT LLXGGCSS 378

## (2) INFORMATION ON SEQ ID NO. 619:

- (i) SEQUENCE CHARACTERISTIC:

09673395-12700

- (A) LENGTH: 269 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

```
GTGSLGXRNG XRKSPREHNG KVKKKKKIHQ EGDALPGHSK PSRSMESSPR KGSKKKPKVKV 60
EAPYIPIISD DPKSSAKKKM KSKKKVEQPV IEEPALKRKT RKKRKESGVA GDPWREETDT120
DLEVVLEKKG NMDEAHIDQV RRKALQEEID RESGKTEASE TRKWTGTQFG QWDTAGFENE180
DQKLKFLRLM GGFKNLSPSF SRPASTIARP NMGALGKKAAD SLQQNLQRDY DRAMSLEVQP240
GSRLAVFSTA PNKIFYIDRN ASKSVKLED                                269
```

(2) INFORMATION ON SEQ ID NO. 620:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 218 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

```
VRVCFLPPRV SCYPTLFPLL PRLPFQSWLL DDWLLYLLFG LHLFLCGGLR VITYGDVFRS 60
LNFDWLLFTS FPRAALHGPG GLGVAWEGIS LLVDFFFLLH LPIVFSGALP XSVSXPKAAC120
SSSFFPTXAS VPNIPLPGL TEPRVLDREG XWGPGXPFFS FLXFFELLAN SGFLLTLSXG180
XGEVFTPEAW DMARGDFLXF LFPTEELQVA KHLLEAG                                218
```

(2) INFORMATION ON SEQ ID NO. 621:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 389 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual

004227" 5555/1960



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNPGPPSSLR RAFRRRELPE 60  
 CACHEIGLGA EAGSGPPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120  
 PGVTEVTIIE KPPAERHMIS SWEQKNNVCM PEDVKNFYLM TNGFHMWTSV KLDEHIIPLG180  
 SMAINSISKL TQLTQSSMYS LPNAPTLADL EDDTHEASDD QPEKPHFDSR SVIFELDSCN240  
 GSGKVCLVYK SGKPALAEDT EIWFLDRALY WHFLTDFTTA YYRLLITHLG LPQWQYAFTS300  
 YGISPQAKQW FSMYKPITYN TNLLTEETDS FVNKLDPSKV FKSKNKIVIP KKKGPVQPAG360  
 GQKGPSGPGS PSTSSTSKSS SGSGNPTRK 389

(2) INFORMATION ON SEQ ID NO. 622:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 109 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

ARPAPAGREG RGEGEATSRR CGVGHRA GPR EPAPHGAAV RPTPGPHHC AALSGAENYR 60  
 SRHAMKLASA LRRGPALHPL PPRANRGREP WRRRHRPRGW AAASRTWRS 109

(2) INFORMATION ON SEQ ID NO. 623:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 96 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

00422T 56224960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

RSAGGFSSMMV TSVTPGEDSR MRVMPRVFS RCGLLQPSPG DDASSSMARD RDSRAAGAGG60  
GPD PASAPRP ISWHAGNGSS RRLKARRSDD GPGPLV 96

(2) INFORMATION ON SEQ ID NO. 624:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 218 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

CCTEHRWPAS MPPQLQETRM NRSIPVEVDE SEPYPSQLLK PIPEYSPEEE SEPPAPNIRN 60  
MAPNSLSAPT MLHNSSGDFS QAHSTLKLAN HQRPVSRQVT CLRTQVLEDS EDSFCRRHPPG120  
LGKAFPSGCS AVSEPASESV VGALPAEHQF SFMEKRNQWL VSQLSAASPD TGHDSKSDQ180  
SLPNASADSL GGSQEMVQRP QPXQEPSRPG SANHRHGI 218

(2) INFORMATION ON SEQ ID NO. 625:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 212 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

0042273395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

NLQITSGLYP GRSPACALKF WRTVKTVSAG DTQAWAKLSL LGALQSASLR LSLWLEPSLQ 60  
 SISFHLWKNV INGWYLSFQR LLLTLAMTQT NQTKVYLMPO QTPWAVARRW CNGPSLHRNR120  
 AGLDLPTIDT GYDSQPQDVL GIRQLERPLX LTSVCYPQDL PRPLRSREFF QFEPQRYPAC180  
 AQMLPPNLSP HAPWNYHYHC PGSPDHQVXI WP 212

## (2) INFORMATION ON SEQ ID NO. 630:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 184 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

FMINVSFFFF LAAGRKKEE MGCDGSKAGK VSHGPQTPFP PLSLSPLPKK KKKETFIMNQ 60  
 QGFSPYQREM WKELKKPPFV PNSTLPIFYA TQTLSEFWVPF LQMDLLRRII VFHVFSPOVT120  
 KINICIYNLY YCYIFVDNTE RWCWVIYYNL NLGISFGLPQ SLLRWGPWYG KTPRYNVTSP180  
 QPLY 184

## (2) INFORMATION ON SEQ ID NO. 631:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 138 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

GPWLTFPAFD PSHPISSSFP LPAAKKKKKE TFIMNQGGFS PYQREMWKEL KKPPFVPNST 60  
 LPIFYATQTL SFWVPFLQMD LLRRIIVFHV FSPQVTKINI CIYNLYYCYI FVDNTEFRWCW120  
 VIYYNLLNLGI SFGLPQSC 138

004221" 85554950

## (2) INFORMATION ON SEQ ID NO. 632:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

WVKGRKGKPW SSNPISSSFP LPAAKKKKKG NVYHESTGFQ SLSKRDVERA KETTLCSQLH60  
 FTHILCNTNT VLLGPFLTDG PLEKNYRIPR F 91

## (2) INFORMATION ON SEQ ID NO. 633:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

RNHAKIQLPM QAPQSLILSS QFCCQATVVW RLVGCCPCCN EWEEVDGMV ETFTSSSPAT 60  
 GIPPRPVLCC GGRFKSKLL FEVGFAVWEK XHDAIAXERP SKDSGLPGLE N 111

## (2) INFORMATION ON SEQ ID NO. 634:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

004227 5666960

(A) ORGANISM: HUMAN

LRRCNPVQRP TFPFAPHLFR TPLHTLQPPK VPGSGFLHPA AATNANSLNS TFSVLPQRF60  
QFQOHRVYN SFSFPGQAAAR YPWMAFPXQ 89

(D) TOPOLOGY: linear

(A) ORGANISM: HUMAN

FIQFSRPGSP LSLDGLSXAI ASCXLNHTAN PTSNSNFLDL NLPPQHNTGL GGIPVAGEEEE60  
VKVSTMPLST SSSLQOQGQQ PTLSHTTVA 89

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529 Rec'd PCT/PTC 17 OCT 2000  
PCT/DE99/01174

WO 99/54461

## Claims

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555 or a complementary or allelic variant thereof.

3. Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, characterized in that they are expressed elevated in uterus tumor tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

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7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

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16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. An antibody according to claim 20, wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. Seq. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

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004222T-56524950



26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 as tools for finding active ingredients against uterus tumors.

28. Use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 for expression of polypeptides that can be used as tools for finding active ingredients against the endometrial tumor.

29. Use of nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 as pharmaceutical agents in gene therapy for treatment of the endometrial tumor.

31. Use of polypeptide partial sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 for the production of a pharmaceutical agent for treatment of the endometrial tumor.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

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35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

## Systematic Gene Search in the Incyte LifeSeq Database

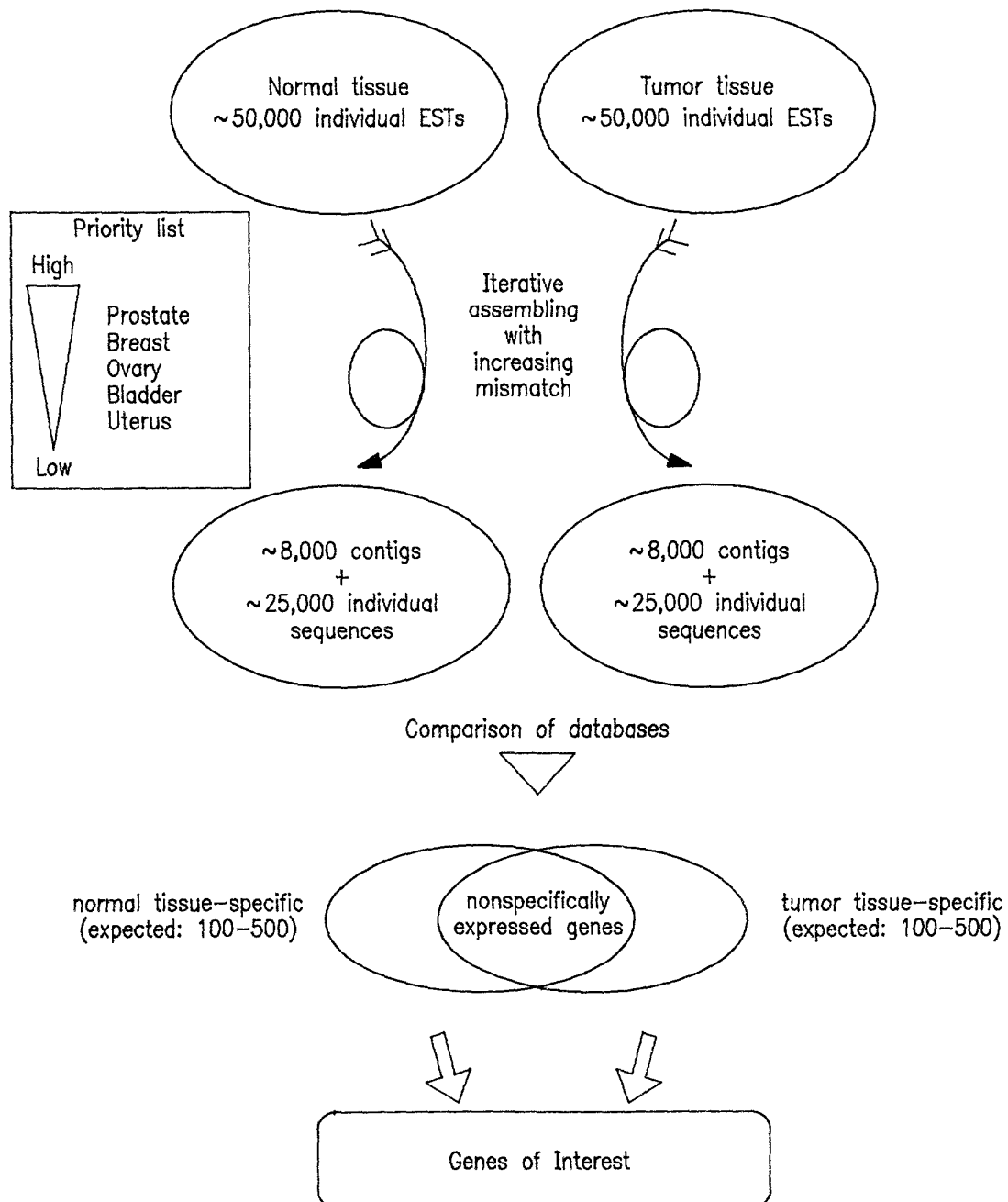


FIG. 1

## Principle of EST Assembly

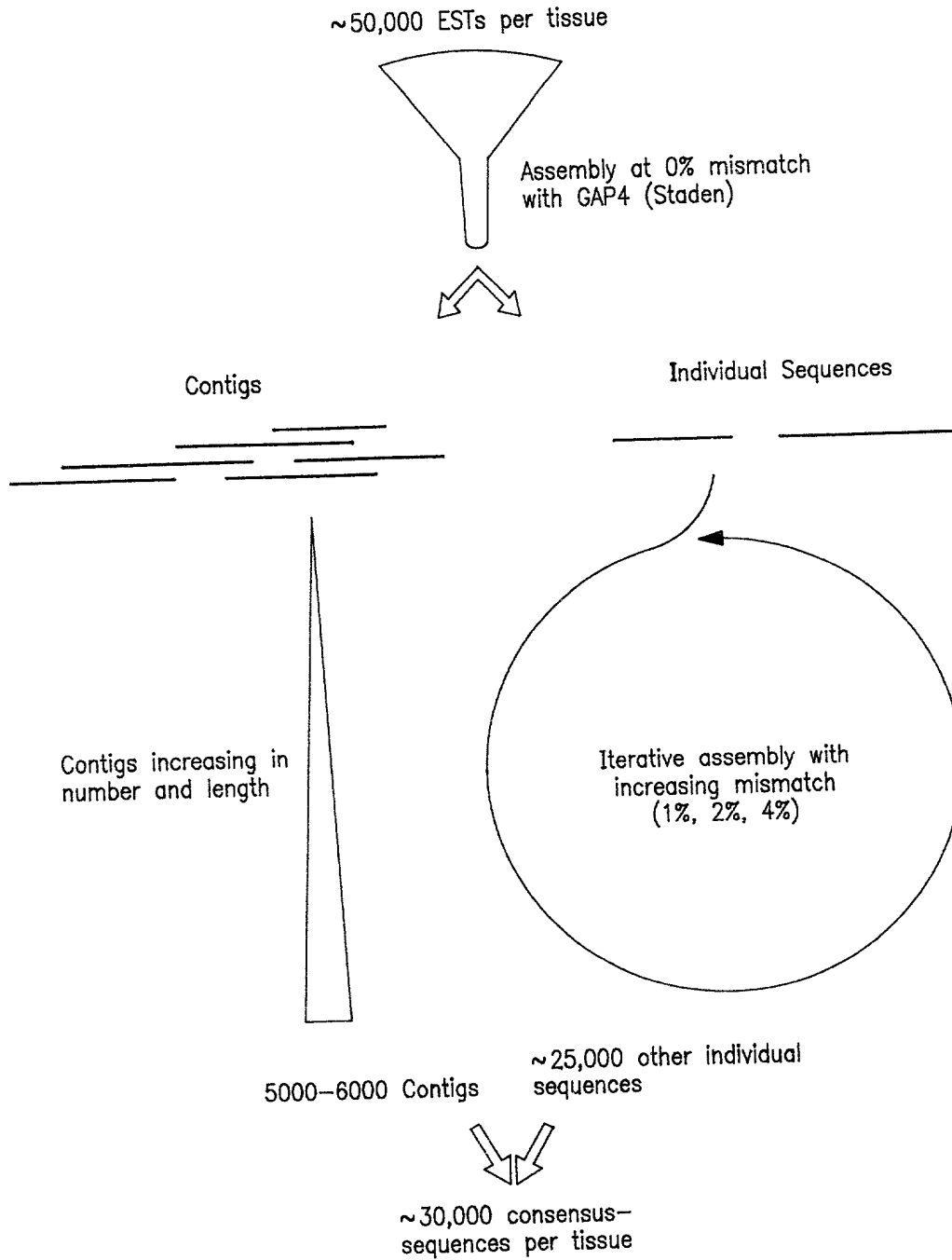


FIG. 2a

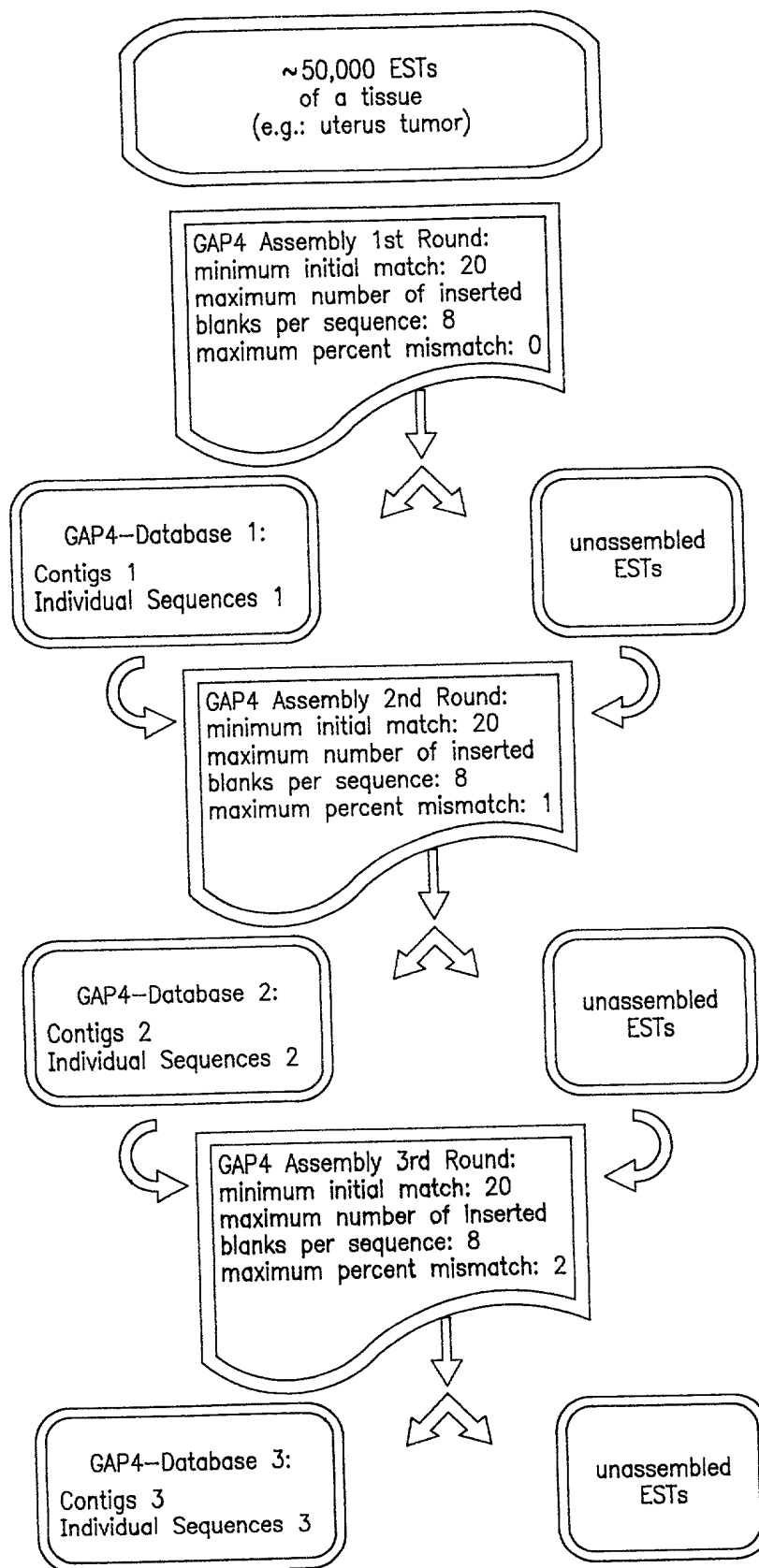


FIG. 2b-I

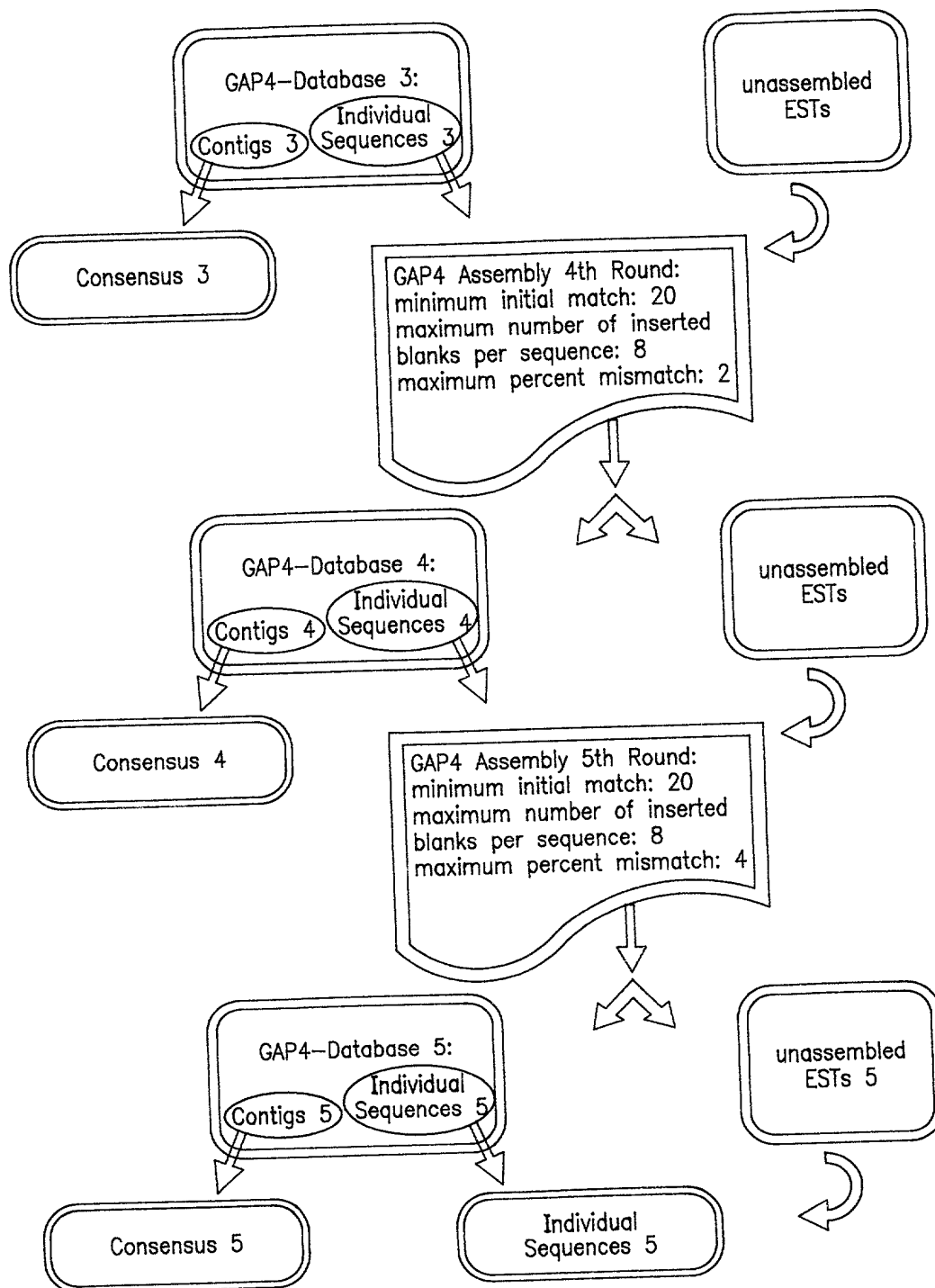


FIG. 2b-2

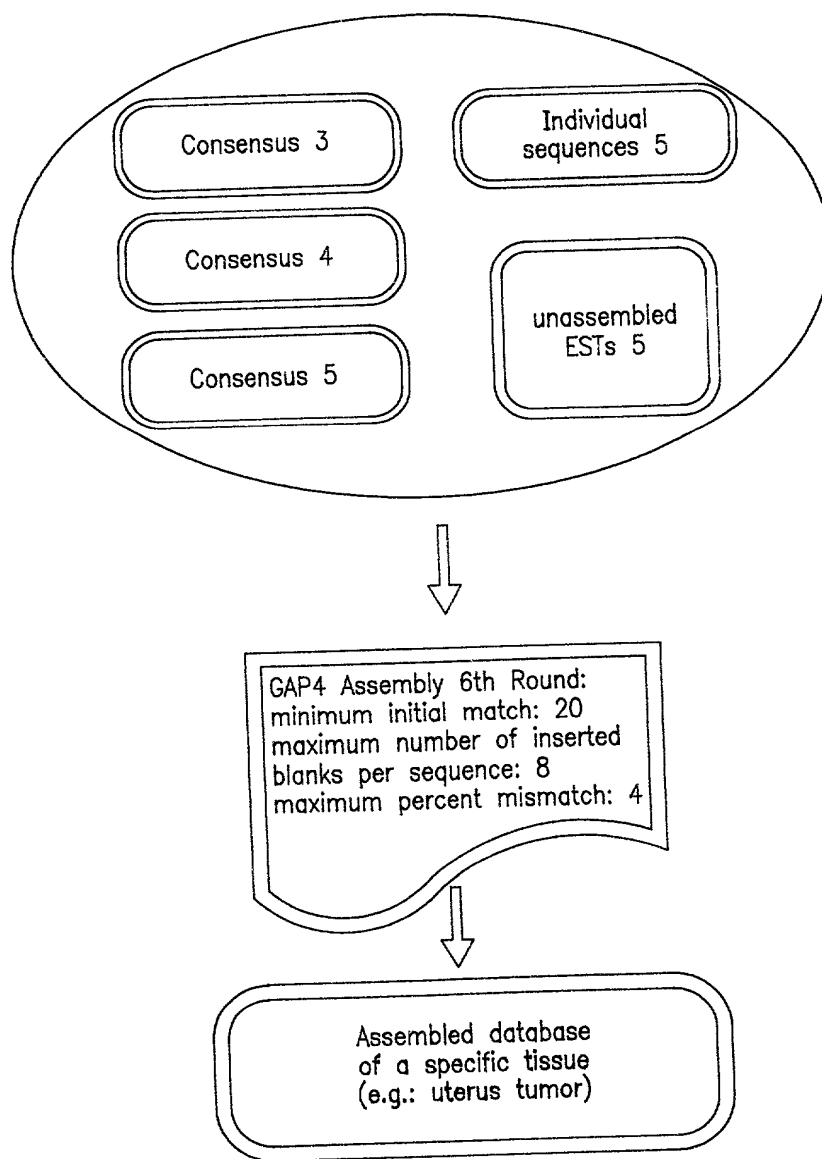


FIG. 2b-3

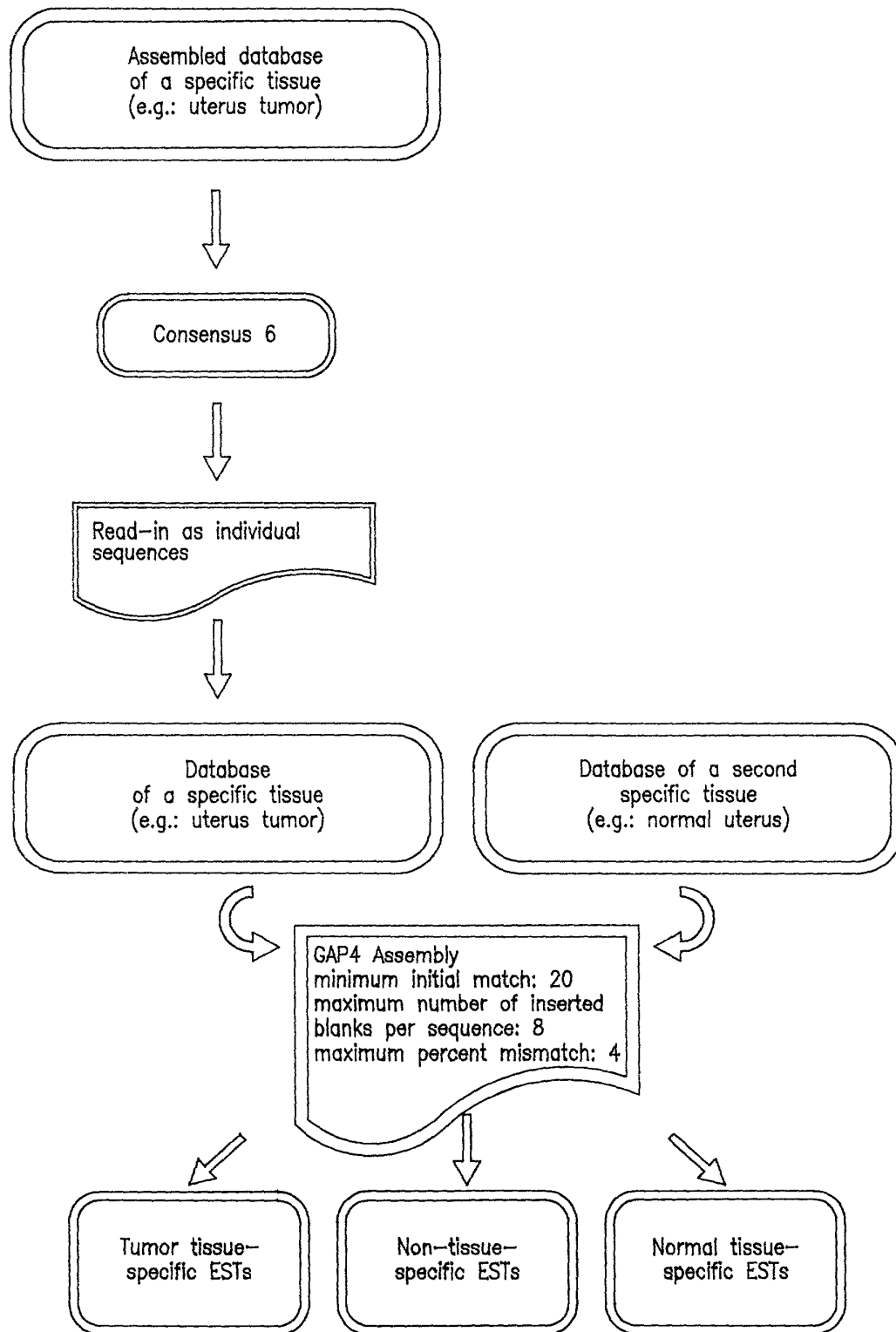


FIG. 2b-4



## In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

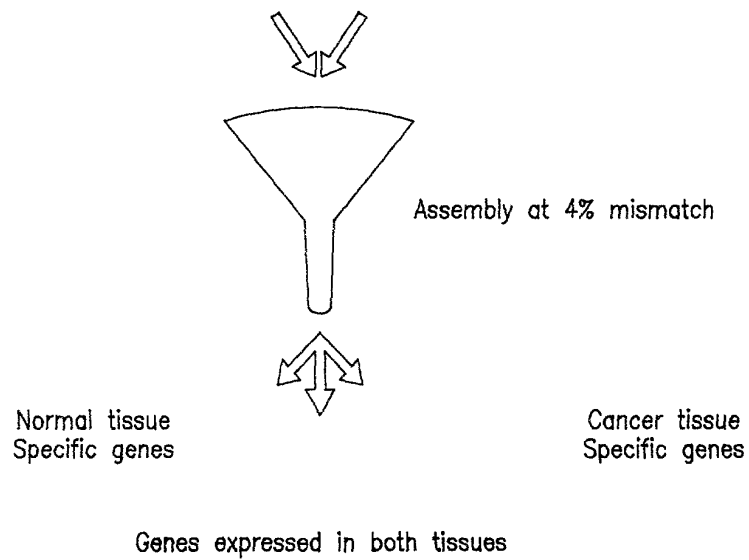


FIG. 3

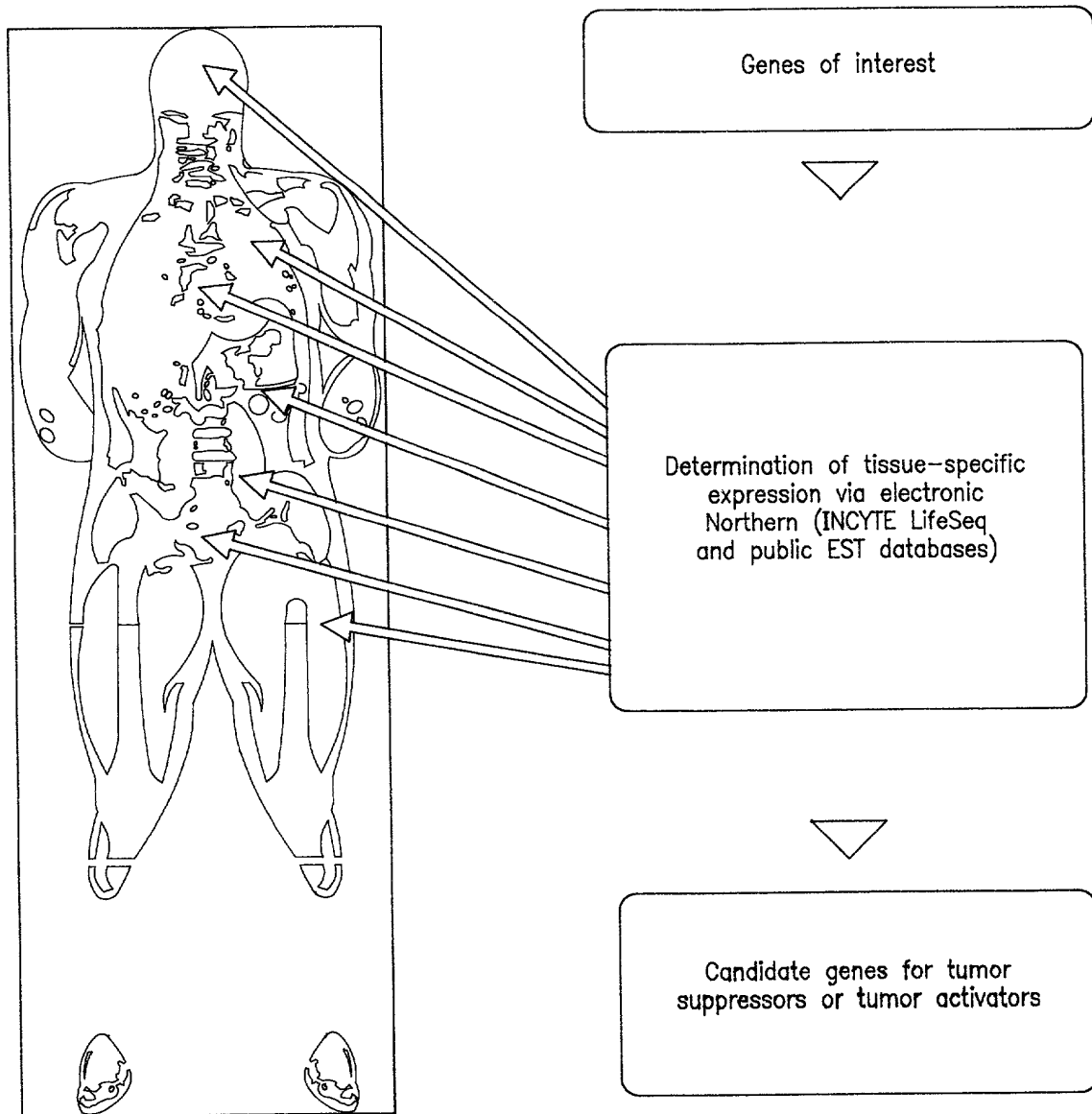


FIG. 4a

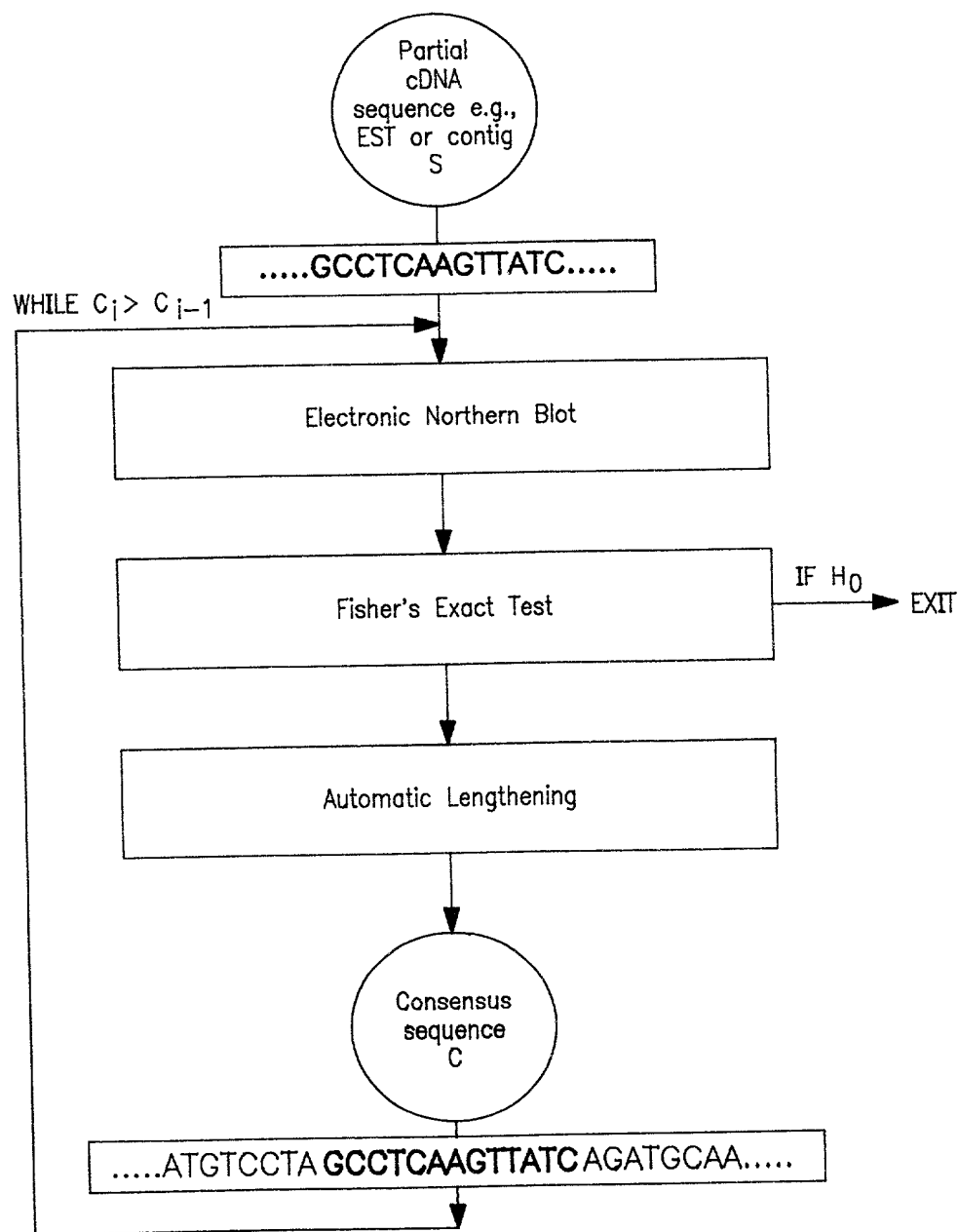


FIG. 4b

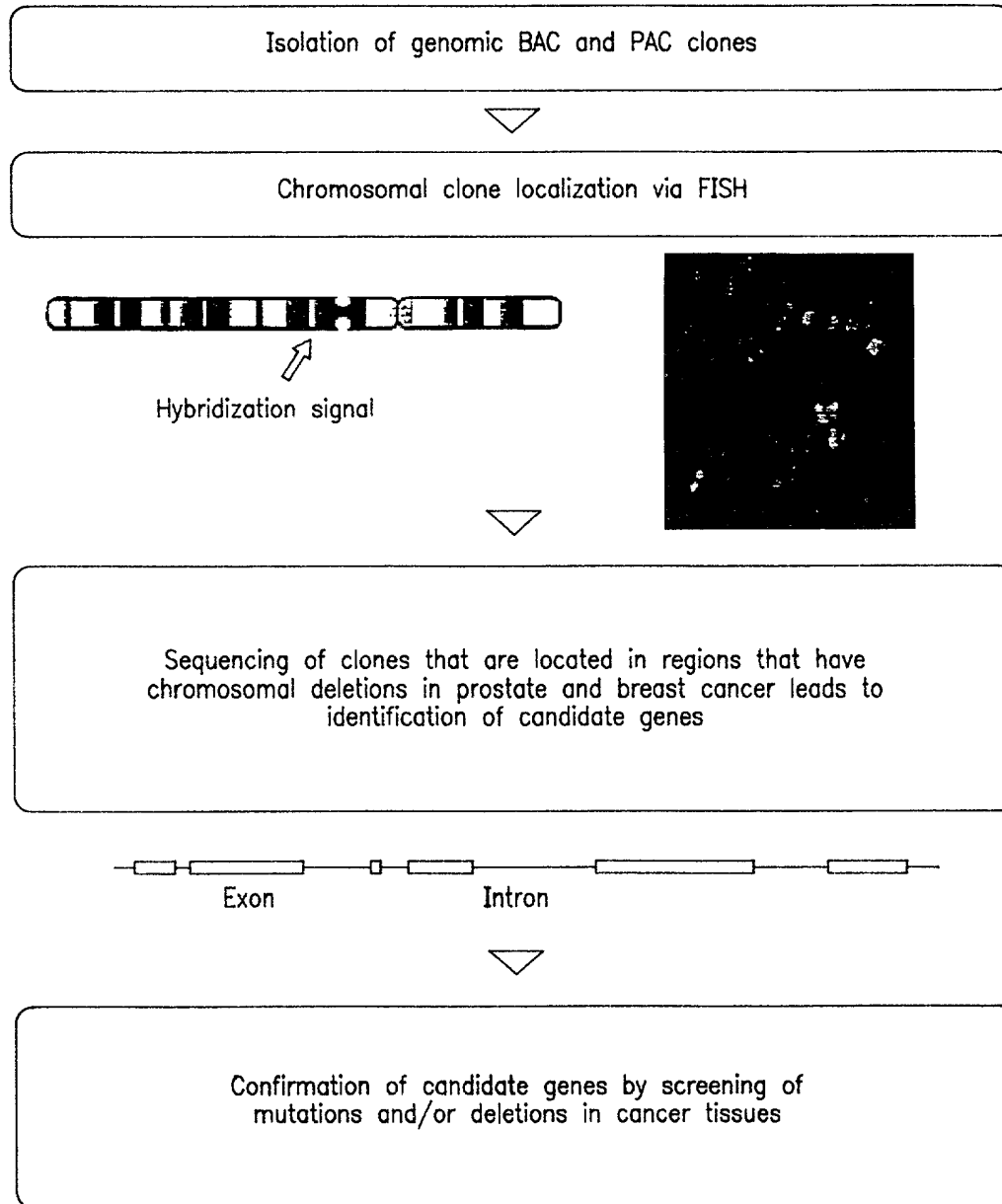


FIG. 5

Attorney Docket Number: SCH 1780**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN NUCLEIC ACID SEQUENCES OF ENDOMETRIUM TUMOR TISSUE**

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01174 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

**PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119**

APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 948.0	Germany	17 April 1998	X

by claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

**PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)**

APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

**PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120**

APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

Attorney Docket Number: SCH 1780**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN NUCLEIC ACID SEQUENCES OF ENDOMETRIUM TUMOR TISSUE**

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01174 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

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I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 948.0	Germany	17 April 1998	X

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

## Declaration for Patent Application (Continued)

Full Name of additional joint inventor (given name family name)

André ROSENTHAL

Signature

Date

Residence

Berlin, Germany

Citizenship

Germany

Post Office Address Kopenplatz 10 D-10115 Berlin, Germany

006227 8622/950

Declaration for Patent Application (Continued)

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FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name, family name)

1-00 **Thomas SPECHT**Signature *Thomas Specht* Date 17.10.00Residence Berlin, Germany *DEX* Citizenship Germany

Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

2-00 **Bernd HINZMANN**Signature *Bernd Hinzmann* Date 17.10.2000Residence Berlin, Germany *DEX* Citizenship Germany

Office Address Parkstrasse 19, D-13127 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

3-00 **Armin SCHMITT**

Signature \_\_\_\_\_ Date \_\_\_\_\_

Residence Berlin, Germany *DEX* Citizenship Germany

Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

4-00 **Stian PILARSKY**Signature *Stian Pilarsky* Date 17.10.00Residence Schönfeld-Weissig, Germany *DEX* Citizenship Germany

Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld-Weissig, Germany

Full Name of additional joint inventor (given name, family name)

5-00 **Edgar DAHL**Signature *Edgar Dahl* Date 17.10.2000Residence Potsdam, Germany *DEX* Citizenship Germany

Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany


☐ Additional joint inventors are named on separately numbered sheets attached hereto



Declaration for Patent Application (Continued)

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Arlington, VA 22201  
TEL (703) 243-6333  
FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name, family name)	
Thomas SPECHT	
Signature	Date
Residence	Citizenship
Berlin, Germany	Germany
Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany	
Full Name of additional joint inventor (given name, family name)	
Bernd HINZMANN	
Signature	Date
Residence	Citizenship
Berlin, Germany	Germany
Post Office Address Parkstrasse 19, D-13127 Berlin, Germany	
Full Name of additional joint inventor (given name, family name)	
Armin SCHMITT	
Signature 	Date October 18, 2000
Residence	Citizenship
Berlin, Germany DEX	Germany
Post Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany	
Full Name of additional joint inventor (given name, family name)	
Christian PILARSKY	
Signature	Date
Residence	Citizenship
Schönfeld-Weissig, Germany	Germany
Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld-Weissig, Germany	
Full Name of additional joint inventor (given name, family name)	
Edgar DAHL	
Signature	Date
Residence	Citizenship
Potsdam, Germany	Germany
Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany	

☒ Additional joint inventors are named on separately numbered sheets attached hereto

## Declaration for Patent Application (Continued)

Full Name of additional joint inventor (given name family name)

André ROSENTHAL

Signature

André Rosenthal

Date

17.10.2000

Residence

Berlin, Germany DEX

Citizenship

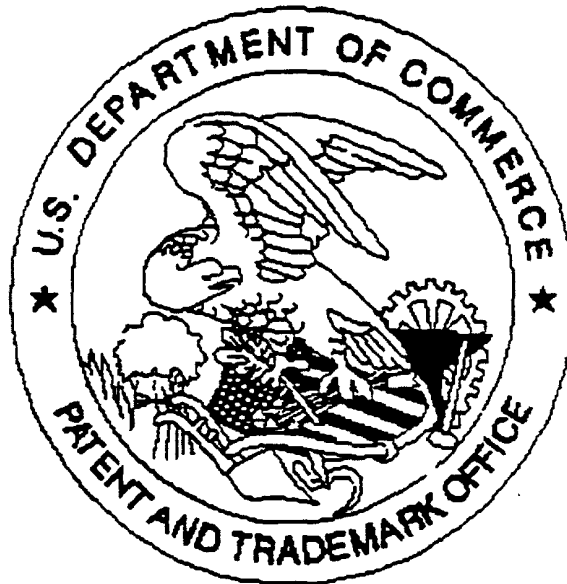
Germany

Post Office Address

Koppenplatz 10 D-10115 Berlin, Germany

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00673395 122700

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started on page 375.